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	PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4		
	PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25		
5	PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88		
	PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22		
	PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45		
10	PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1		
	PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44		
	PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84		
	PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85		
15	PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3		
	PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49		
	PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68		
	PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37		
20	PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
	PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
	PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
25	PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
	PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
	PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
	PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
30	PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
	PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
	PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
35	PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
	PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
	PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		
	PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
40	PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
	PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
	PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
45	PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
	PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
	PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
	PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
50	PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
	PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
	PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
	PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
55	PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		

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	PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
	PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
5	PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		
	PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
	PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
	PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
10	PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
	PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
	PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
15	PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
	PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
	PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
	PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
20	PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
	PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
	PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		
25	PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
	PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
	PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
	PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
30	PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
	PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
	PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
35	PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
	PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		
	PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
	PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
40	PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
	PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
	PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
	PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
45	PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
	PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
	PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
50	PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
	PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
	PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
	PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
55	PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+



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	PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
	PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
5	PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
	PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
	PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
	PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
10	PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
	PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
	PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
15	PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
	PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
	PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
	PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
20	PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
	PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
	PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
25	PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
	PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
	PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
	PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
30	PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
	PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
	PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
	PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
35	PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
	PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
	PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
40	PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
	PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
	PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
	PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
45	PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
	PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
	PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
50	PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
	PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
	PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
	PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		
55	PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46		

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	PLACE1005477	1.58	2.26	2.51	3	2.93	2.74		
	PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53		
5	PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44		
	PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06		
	PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62		
10	PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91		
	PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49		
	PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49		
	PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98		
15	PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78		
	PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83		
	PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71		
	PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33		
20	PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67		
	PLACE1005536	1.74	1	2.74	3.12	2.43	2.88		
	PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22		
25	PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57		
	PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27		
	PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86		
	PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17		
30	PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7		
	PLACE1005563	0.51	4	1.89	1.45	2.07	1.06		
	PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09		
35	PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22		
	PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03		
	PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02		
	PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89		
40	PLACE1005601	2	5.66	4.22	3.77	4	4.02		
	PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94		
	PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46		
	PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89		
45	PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26		
	PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61		
	PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	**	+
50	PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18		
	PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55		
	PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25		
	PLACE1005648	3	8.11	9.21	8.34	10.59	8.22		
55	PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67		

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	PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58		
	PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32		
5	PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34		
	PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19		
	PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97		
	PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6		
10	PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47		
	PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38		
	PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76		
15	PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29		
	PLACE1005727	2.97	4.54	4.15	3.9	3.49	4		
	PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28		
	PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
20	PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
	PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
	PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
	PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
25	PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
	PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
	PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
30	PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
	PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
	PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
	PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
35	PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
	PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
	PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
40	PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
	PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
	PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
	PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
45	PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
	PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
	PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
50	PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
	PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
	PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
	PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
55	PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		

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	PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
	PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
5	PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
	PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
	PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
10	PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
	PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
	PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
	PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
15	PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
	PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
	PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
	PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
20	PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
	PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
	PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
25	PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
	PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
	PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
	PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
30	PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
	PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
	PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
35	PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
	PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		
	PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
	PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
40	PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
	PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
	PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
	PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
45	PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
	PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
	PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		
50	PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
	PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
	PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
	PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
55	PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		

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	PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
	PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
5	PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
	PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
	PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
10	PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
	PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
	PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
	PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
15	PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
	PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		
	PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
	PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
20	PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
	PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
	PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
25	PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
	PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
	PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
	PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
30	PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
	PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
	PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
35	PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		
	PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
	PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
	PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
40	PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
	PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
	PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
	PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
45	PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
	PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
	PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
50	PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
	PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
	PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
	PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		
55	PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		

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	PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
	PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
5	PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
	PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
	PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
10	PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
	PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
	PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
	PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
15	PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
	PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
	PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
20	PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
	PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
	PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
	PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
25	PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
	PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
	PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
	PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
30	PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
	PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
	PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
35	PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
	PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
	PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
	PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
40	PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
	PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
	PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
45	PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
	PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
	PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
	PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
50	PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
	PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
	PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
	PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
55	PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		

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	PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
	PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
5	PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
	PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
	PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
10	PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
	PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
	PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
	PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
15	PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
	PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
	PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		
	PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
20	PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
	PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
	PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
25	PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
	PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
	PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
	PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
30	PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
	PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
	PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
35	PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
	PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
	PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
	PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
40	PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
	PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
	PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
	PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
45	PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
	PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
	PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
50	PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
	PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
	PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
	PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
55	PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		

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	PLACE1006860	1	4.29	1.62	1.61	2.1	1		
	PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
5	PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
	PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
	PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
10	PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
	PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
	PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
	PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
15	PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
	PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
	PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
	PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
20	PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
	PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
	PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
25	PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
	PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
	PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
	PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
30	PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
	PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
	PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
35	PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
	PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		
	PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
	PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
40	PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
	PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
	PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
	PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
45	PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
	PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
	PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
50	PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
	PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
	PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
	PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
55	PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		



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	PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
	PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
5	PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
	PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
	PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
10	PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
	PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
	PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
	PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
15	PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
	PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
	PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
20	PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
	PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
	PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
	PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
25	PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
	PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
	PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
	PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
30	PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
	PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
	PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
35	PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
	PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
	PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
	PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
40	PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
	PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
	PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
	PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
45	PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
	PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
	PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
50	PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
	PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
	PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
	PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		
55	PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51		

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	PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8		
	PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02		
5	PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52		
	PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	*	+
	PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91		
	PLACE1007450	0.79	1.22	2.65	3	2.99	2.39		
10	PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45		
	PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61		
	PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58		
15	PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92		
	PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69		
	PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46		
	PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11		
20	PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42		
	PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9		
	PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96		
25	PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24		
	PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1		
	PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61		
	PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4		
30	PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41		
	PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59		
	PLACE1007565	0.37	2.27	1	1	1.16	0.91		
35	PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	**	+
	PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09		
	PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07		
	PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71		
40	PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5		
	PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41		
	PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38		
	PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53		
45	PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63		
	PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37		
	PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95		
50	PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13		
	PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9		
	PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4		
	PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91		
55	PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98		

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	PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61		
	PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8		
5	PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08		
	PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75		
	PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49		
	PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39		
10	PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99		
	PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32		
	PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17		
15	PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03		
	PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97		
	PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94		
	PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58		
20	PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17		
	PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87		
	PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29		
25	PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27		
	PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3		
	PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44		
	PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06		
30	PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39		
	PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39		
	PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86		
	PLACE1007845	1.76	3	4.11	3.45	3.42	2.36		
35	PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5		
	PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25		
	PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24		
40	PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	**	+
	PLACE1007866	19.42	25.98	40.48	43	80.39	56.73		
	PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08		
	PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53		
45	PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9		
	PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93		
	PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01		
50	PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41		
	PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24		
	PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54		
	PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94		
55	PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63		

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	PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51		
	PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05		
5	PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22		
	PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8		
	PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17		
10	PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21		
	PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92		
	PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88		
	PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66		
15	PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51		
	PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02		
	PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16		
20	PLACE1008045	0.4	4.07	1.54	1.75	2	1.65		
	PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78		
	PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86		
	PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23		
25	PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74		
	PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68		
	PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04		
30	PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	*	+
	PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5		
	PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91		
	PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63		
35	PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8		
	PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46		
	PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
	PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
40	PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
	PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
	PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
45	PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
	PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
	PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
	PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
50	PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
	PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
	PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
	PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
55	PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		

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	PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
	PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
5	PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
	PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
	PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
	PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
10	PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
	PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
	PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
15	PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
	PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
	PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
	PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
20	PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
	PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
	PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
25	PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
	PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		
	PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
	PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
30	PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
	PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
	PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
	PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
35	PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
	PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
	PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
40	PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
	PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
	PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
	PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
45	PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
	PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
	PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
	PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
50	PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
	PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
	PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		
55	PLACE1008532	2.12	3	5.51	5.66	4.72	4.19		

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	PLACE1008533	2.01	4	4.07	5.53	5.18	3.77		
	PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72		
5	PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53		
	PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47		
	PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38		
10	PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21		
	PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6		
	PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31		
	PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57		
15	PLACE1008603	5.9	7.25	31	30.55	43.67	29.76		
	PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16		
	PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03		
	PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95		
20	PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7		
	PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41		
	PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51		
25	PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94		
	PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24		
	PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91		
	PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13		
30	PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2		
	PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
	PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
35	PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
	PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
	PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
	PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
40	PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
	PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
	PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
	PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
45	PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
	PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
	PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
50	PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
	PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
	PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		
	PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
55	PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		

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	PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
	PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
5	PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
	PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
	PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
10	PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
	PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
	PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
	PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
15	PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
	PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		
	PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		
	PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
20	PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
	PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
	PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
25	PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
	PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
	PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
	PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
30	PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
	PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
	PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
35	PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
	PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
	PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
	PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
40	PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
	PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
	PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
	PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
45	PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
	PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
	PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
50	PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
	PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
	PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
	PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
55	PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		

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	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
5	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
10	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
15	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
20	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
25	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
30	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
35	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		
	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
40	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
45	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
50	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
55	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		



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	PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
	PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
5	PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
	PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
	PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
10	PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
	PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
	PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
	PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
15	PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
	PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
	PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
20	PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
	PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
	PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
	PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
25	PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
	PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
	PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
	PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
30	PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
	PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
	PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
35	PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
	PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
	PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
	PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
40	PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
	PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
	PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
	PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
45	PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
	PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
	PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
50	PLACE1009731	1.36	3.59	3	3.58	6.53	5		
	PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
	PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
	PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		
55	PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68		

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	PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39
	PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75
5	PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89
	PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74
	PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03
10	PLACE1009798	1.59	5.37	4	6.26	5.57	5.67
	PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92
	PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59
	PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56
15	PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11
	PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73
	PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32
	PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34
20	PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72
	PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94
	PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9
25	PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15
	PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47
	PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57
	PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04
30	PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5
	PLACE1009931	2.78	5.21	9	8.71	6.93	8.09
	PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5
35	PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03
	PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9
	PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45
	PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96
40	PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68
	PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23
	PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64
	PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46
45	PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68
	PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68
	PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06
50	PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14
	PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82
	PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19
	PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64
55	PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37

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	PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05		
	PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3		
5	PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09		
	PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22		
	PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82		
	PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85		
10	PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*	+
	PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26		
	PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48		
15	PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2		
	PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57		
	PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82		
	PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
20	PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
	PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
	PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
25	PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
	PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
	PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
	PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
30	PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
	PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
	PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
	PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
35	PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
	PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
	PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
40	PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
	PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
	PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
	PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
45	PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
	PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
	PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
50	PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
	PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
	PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
	PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
55	PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		

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	PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
	PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
5	PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
	PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
	PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
10	PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
	PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
	PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
	PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
15	PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
	PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
	PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
	PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
20	PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
	PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
	PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
25	PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
	PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
	PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
	PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
30	PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
	PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
	PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
35	PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
	PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		
	PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
	PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
40	PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
	PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
	PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
	PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
45	PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
	PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
	PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
50	PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		
	PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
	PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
	PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
55	PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		

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	PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5		
	PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29		
5	PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67		
	PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*	+
	PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22		
10	PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61		
	PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75		
	PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2		
	PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25		
15	PLACE1010713	7	10.81	14.7	9.14	8.16	15.14		
	PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47		
	PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93		
20	PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61		
	PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49		
	PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93		
	PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21		
25	PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53		
	PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08		
	PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42		
	PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34		
30	PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21		
	PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17		
	PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93		
35	PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3		
	PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18		
	PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7		
	PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81		
40	PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09		
	PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13		
	PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59		
45	PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56		
	PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94		
	PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62		
	PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51		
50	PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95		
	PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47		
	PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85		
	PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2		
55	PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		

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	PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
	PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
5	PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
	PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
	PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
10	PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
	PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
	PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
	PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
15	PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
	PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
	PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
20	PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
	PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
	PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
	PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
25	PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
	PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
	PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
	PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
30	PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
	PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
	PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
35	PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
	PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
	PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
	PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
40	PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
	PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
	PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
	PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
45	PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
	PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
	PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
50	PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
	PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
	PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
	PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
55	PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		

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	PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
	PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
5	PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
	PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
	PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
10	PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
	PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
	PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
	PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
15	PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
	PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
	PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		
	PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
20	PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
	PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
	PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
25	PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
	PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		
	PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
	PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
30	PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
	PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
	PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
35	PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
	PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
	PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
	PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
40	PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
	PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
	PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
45	PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
	PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
	PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
	PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		
50	PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
	PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
	PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
	PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
55	PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		

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	PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
	PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
5	PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
	PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
	PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
	PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
10	PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
	PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		
	PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
15	PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
	PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
	PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
	PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
20	PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
	PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
	PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
25	PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
	PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
	PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
	PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
30	PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
	PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
	PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
	PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		
35	PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		
	PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
	PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
40	PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
	PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
	PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
	PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
45	PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
	PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
	PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
50	PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
	PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
	PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
	PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
55	PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		



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	PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
	PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
5	PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
	PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
	PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
10	PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
	PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
	PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
	PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
15	PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
	PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
	PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
	PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
20	PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		
	PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
	PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
25	PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
	PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
	PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
	PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
30	PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
	PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
	PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
35	PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
	PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
	PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
	PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		
40	PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
	PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
	PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
45	PLACE2000003	1.18	3.64	6.86	7.38	8.12	8.92		
	PLACE2000005	1.16	2.41	2.16	2.76	2.03	1.89		
	PLACE2000006	2.52	4.13	15.6	11.34	16.58	13.4		
	PLACE2000007	0.96	4.85	4.24	3.94	5.13	3.33		
50	PLACE2000011	1.72	3.27	3.34	4.3	5.06	3.62		
	PLACE2000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
	PLACE2000015	1.27	4.79	3.52	2.77	3.31	2.69		
	PLACE2000017	0.48	4.78	2.15	2.65	2.56	2.45		
55	PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61		

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	PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
	PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
5	PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
	PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
	PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
10	PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
	PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
	PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
	PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
15	PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
	PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
	PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
	PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
20	PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
	PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
	PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
25	PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
	PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
	PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
	PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
30	PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
	PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
	PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
35	PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
	PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
	PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
	PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
40	PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
	PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
	PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
	PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
45	PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
	PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
	PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
50	PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
	PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
	PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
	PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
55	PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48

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	PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47		
	PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97		
5	PLACE2000246	1.93	2	6.06	4.58	5.09	3.93		
	PLACE2000264	0.67	1.39	1.85	2.45	3.74	3	*	+
	PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1		
10	PLACE2000287	0.81	4.44	1.49	2	2.59	1.34		
	PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69		
	PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45		
	PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02		
15	PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4		
	PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3		
	PLACE2000334	3.52	5	6.6	7.33	8.12	5.88		
	PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
20	PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
	PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
	PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
25	PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
	PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
	PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
	PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
30	PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
	PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
	PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		
35	PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
	PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
	PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
	PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
40	PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
	PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
	PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
	PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
45	PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
	PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
	PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
50	PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
	PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+
	PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
	PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
55	PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		

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	PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
	PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
5	PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
	PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
	PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
	PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
10	PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
	PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
	PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
15	PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
	PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
	PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
	PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		
20	PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
	PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
	PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
25	PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
	PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
	PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
	PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
30	PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
	PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
	PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
	PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
35	PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		
	PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		
	PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
40	PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
	PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
	PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
	PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
45	PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
	PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
	PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
	PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
50	PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
	PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
	PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
55	PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		

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	PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
	PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
5	PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		
	PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
	PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
	PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
10	PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
	PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
	PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
15	PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
	PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
	PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
	PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
20	PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
	PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
	PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		
	PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
25	PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
	PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
	PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
30	PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
	PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
	PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
	PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
35	PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
	PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
	PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
40	PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
	PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
	PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
	PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
45	PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		
	PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
	PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
	PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
50	PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
	PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
	PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		
55	PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29		

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	PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22		
	PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05		
5	PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82		
	PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	*	+
	PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79		
	PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01		
10	PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42		
	PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52		
	PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72		
15	PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92		
	PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14		
	PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91		
	PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21		
20	PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42		
	PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31		
	PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84		
25	PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82		
	PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19		
	PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25		
	PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91		
30	PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86		
	PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02		
	PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71		
	PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73		
35	PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84		
	PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98		
	PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94		
40	PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9		
	PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21		
	PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4		
	PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78		
45	PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22		
	PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61		
	PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07		
50	PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84		
	PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76		
	PLACE4000192	1.3	2.27	3.6	2.36	2	1.25		
	PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02		
55	PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44		

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	PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69		
	PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5		
5	PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38		
	PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48		
	PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15		
	PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51		
10	PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35		
	PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35		
	PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8		
15	PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64		
	PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02		
	PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12		
	PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51		
20	PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85		
	PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59		
	PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87		
25	PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	*	+
	PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21		
	PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82		
	PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59		
30	PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18		
	PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	*	+
	PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79		
	PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38		
35	PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82		
	PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07		
	PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12		
40	PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63		
	PLACE4000399	10.99	17.08	75.17	59.11	80.22	58		
	PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4		
	PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87		
45	PLACE4000411	2.22	2.28	4	2.27	2.6	1.82		
	PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78		
	PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83		
50	PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51		
	PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79		
	PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14		
	PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27		
55	PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04		

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	PLACE4000455	5.18	7.39	9.55	8	7.21	4.63		
	PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34		
5	PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31		
	PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22		
	PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05		
	PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69		
10	PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08		
	PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37		
	PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2		
15	PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11		
	PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22		
	PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32		
	PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15		
20	PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44		
	PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25		
	PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83		
25	PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74		
	PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58		
	PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16		
	PLACE4000651	2.42	6.4	7.48	5	7.01	6.07		
30	PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47		
	PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67		
	PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77		
	PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12		
35	PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07		
	PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76		
	PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79		
40	PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32		
	PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09		
	PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	*	+
	PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84		
45	PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87		
	PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54		
	PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64		
50	PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73		
	PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57		
	PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8		
	PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87		
55	PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82		



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	SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96		
	SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77		
5	SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44		
	SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96		
	SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44		
	SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56		
10	SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55		
	SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12		
	SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73		
15	SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92		
	SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39		
	SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	**	+
	SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18		
20	SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43		
	SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89		
	SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67		
25	SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1		
	SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11		
	SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02		
	SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3		
30	SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88		
	SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26		
	SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52		
35	SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99		
	SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84		
	SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99		
	SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68		
40	SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47		
	SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64		
	SPLEN1000072	1	8.5	4.7	2.82	3	2.21		
	SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63		
45	SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76		
	SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04		
	SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32		
50	SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99		
	SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52		
	SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8		
	SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51		
55	SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61		

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	SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68		
	SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15		
5	SPLEN1000182	0.98	2.66	-0.23	0.83	0.6	0.67		
	SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95		
	THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6		
10	THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1		
	THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	*	+
	THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38		
	THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6		
15	THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14		
	THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31		
	THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45		
	THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28		
20	THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23		
	THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11		
	THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55		
25	THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04		
	THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74		
	THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94		
	THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	*	+
30	THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74		
	THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27		
	THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93		
	THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97		
35	THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66		
	THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11		
	THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36		
40	THYRO1000034	0.49	4.16	1.59	1.99	2	1.82		
	THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11		
	THYRO1000036	0.93	8.32	4	3.08	4.36	5.59		
	THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93		
45	THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61		
	THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3		
	THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45		
50	THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06		
	THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42		
	THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85		
	THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15		
55	THYRO1000087	0.72	3.86	1.01	0	0.58	0.17		

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	THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5		
	THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95		
5	THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39		
	THYRO1000107	0.5	2.95	2.7	2.86	3.22	2		
	THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36		
10	THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95		
	THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64		
	THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92		
	THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39		
15	THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26		
	THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73		
	THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33		
	THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
20	THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
	THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
	THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
25	THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
	THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
	THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
	THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
30	THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
	THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
	THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
	THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
35	THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
	THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
	THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
40	THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
	THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
	THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
	THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
45	THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
	THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
	THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
50	THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
	THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
	THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
	THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
55	THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		

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	THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
	THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
5	THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
	THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
	THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
10	THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
	THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
	THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
	THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
15	THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
	THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
	THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
	THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
20	THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
	THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
	THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
25	THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
	THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
	THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
	THYRO1000501	1.12	4.01	2.78	3	1.92	1.82		
30	THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
	THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
	THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
35	THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
	THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		
	THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88		
	THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49		
40	THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42		
	THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78		
	THYRO1000577	1.06	5	1.34	0.96	1.22	0.71		
	THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79		
45	THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58		
	THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52		
	THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21		
50	THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97		
	THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56		
	THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29		
	THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78		
55	THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67		

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	THYR01000637	0.91	3.96	1.71	1.18	2.03	1.54
	THYR01000641	0.38	4.19	2.49	1.36	1.67	1.64
5	THYR01000657	2.99	3.69	5.42	7.67	12.28	3.86
	THYR01000658	2.68	3.62	5.39	5.4	5.55	6.09
	THYR01000662	1.1	3.19	2.09	2.42	2.69	1.66
10	THYR01000666	0.57	3.19	2.28	1.63	1.48	1.43
	THYR01000676	1.37	4.53	2.01	1.75	1.83	1.56
	THYR01000678	0.52	5.86	0.99	1.29	1.4	0.53
	THYR01000684	0.95	4.98	2.94	1.92	2.65	1.47
15	THYR01000694	2.08	6.64	4.65	2.8	2.48	3.59
	THYR01000699	2.98	2.14	5.55	4.86	7.08	7.12
	THYR01000712	1.88	4.25	5.9	6.25	6.75	7.78
20	THYR01000715	5.74	5.67	27.37	21.74	28.63	16.99
	THYR01000716	0.92	3.26	3.2	1.88	1.78	1.35
	THYR01000717	1.58	5	4.36	2.98	4.63	1.91
	THYR01000723	0.6	4.54	1.6	0.55	1.06	0.85
25	THYR01000734	-0.01	4.81	1.89	1.49	1.73	1.07
	THYR01000748	0.98	5.51	5.23	2.35	3.85	3.18
	THYR01000755	1.74	3.26	4.32	4.33	3.47	4.38
	THYR01000756	2.79	4.24	3.24	3.46	4.2	3.41
30	THYR01000776	0.48	2.17	3.02	3.36	3.99	3.34
	THYR01000777	1.81	3.39	4.54	4.99	2.05	2.37
	THYR01000779	1.45	3.55	0.88	0.18	1.01	-0.26
35	THYR01000782	3.92	10.13	12.52	10.76	15.05	14.05
	THYR01000783	0.12	5.51	1.2	1.11	1.41	0.92
	THYR01000786	6.65	9.54	19.71	15.74	7.92	13.7
	THYR01000787	0.23	1.88	1.67	1.31	1.54	0.78
40	THYR01000792	1.51	3.13	2.29	3.09	3.13	2.11
	THYR01000793	0.11	3.13	0.84	1.51	1.86	1.16
	THYR01000795	1.23	6.03	3.54	2.76	3.1	3.05
	THYR01000796	0.6	7.73	2.44	2.26	2.95	1.66
45	THYR01000798	1.89	5.82	2.51	2.59	3.57	3.53
	THYR01000800	9.26	17.2	24.74	17.74	20.68	21.06
	THYR01000805	0.49	3.04	1.08	0.72	2.66	1.38
50	THYR01000815	2.54	3.49	9.48	7.61	5.47	7.87
	THYR01000829	5.55	7.83	10.57	3.78	8.32	10.01
	THYR01000835	0.96	3.2	1.93	1.07	2.36	1.8
	THYR01000843	1.09	11.48	3.56	3.69	4.41	3.62
55	THYR01000846	0.76	5.71	1.32	2.67	1.62	1.26

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	THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32		
	THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	*	+
5	THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95		
	THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01		
	THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	*	+
10	THYRO1000894	0.33	3.95	1.36	1.75	1.48	1		
	THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82		
	THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29		
	THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89		
15	THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82		
	THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46		
	THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9		
	THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24		
20	THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87		
	THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48		
	THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64		
25	THYRO1000964	0.42	11.59	0.76	1	1.27	1.06		
	THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19		
	THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71		
	THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68		
30	THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12		
	THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26		
	THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67		
35	THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2		
	THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26		
	THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56		
	THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66		
40	THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24		
	THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41		
	THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16		
	THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02		
45	THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62		
	THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84		
	THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76		
50	THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78		
	THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5		
	THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78		
	THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93		
55	THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18		

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	THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99		
	THYRO1001113	11.41	17.42	32	21.81	26.65	18.72		
5	THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72		
	THYRO1001121	1.57	4.28	4.19	3.92	2.72	3		
	THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09		
10	THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12		
	THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38		
	THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22		
	THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62		
15	THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52		
	THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97		
	THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94		
	THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31		
20	THYRO1001204	2.17	3.58	4.27	4.03	4.74	4		
	THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9		
	THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33		
25	THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	*	+
	THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46		
	THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46		
	THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66		
30	THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69		
	THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66		
	THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97		
	THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2		
35	THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36		
	THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5		
	THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18		
40	THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5		
	THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48		
	THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83		
	THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23		
45	THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01		
	THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49		
	THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18		
50	THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65		
	THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1		
	THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28		
	THYRO1001365	0.86	3	1.6	2.19	2.6	1.96		
55	THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21		

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	THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29		
	THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94		
5	THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63		
	THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36		
	THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12		
	THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87		
10	THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18		
	THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81		
	THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73		
15	THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4		
	THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67		
	THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23		
	THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21		
20	THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64		
	THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75		
	THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57		
25	THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13		
	THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48		
	THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55		
	THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6		
30	THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35		
	THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54		
	THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38		
	THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51		
35	THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26		
	THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52		
	THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98		
40	THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54		
	THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23		
	THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73		
	THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16		
45	THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54	*	+
	THYRO1001563	9.49	14.06	15.89	10	15.49	22.09		
	THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41		
50	THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67		
	THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29		
	THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52		
	THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29		
55	THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51		



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	THYR01001602	1.49	3.26	3.52	4.95	5.22	3.41		
	THYR01001605	1.58	4.48	3.22	3.2	3.43	2.42		
5	THYR01001608	1.87	9.45	5.1	5.04	8.23	4.7		
	THYR01001617	6.06	13.68	11.47	9.75	10.87	9.61		
	THYR01001634	1.87	9.08	3.46	2.93	5.59	2.05		
	THYR01001637	3.51	3.13	9.65	8.72	7.94	9.07		
10	THYR01001641	2.57	3.73	5.09	4.03	3.08	2.94		
	THYR01001656	1.59	2.94	4.16	2.82	5.36	2.33		
	THYR01001658	22.34	29.19	40.11	34.98	33.16	42.01		
15	THYR01001661	1.4	5.83	2.31	2.93	3.31	2.05		
	THYR01001671	0.67	7.36	2.68	1.89	1.34	1.8		
	THYR01001672	1.1	9.24	2.1	1.14	1.52	1.66		
	THYR01001673	1.59	7.6	3.49	2.86	4.74	2.16		
20	THYR01001677	1.6	2.27	3.87	3.03	3.54	3.36		
	THYR01001683	12.71	17.66	29.06	24.4	15.4	16.72		
	THYR01001700	1.39	2.52	2.67	2.09	1.58	1.37		
25	THYR01001702	11.83	15.98	16.19	15.63	14.35	14.29		
	THYR01001703	1.63	6.74	4.25	4.72	3.27	4.21		
	THYR01001706	1.7	6.47	3.01	2.96	5.6	3.53		
	THYR01001721	1.84	5.66	3.2	2.73	6.37	2.77		
30	THYR01001725	5.3	6.55	9.69	8.97	8.65	8.29		
	THYR01001730	17.72	20.4	40.1	30.61	26.56	34.8		
	THYR01001738	1.35	3.18	4.65	3.52	2.82	1.78		
	THYR01001743	0.19	2.13	1.85	1.8	1.64	1.06		
35	THYR01001745	0.47	2.88	1.55	1.05	1.2	1.27		
	THYR01001746	1.9	6.25	4.04	6.12	4.01	3.88		
	THYR01001770	15.49	20.38	35.39	41.65	44.42	40.17	*	+
40	THYR01001772	1.12	4.88	3.64	4.78	4.24	3.06		
	THYR01001778	3.89	6.68	9.89	14.67	13.47	14.25	*	+
	THYR01001793	3.85	3.77	9.43	10.3	10.42	4.92		
	THYR01001796	1.35	2.28	2.28	3.45	4.22	3.24	*	+
45	THYR01001800	1.82	2.99	2.75	4.17	5.12	2.09		
	THYR01001803	3.42	6.03	5.21	4.31	4.14	3.42		
	THYR01001809	1.6	4.26	3.4	5.9	4.23	3.39		
50	THYR01001817	8.69	18.33	24.88	22.11	22.77	25.27		
	THYR01001819	4.68	8.46	9.01	7.84	10.46	6.77		
	THYR01001828	21.89	24.53	104.32	106.68	121.95	68.55		
	THYR01001854	6.67	6.12	12.45	13.43	15.86	13.31		
55	THYR01001895	0.85	1.31	2.52	3.54	4.31	1.28		

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	THYR01001907	2.16	3.08	3.37	3.9	4.53	2.74		
	TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22		
5	TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65		
	TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77		
	TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11		
	TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65		
10	TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09		
	TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54		
	TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75		
15	TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72		
	TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69		
	VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02		
	VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94		
20	VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88		
	VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	*	+
	VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27		
25	VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59		
	VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48		
	VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79		
	VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5		
30	VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65		
	VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27		
	VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87		
35	VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	*	+
	VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59		
	VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7		
	VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36		
40	VESEN1000410	1.11	5	1.78	2.36	2.71	3.69		
	VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	*	+
	VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29		
	VESEN1000440	7	5.53	7.81	3.79	9.4	12.22		
45	VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11		
	VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	*	+
	VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58		
50	VESEN1000557	4.22	7.94	7.73	6.55	9.07	10		
	VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8		
	VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08		
	VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46		
55	VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91		

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	VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51		
	VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21		
5	VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96		
	VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	*	+
	VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1		
	VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61		
10	VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66		
	VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59		
	VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47		
15	VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12		
	VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6		
	VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33		
	VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
20	VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
	VESEN2000272	2.29	4	8.92	7	8.31	5.88		
	VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
25	VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
	VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
	VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
	VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
30	VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
	VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
	VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
	VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
35	VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
	VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
	VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
40	VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
	VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
	VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
	VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
45	VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
	VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
	VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
50	VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
	VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
	VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
	VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
55	Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		

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	Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
	Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
5	Y79AA1000037	1.38	3.36	-5.71	4.84	6.82	4.49		
	Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
	Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
10	Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
	Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
	Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
	Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
15	Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
	Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
	Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
	Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
20	Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
	Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
	Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
25	Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
	Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
	Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
	Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
30	Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
	Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
	Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
35	Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
	Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		
	Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
	Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
40	Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
	Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
	Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
45	Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
	Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
	Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
	Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
50	Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
	Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
	Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
	Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
55	Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		

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	Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
	Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
5	Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
	Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
	Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
10	Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
	Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
	Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
	Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
15	Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
	Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
	Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
20	Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
	Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
	Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
	Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
25	Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
	Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
	Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
	Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
30	Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
	Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
	Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
35	Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
	Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
	Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
	Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
40	Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
	Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
	Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
	Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
45	Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
	Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
	Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
50	Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
	Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
	Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
	Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		
55	Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45		

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	Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22		
	Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17		
5	Y79AA1000697	21.76	27.52	-43.01	21.93	24.76	27.31		
	Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97		
	Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	**	+
	Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18		
10	Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45		
	Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7		
	Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	**	+
15	Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95		
	Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71		
	Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94		
	Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56		
20	Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62		
	Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38		
	Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21		
25	Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11		
	Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01		
	Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44		
	Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96		
30	Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	**	+
	Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23		
	Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39		
	Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1		
35	Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6		
	Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	*	+
	Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56		
40	Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79		
	Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14		
	Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	**	+
	Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	*	+
45	Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21		
	Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51		
	Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59		
50	Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	**	+
	Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48		
	Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68		
	Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	*	+
55	Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07		

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	Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79		
	Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13		
5	Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1		
	Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3		
	Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	*	+
	Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41		
10	Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43		
	Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56		
	Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89		
15	Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	*	+
	Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23		
	Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	*	+
	Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
20	Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
	Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
	Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
25	Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
	Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
	Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
	Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
30	Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
	Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
	Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
35	Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
	Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
	Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
	Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
40	Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
	Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
	Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
	Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
45	Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
	Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
	Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
50	Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
	Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
	Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
	Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
55	Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		

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	Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
	Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
5	Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
	Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
	Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
10	Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
	Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
	Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
	Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
15	Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
	Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
	Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
	Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
20	Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
	Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
	Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
25	Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
	Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
	Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
	Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
30	Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
	Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
	Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
35	Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
	Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		
	Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94		
	Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2		
40	Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94		
	Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14		
	Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25		
	Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	*	+
45	Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82		
	Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53		
	Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	**	+
50	Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	*	+
	Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57		
	Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46		
	Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47		
55	Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1		



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	Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	**	+
	Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	*	+
5	Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19		
	Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34		
	Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1		
10	Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	*	+
	Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83		
	Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54		
	Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05		
15	Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02		
	Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73		
	Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66		
20	Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66		
	Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67		
	Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65		
	Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73		
25	Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75		
	Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35		
	Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51		
	Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55		
30	Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85		
	Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21		
	Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14		
35	Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43		
	Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77		
	Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33		
	Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24		
40	Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28		
	Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42		
	Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15		
	Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35		
45	Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8		
	Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	*	+
	Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9		
50	Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33		
	Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17		
	Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15		
	Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79		
55	Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		

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	Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
	Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
5	Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
	Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
	Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
	Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51		
10	Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
	Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
	Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		
15	Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
	Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
	Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
	Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
20	Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
	Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
	Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
25	Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
	Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
	Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
	Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
30	Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
	Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
	Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
	Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
35	Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		
	Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
	Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
40	Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
	Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
	Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
	Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
45	Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
	Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
	Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
50	Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
	Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
	Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
	Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		
55	Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		

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	Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
	Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
5	Y79AA1002101	1.11	8.58	-2.98	6.54	5.58	6.6		
	Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
	Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
10	Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
	Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
	Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
	Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
15	Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
	Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
	Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		
20	Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
	Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
	Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
	Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
25	Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
	Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
	Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
	Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
30	Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
	Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
	Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
35	Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
	Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
	Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
	Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
40	Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
	Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
	Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
	Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
45	Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
	Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
	Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
50	Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
	Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
	Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
	Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
55	Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		

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	Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
	Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
5	Y79AA1002376	110.81	135.82	-249.8	205.99	213.25	191.69		
	Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
	Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
10	Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
	Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
	Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
15	Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
	Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
	Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
20	Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
	Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
	Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
25	Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
	Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
	Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
	Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
30	Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
	Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
	Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
35	Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
	Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
	ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

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Table 353

5 Expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light (the table also includes clones that are not described in Examples)

10 In the table, UV\_0h represents skin-derived fibroblast cells without ultraviolet irradiation; UV\_4h and UV\_24h represent skin-derived fibroblast cells 4 and 24 hours, respectively, after the irradiation. The assay was performed in triplicate (n=3) and each result is shown in the column of Exp1, Exp2, or Exp3. "t-test 0/4" and "t-test 0/24" represent the results of the test for significant difference between the unexposed cells and the cells 4 hours after the irradiation, and between the unexposed cells and the cells 24 hours after the irradiation, respectively. The table also includes the information on an increase (+) or decrease (-) in the expression level of the gene in the exposed cells 4 hours or 24 hours after the ultraviolet light irradiation. The results of the test for significant difference are shown in the columns of \*p<0.05 and \*\*p<0.01.

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	Clone	UV 0h			UV 4h			UV 24h			t test		4h 24h
		Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	0/4	0/24	+/- +/-
5	GAPDH(Cr1)	0	1.29	0.1	0.9	0.06	1.18	1.49	0.47	0			
	$\beta$ actin(Cr2)	256.82	283.53	414.29	388.38	117.29	329.8	189.18	190.26	157.87	*		-
	ADRGL1000005	15.9	10.68	19.67	3.3	6.44	12.69	6	3.06	5	*		-
	ADRGL1000007	47.47	31.62	85.7	41.54	41.35	40.62	31.64	14.77	31.5			
	ADRGL1000009	3.97	2.45	8.72	6.06	2.65	3.32	3.72	1.8	2.91			
10	ADRGL1000011	21.55	13.26	21.8	18.36	12.63	13.95	15.62	6.5	14.45			
	ADRGL1000027	2.4	1.68	5.6	4.02	2.48	2.04	3.18	0.81	3.55			
	ADRGL1000058	84.24	29.04	76.55	95.27	68.98	72.58	39.84	22.31	39.98			
	ADRGL1000069	7.61	6.31	10.67	3.58	5.86	4.59	2.92	1.14	2.62	*		-
	ADRGL1000077	4.08	5.99	6.34	5.76	3.87	4.68	4.23	2	3.08			
15	ADRGL1000092	41.45	38.57	55.77	73.06	40.91	54.59	24.67	18.9	27.36	*		-
	ADRGL1000099	43.57	33.01	48.6	56.04	29.24	45.47	24.87	18.08	20.27	*		-
	ADRGL1000136	52.22	43.6	70.27	58.84	40.95	44.91	35.09	21.07	29.76	*		-
	ADRGL1000147	6.66	6.78	11.64	6.52	5.38	7	5.38	2.59	5.89			
	ADRGL1000159	7.28	7.31	7.55	10.23	10.38	9.89	7.3	4.68	8.62	**		+
	ADRGL1000160	11.62	12.89	8.28	9.39	13.77	23.6	7.39	5.18	9.59			
20	ADRGL1000171	4.47	4.72	5.01	4.83	6.43	4.19	3.69	1.77	4.29			
	ADRGL1000181	9.73	12.6	18.02	18.65	11.48	13.93	9.96	11.18	7.77			
	BGG111000015	25.13	21.03	22.91	10.68	12.73	20.09	10.32	15.5	18.5	*		-
	BGG111000016	63.98	55.25	74.82	18.05	36.94	8.26	17.67	40.65	37.24	*	*	-
	BGG111000017	8.13	6.51	11.46	3.65	5.27	5.54	2.72	4.69	3.8	*		-
	BGG111000022	12.98	14.45	15.11	7.84	9.62	8.77	7.97	8.92	10.08	**	**	-
25	BGG111000031	13.67	9.32	14.45	9.12	13.53	12.58	6.75	10.28	15.5			
	BGG111000042	78.81	92.28	77.71	51.19	53.47	19.5	23.41	16.53	22.63	*	**	-
	BGG111000046	59.14	59.17	43.06	30.88	42.51	35.11	16	15.29	7.23	**		-
	BNGH41000025	34.23	58.36	71.87	11.96	22.6	19.45	12.51	15.56	19.08	*	*	-
	BNGH41000026	8.61	10.35	11.92	5.79	4.65	4.41	2.7	3.65	4.11	**	**	-
30	BNGH41000027	36.04	26.15	57.91	21.21	34.28	46.33	28.86	28.53	19.37			
	BNGH41000035	71.93	95.4	103.3	77.48	91.38	82.2	85.4	91.4	89.21			
	BNGH41000037	11.37	8.43	18.43	4.88	12.04	10.79	4.26	3.88	5.78			
	BNGH41000042	153.34	222.69	94.88	128.41	120.85	102.56	66.52	26.75	52.39	*		-
	BNGH41000048	115.13	80.94	131.08	158.03	99.22	95.02	70.52	58.67	62.66	*		-
	BNGH41000056	6.81	7.33	32.46	17.81	11.49	11.22	6.84	4.36	6.34			
35	BNGH41000087	7.57	4.78	6.77	6.26	6.74	6.12	2.23	3.11	5.45			
	BNGH41000091	5.88	4.66	7.21	3.92	3.81	2.29	2.51	1.95	5.23	*		-
	BNGH41000157	24.78	9.57	39.68	15.95	28.36	14.05	14.96	12.43	25.4			
	BNGH41000169	4.77	2.7	8.76	3.03	4.07	2.47	2.48	1.85	2.4			
	BNGH41000181	15.03	14.16	15.82	9.14	8.43	9.02	9.57	5.48	4.7	**	**	-
	BNGH41000198	5.23	7.17	13.44	2.81	5.92	4	2.64	2.63	2.78			
40	BNGH41000219	55.36	63.96	42.98	30.63	34.86	27.19	11.04	4.75	5.11	*	**	-
	BNGH41000229	41.48	41.07	32.45	12.86	20.86	15.06	12.11	29.5	42.2	**		-
	BNGH41000237	30.57	28.92	29.88	23.95	17.14	16.36	7.62	11.39	18.2	*	**	-
	BNGH41000238	12.97	6.92	11.13	3.1	5.96	5.05	3.21	2.99	4.83	*	*	-
	BNGH41000243	37.29	22.23	38.12	21.69	20.76	22.29	17.48	13.04	12	*		-
	BNGH41000270	7.24	2.74	13.66	5.03	4.81	3.91	2.55	1.06	3.15			
45	BRAWH1000004	26.05	12.1	22.36	14.77	13.7	15.56	10.21	9.28	9.3			
	BRAWH1000018	16.02	18.04	23.1	10.35	11.87	13.62	8.4	6.81	8.26	*	**	-
	BRAWH1000021	13.77	12.07	18.61	14.58	14.48	10.65	13.45	8.59	11.48			
	BRAWH1000027	4.8	4.82	5.71	4.63	4.59	5.52	2.19	2.04	7.42			
	BRAWH1000029	7.2	4.85	5.05	4.67	2.83	2.65	2.93	2.18	1.97	*		-
50	BRAWH1000040	20.85	33.58	27.15	16.04	13.44	12.14	8.98	5.99	6.77	*	**	-
	BRAWH1000050	86.78	63.26	107.91	121.47	88.32	92.39	77.36	45.55	64.9			
	BRAWH1000051	3.25	3.15	8.62	2.34	1.27	1.81	2.29	1.14	1.52			
	BRAWH1000060	103.56	87.24	102.14	122.05	99.97	107.12	58.34	59.07	66.98	**		-
	BRAWH1000075	6.97	6.63	15	3.29	4.01	3.69	3.52	2.95	3.34			
	BRAWH1000081	23.41	12.71	28.79	20.72	20.86	22.65	19.13	9.85	15.04			
55	BRAWH1000084	219.94	140.27	3.27	8.21	5.55	1.75	106.89	121.2	155.45			
	BRAWH1000095	6.67	5.04	6.84	7.47	5.22	4.62	3.81	0.91	1.79	*		-

Table 354

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BRANH1000096	5.38	6.14	9.95	5.23	5.99	6.41	5.29	2.17	4.29			
BRANH1000097	32.73	36.25	38.91	16.1	26.45	25.46	34.97	22.26	21.98	*	-	
BRANH1000100	3.44	3.77	6.36	1.33	1.79	1.51	2.06	0.88	1.83	*	*	-
BRANH1000101	151.17	188.03	182.43	124.31	137.07	112.48	156.93	114.91	72.6	*	-	
BRANH1000104	3.11	5.16	13	2.27	6.18	12.04	5.42	9.52	5.16			
BRANH1000107	4.13	9.11	10.29	5.8	8.93	4.46	6.91	1.75	1.45			
BRANH1000110	63.35	48.25	85.05	53.28	34.71	42.03	42.56	51.83	49.06			
BRANH1000111	17.89	14.24	19.42	6.38	13.57	14.32	11.88	11.36	7.34	*	-	
BRANH1000135	7.97	7.93	10.18	6.35	4.56	3.75	5.18	4.92	2.5	*	*	-
BRANH1000190	13.15	11.52	18.33	11.13	9.11	7.4	12.15	9.59	8.37			
HEMBA1000005	35.95	34.82	38.35	20.64	26.11	18.05	30.81	17.47	24.15	**	*	-
HEMBA1000006	9.78	9.8	11.36	1.4	5.53	2.46	3.8	1.71	7.12	**	*	-
HEMBA1000012	142.4	148.44	163.52	136.28	167.18	112.45	92.75	76.02	85.25	**	-	
HEMBA1000020	190.7	248.05	252	200.63	259.1	183.87	186.01	114.55	161.9			
HEMBA1000030	20.38	15.29	27.68	14.24	16.3	11.52	9.94	9.08	14.21			
HEMBA1000034	15.22	17.47	15.15	7.36	10.81	14.4	7.69	4.87	8.91	**	-	
HEMBA1000042	22.23	17.73	35.18	17.22	20.39	12.68	19.66	13.46	21.05			
HEMBA1000045	12.71	14.02	2.46	0.7	7.88	1.39	4.27	2.85	2.17			
HEMBA1000046	10.19	13.7	20.59	6.92	10.64	7.67	13.72	12.92	11.87			
HEMBA1000047	4.05	7.12	13.48	2.54	4.15	2.97	2.37	0.81	3.55			
HEMBA1000048	10.63	14.86	15.51	2.18	6.64	3.23	4.43	0.94	3.67	**	**	-
HEMBA1000050	3.15	3.21	10.5	2.13	3.59	2.35	2.36	0.05	2.24			
HEMBA1000053	5.98	3.98	9.78	8.93	5.91	6.48	2.35	1.85	5.68			
HEMBA1000060	10.62	11.2	18.18	10.13	8.71	11.8	7.34	2.99	9.16			
HEMBA1000072	530.32	492.25	767.01	366.98	521.7	354.83	288.04	399.85	194.47	*	-	
HEMBA1000073	26.51	17.12	39.76	19.17	28.84	19.97	20.8	18.82	12.3			
HEMBA1000076	30.89	23.42	46.09	20.74	16.14	16.31	22.31	20.51	20.54			
HEMBA1000084	46.03	48.38	54.47	61.64	67.48	73.34	43.23	26.25	43.33	*	+	
HEMBA1000087	2.35	3.13	9.77	1.66	2.08	0.86	1.69	0.8	1.37			
HEMBA1000088	3.05	3.73	12.72	2.97	3.67	2.66	4.68	0.94	2.56			
HEMBA1000091	38.82	23.63	75.02	58.3	74.93	71.96	24.1	16.38	30.08			
HEMBA1000111	21.39	20.11	44.78	24.89	20.7	26.97	20.62	12.93	18.49			
HEMBA1000121	18.15	14.06	45.72	26.38	18.11	19.11	16.09	9.88	11.04			
HEMBA1000128	6.74	4.73	14.38	8.16	5.93	6.25	3.31	1.93	2.79			
HEMBA1000129	6.94	5.68	13.44	7.51	6.89	6.55	4.13	5.51	3.96			
HEMBA1000141	12.4	7.44	22.8	8.83	6.54	5.23	5.19	3.51	3.66			
HEMBA1000146	6.55	7.84	15.71	4.62	7.62	7.46	5.3	2.57	3.09			
HEMBA1000150	28.41	41.35	48.05	22.83	16.47	23.82	28.66	15.99	24.53	*	-	
HEMBA1000154	717.61	696.56	881.96	454.74	531.19	670.47	527.79	542.09	612.33	*	*	-
HEMBA1000156	10.8	18.5	21	9.98	4.23	6.43	3.69	3.2	3.36	*	*	-
HEMBA1000158	18.74	13.45	14.16	7.7	2.81	4.64	5.39	2.06	3.26	**	**	-
HEMBA1000168	8.01	6.75	7.08	5.88	4.99	5.86	6.83	2.42	4.44	*	-	
HEMBA1000180	3.02	3.26	4.77	4.2	2.93	2.73	2.69	1.65	3.39			
HEMBA1000185	19.4	18.46	23.05	27.72	15.45	13.55	13.51	10.97	19.3			
HEMBA1000188	6.28	5.61	7.48	5.62	6.91	3.78	3.34	2.85	4.56	*	-	
HEMBA1000193	7.66	7.79	11.97	13.74	5.68	7.85	5.99	5.1	6.65			
HEMBA1000194	31.21	25.82	29.1	20.52	12.15	13.24	9	11.15	12.72	*	**	-
HEMBA1000201	13.81	8.63	14.31	11.15	8.36	7.64	5.43	4.05	4.24	*	-	
HEMBA1000213	2.97	4.59	8.02	5.36	2.78	4.45	3.2	1.24	3.2			
HEMBA1000216	7.62	8.45	11.73	6.7	6.96	6.62	6.13	4.35	5.56	*	-	
HEMBA1000227	2.73	4.56	8.5	4.18	3.58	2.84	3.35	1.71	2.27			
HEMBA1000231	24.52	27.31	24.37	15.72	17.43	21.38	21.29	12.5	20.49	*	-	
HEMBA1000237	76.81	74.32	83.86	66.84	69.97	42.93	44.61	22.46	38.37	**	-	
HEMBA1000243	13.82	10.47	25.88	21.77	11.3	17.41	12.09	8.84	11.38			
HEMBA1000244	9	7.04	9.25	7.59	2.86	4.81	3.47	4.91	3.18	**	-	
HEMBA1000251	4.62	4.41	5.87	4.22	1.63	3.25	2.37	2.22	2.32	**	-	
HEMBA1000254	10.09	13.73	13.57	7.22	5.82	7.35	8.91	6.98	9.5	*	*	-
HEMBA1000264	5.1	3.56	11.16	4.22	2.15	2.47	2.98	1.73	5.35			
HEMBA1000269	4.34	6.24	5.63	3.94	4.73	5.35	3.13	1.23	3.19	*	-	
HEMBA1000275	22.4	40.99	22.83	21.15	22.57	23.38	10.3	5.45	12.41	*	-	
HEMBA1000280	6.51	8.26	15.12	7.28	7.37	8.84	7.59	2.9	7.78			
HEMBA1000282	18.71	16.98	38.85	19.86	12.71	13.67	18.74	14.02	21.9			
HEMBA1000287	10.5	12.84	12.5	3.76	7.11	6.81	3.4	8.14	8.93	**	-	
HEMBA1000288	14.15	21.12	36.73	13.92	11.11	18.3	14.48	11.79	19.51			

Table 355

	HEMBA1000290	5.54	5.24	10.06	5.33	1.73	3.05	3.54	2.47	2.22			
	HEMBA1000296	9.5	13.84	20.76	5.15	12.54	6.86	5.85	5.2	3.4	*		-
5	HEMBA1000300	35.72	34.39	45.53	27	31.39	25.7	26.91	18.61	28.62	*		-
	HEMBA1000302	3.92	5.7	9.9	1.71	5.14	2.38	3.51	1.14	3.24			
	HEMBA1000303	7.88	7.6	13.76	3.6	4.76	4.02	4.64	2.88	3.92	*		-
	HEMBA1000304	20.77	16.02	19.73	12.6	11.48	11.65	12.2	13.31	13.14	**	*	-
	HEMBA1000307	7.67	8.03	6.72	5.49	4.16	4.06	1.61	1.51	3.67	**	**	-
10	HEMBA1000312	26.83	27.01	36.09	21.32	17.54	18.68	18.71	13.82	23.54	*		-
	HEMBA1000318	14.81	10.63	16.92	6.25	7.77	8.66	2.82	1.83	3.66	*	**	-
	HEMBA1000327	16.1	19.56	31.73	13.19	19.56	35.1	16.48	11.24	13.77			
	HEMBA1000333	4.8	4.82	8.3	2.23	3.1	2.42	2.41	0.71	1.87	*	*	-
	HEMBA1000338	14.85	18.8	25.1	10	13.67	12.74	13.23	10.79	10.59			
	HEMBA1000343	9.76	12.6	14.72	7.21	10.87	8.74	6.58	5.91	8.76	*		-
15	HEMBA1000349	7.48	9.48	16.3	4.37	4.58	5.11	3.79	2.9	11.15			
	HEMBA1000351	16.95	12.69	26.79	18.1	17.55	14.44	11.22	7.92	17.2			
	HEMBA1000355	11.99	7.36	8.03	7.48	3.22	2.44	1.27	2.39	3.56	*		-
	HEMBA1000356	34.47	36.59	32.24	39.62	29.15	32.82	22.27	24.67	20.29	**		-
	HEMBA1000357	16.16	16.75	30.37	11.91	12.99	11.46	14.62	9.28	12.57			
20	HEMBA1000366	10.73	7.46	15.42	5.17	5.07	3.55	5.42	3.22	6.53	*		-
	HEMBA1000369	10.72	11.69	16.34	4.55	5.5	4.39	6.76	3.13	5.67	*	*	-
	HEMBA1000370	9	13.55	13.78	4.72	8.24	7.37	5.92	3.13	3.05	*	*	-
	HEMBA1000376	90.99	73.26	0.51	1.99	5.8	2.22	56.72	52.09	77.09			
	HEMBA1000387	26.37	30.02	2.06	0.67	28.79	0	22.74	18.21	26.75			
	HEMBA1000389	16.44	15.64	23.44	8.78	10.05	15.24	16.41	8.42	9.96			
	HEMBA1000390	10	6.3	9.6	4.59	5.15	2.55	7.47	3.11	6.96	*		-
25	HEMBA1000392	7.7	8.4	14.19	5.19	4.42	2.87	4.91	3.87	4.75			
	HEMBA1000396	9.8	6.67	9.18	1.73	1.25	0.34	3.88	1.99	4.11	**	*	-
	HEMBA1000411	4.32	4.84	13.72	2.13	3.17	1.91	3.36	1.45	2.17			
	HEMBA1000418	10.46	14.65	17.48	5.45	8.2	5.71	4.56	2.35	3.71	*	**	-
	HEMBA1000422	9.96	6.26	0	0.69	0.58	0.28	3.62	3.45	7.58			
	HEMBA1000428	8.49	7.69	1.25	0.25	8.33	0	5.22	5.3	9.15			
30	HEMBA1000434	6.78	3.73	4.63	2.97	2.1	1.84	5.95	1.48	3.75	*		-
	HEMBA1000442	3.73	3.34	8.65	2.11	3.23	1.05	2.87	2.62	6.58			
	HEMBA1000443	6.03	7.17	14.31	3.08	6.26	3.05	8.49	4.27	7.22			
	HEMBA1000446	56.88	47.2	7.47	1.38	1.35	0.83	46.56	24.3	38.67			
	HEMBA1000456	14.88	20.85	28.05	5.95	15.86	10.1	10.12	2.72	7.69	*		-
	HEMBA1000459	15.34	18.32	27.74	11	17.98	14.9	11.74	7.37	11.06			
35	HEMBA1000460	23.55	16.11	28.93	19.24	20.63	19.37	10.12	7.72	17.35			
	HEMBA1000462	25.82	7.48	2.26	1.21	3.05	10.25	13.12	8.17	7.37			
	HEMBA1000464	7.56	4.51	6.06	3.68	3.64	2.38	3.55	1.26	2.53	*	*	-
	HEMBA1000468	3	4	6.33	1.85	2.29	0.39	1.45	0.17	1.64	*	*	-
	HEMBA1000469	22.54	28.03	34.83	17.42	17.27	14.02	27.65	14.61	18.23	*		-
	HEMBA1000477	17.38	15.06	7.59	1.07	12.5	0.35	11.11	7.11	9.19			
40	HEMBA1000481	63.47	80.18	49.05	5.51	28	7.01	17.9	5.67	5.55	*	**	-
	HEMBA1000488	14.11	13.36	8.09	0.4	9.3	4.86	6.34	1.81	3.54	*	*	-
	HEMBA1000490	9	6.13	11.44	3.85	4.12	5.04	6.84	2.63	7.56	*		-
	HEMBA1000491	5.32	6.61	17.42	8.34	8.06	9.74	6.93	4.28	9.22			
	HEMBA1000498	14.5	18.25	24.06	10.95	15.11	14.4	16.82	10.93	14.38			
	HEMBA1000501	7.87	9.11	2.74	0.21	2.74	4.51	6.04	4.62	6.97			
45	HEMBA1000504	12.54	5.58	11.75	3.41	4.13	2.59	2.67	4.18	4.58	*		-
	HEMBA1000505	6.92	8.54	7.08	0	1.28	0.84	5.6	2.13	4.7	**	*	-
	HEMBA1000507	0.45	1.56	8.28	0	1.2	0.18	0.77	0	0.38			
	HEMBA1000508	26.91	34.97	50.59	22.03	32.11	27.29	38.18	21.05	20.98			
	HEMBA1000518	3.76	3.28	6.48	5.32	4.44	6.01	3.59	1.86	3.38			
	HEMBA1000519	85.07	91.86	141.09	42.18	50.11	71.14	47.48	35.9	57.59	*		-
50	HEMBA1000520	6.49	7.75	13.06	6.32	6.26	4.22	5.77	4.5	4.14			
	HEMBA1000523	11.85	6.14	1.44	0	1.42	0.29	4.15	3.58	2.35			
	HEMBA1000531	8.26	6.64	16	4.73	9.37	11.46	9.54	4.57	6.14			
	HEMBA1000534	28.94	37.16	55.86	24.81	22.76	20.48	41.37	29.08	32.84			
	HEMBA1000538	14.97	19.18	30.49	12.11	14.95	11.04	13.25	9.03	10.27			
	HEMBA1000540	18.41	10.82	26.42	7.05	8.02	12.43	11.49	5.58	4.88			
55	HEMBA1000542	68.21	65.66	96.9	105.13	126.6	107.62	49.4	38.5	50.6	*	*	+
	HEMBA1000545	10.72	9.72	19.53	13.15	9.91	10.84	7.59	4.75	4.2			
	HEMBA1000547	16.09	12.61	26.19	11.54	11.54	13.04	5.83	5.77	5.14	*		-



Table 356

	HEMBA1000551	31.43	29.13	74.52	42.08	38.34	36.48	27.97	18.18	17.63			
	HEMBA1000555	23.07	51.65	28.63	16.75	19.18	84.47	21.47	21.24	16.53			
5	HEMBA1000557	20.2	22.07	26.42	16.84	15.85	18.08	21.6	11.99	15.53	*	-	
	HEMBA1000561	6.79	6.3	13.7	3.18	1.89	4.15	4.27	2.09	3.68			
	HEMBA1000563	5.71	6.02	9.65	3.7	5.59	3.42	4.89	1.86	4.27			
	HEMBA1000567	2.91	1.55	3.34	2.35	0.99	3.67	2.89	1.41	2.17			
	HEMBA1000568	8.19	5.62	14.84	8.57	7.03	7.81	7.88	3.61	9.31			
	HEMBA1000569	2.57	3.31	7.08	4.64	2.77	3.17	2.3	1.18	2.24			
10	HEMBA1000575	24.44	15.32	39.5	24.17	18.92	19.53	17.36	14	17.06			
	HEMBA1000588	7.1	5.81	8.91	7.39	8.88	8.85	8.33	2.25	5.9			
	HEMBA1000590	5.23	6.06	5.7	5.36	6.93	6.66	4.07	2.31	4.39	*	-	
	HEMBA1000591	24.12	22.46	26.56	10.74	18.87	21.61	11.03	5.76	13.01	**	-	
	HEMBA1000592	30.95	41.43	24.53	10.67	31.41	23.82	10.57	11.36	12.37	*	-	
	HEMBA1000594	5.11	7.29	6.57	8.37	4.71	6.68	5.32	3.27	3.89			
15	HEMBA1000604	21.62	17.48	22.7	28.09	18.45	20.99	13.92	9.43	17.25			
	HEMBA1000607	59.03	59	91.06	71.67	51.82	56.83	60.28	42.6	51.42			
	HEMBA1000608	9.41	4.42	6.41	8.42	5.12	4.07	7.92	3.99	8.94			
	HEMBA1000622	7.92	7.76	16.15	9.11	9.27	13.89	9.94	3.81	11.14			
	HEMBA1000634	52.78	74.71	70.68	39.88	65.82	64.7	32.15	24.17	25.34	**	-	
	HEMBA1000636	27.22	28.11	25.27	25.4	22.96	20.49	9.12	9.28	12.36	**	-	
20	HEMBA1000637	8.86	11.75	7.97	5.21	9.26	6.88	4.93	3.34	3.68	*	-	
	HEMBA1000655	30.73	31.69	54.9	27.54	16.27	22.75	21.5	18.39	24.41			
	HEMBA1000657	14.08	9.28	10.28	5.96	7.53	6.3	3.93	18.82	5.24	*	-	
	HEMBA1000662	6.27	5.79	10.27	3.02	6.27	5.29	2.93	4.16	3.38			
	HEMBA1000664	6.29	6.77	9.71	5.57	5.25	9.62	2.22	2.8	4.62	*	-	
	HEMBA1000671	30.41	19.43	27.86	31.58	22.01	24.63	20.58	14.98	15.56			
25	HEMBA1000673	24.11	24.74	28.83	18.72	18.93	18.52	21.96	17.14	28.31	**	-	
	HEMBA1000675	11.22	13.93	16.24	11.01	14.94	12.36	11.46	6.91	7.33			
	HEMBA1000678	5.24	8.15	11.3	5.35	7.05	6.17	5.02	1.55	1.87			
	HEMBA1000682	34.57	35.39	53.17	14.17	19.8	19.96	13.73	23.76	33.18	*	-	
	HEMBA1000686	21.71	40.16	35.85	10.91	16.11	14.54	4.3	11.52	5.8	*	*	-
30	HEMBA1000702	10.84	17.35	25.73	7.39	11.25	13.13	7.56	7.08	9.42			
	HEMBA1000705	4.6	3.75	8.97	3.21	1.09	3.11	3.08	4.72	3.61			
	HEMBA1000713	10.43	11	19.66	5.79	9.41	8.35	11.72	6.95	13.37			
	HEMBA1000718	27.65	31.72	34.47	19.34	17.98	21.82	22.89	15.55	26.61	**	-	
	HEMBA1000719	21.36	28.6	18.8	18.63	23.29	31.74	21.77	16.83	13.89			
	HEMBA1000722	10.72	14.07	15.25	12.4	11.9	8.36	7.24	4.41	3.46	**	-	
35	HEMBA1000726	32.15	32.06	69.89	34.36	26.18	30.36	36.32	22.04	41.04			
	HEMBA1000727	16.97	26.82	19.68	5.88	11.41	11.31	4.45	8.11	7.29	*	**	-
	HEMBA1000732	8.15	9.73	16.83	6.74	7.08	9.59	5.57	4.8	5.38			
	HEMBA1000736	9.38	7.92	11.45	7.38	12.77	8.49	9.33	6.94	12.57			
	HEMBA1000743	6.76	5.78	11.72	5.12	7.77	27.92	5.16	3.39	8.47			
	HEMBA1000745	7.61	8.54	13.88	4.04	5.82	4.46	4.98	2.87	5.45			
40	HEMBA1000747	5.32	4.72	12.62	2.69	5.68	3.35	3.85	2.1	3.4			
	HEMBA1000748	7.08	6.97	13.44	6.2	9.91	9.41	8.23	3.96	6.55			
	HEMBA1000749	18.03	20.17	33.28	13.55	12.82	15.47	12.43	12.59	18.76			
	HEMBA1000752	9.61	11.01	10.43	7	5.98	6.12	4.8	4.54	8.58	**	*	-
	HEMBA1000753	14.73	8.44	14.96	4.78	5.04	11.61	5.39	6.35	8.17			
	HEMBA1000757	11.82	6.81	16.04	4.91	5.14	4.63	2.56	3.42	2.84	*	-	
45	HEMBA1000760	13.51	13.09	20.98	7.09	10.48	10.58	5.68	4.5	6.77	*	-	
	HEMBA1000769	7.76	13.89	13.94	4.47	6.26	7.04	9.68	6.14	7.78			
	HEMBA1000773	3.65	4.13	15.13	0.99	5.68	8.11	2.71	1.47	3.38			
	HEMBA1000774	21.34	27.53	42.71	22.13	28.3	22.38	30.47	15.88	17.88			
	HEMBA1000780	6.15	5.35	9.22	6.03	4.9	4.38	2.5	2.74	2.78	*	-	
	HEMBA1000783	8.54	7.55	8.23	4.94	5.39	5.68	3.76	3.66	3.46	**	**	-
50	HEMBA1000791	29.92	28.02	44.77	28.48	22.57	21.5	32.85	19.21	32.35			
	HEMBA1000793	30.39	19.19	19.38	8.64	16.27	16.1	13.32	16.07	12.64			
	HEMBA1000802	4.74	2.72	8.7	3.43	2.84	2.21	2.09	1.11	2.74			
	HEMBA1000813	46.62	47.69	50.56	27.4	35.01	30.28	30.89	15.81	34.56	**	*	-
	HEMBA1000817	12.55	12.98	16.93	6.72	11.22	3.95	2.79	1.89	3.94	**	-	
	HEMBA1000822	6.54	19.54	13.74	4.86	7.54	6.86	4.29	1.48	3.36			
55	HEMBA1000827	13.88	14.84	28.11	13.31	20.08	16.37	7.68	5.83	12.73			
	HEMBA1000833	12.7	15.8	16.64	5.65	5.56	4.66	3.19	1.79	1.87	**	**	-
	HEMBA1000835	118.36	117.03	136.17	175.69	117.43	151.33	112.03	74.79	83.7			

Table 357

	HEMBA1000843	12.55	15.69	27.26	12.49	12.36	9.92	12.67	6.01	13.01				
	HEMBA1000851	7.99	8.88	11.08	3.31	3.75	3.94	6.33	2.77	2.83	**	*	-	-
5	HEMBA1000852	16.57	13.81	23	7.9	10.22	6.68	11.13	8.47	9.44	*	*	-	-
	HEMBA1000867	6.41	40.09	21.59	7.82	12.17	12.73	16.16	8.86	5.82				
	HEMBA1000869	6.66	6.92	14.84	4.94	6.58	4.87	5.66	1.59	2.82				
	HEMBA1000870	16.63	14.8	15.74	6.74	7.25	8.9	6.35	3.09	4.06	**	**	-	-
	HEMBA1000872	19	16.2	19.95	12.25	11.2	8.26	7.42	4.77	5.4	**	**	-	-
	HEMBA1000875	7.38	6.41	11.16	2.07	4.19	4.92	3.96	2.9	2.7		*	-	-
10	HEMBA1000876	12.29	12.13	19.01	9.58	10.69	6.67	12.67	6.89	9.73				
	HEMBA1000907	4.99	12.04	11.83	5.83	7.88	10.61	8.24	2.82	6.62				
	HEMBA1000908	7.89	3.64	11.79	2.7	10.96	1.89	2.83	0.62	3.13				
	HEMBA1000910	4.91	8.05	12.14	3.81	5.91	4.56	6.84	3.7	4.74				
	HEMBA1000918	21.04	31.68	45	25.17	23.52	19.82	25.88	9.86	18.68				
	HEMBA1000919	4.44	2.5	5.8	3.35	2.86	3.17	3.08	0.43	2.37				
15	HEMBA1000934	4.04	4.57	5.7	3.99	3.21	2.45	2.55	1.54	2.64		*	-	-
	HEMBA1000935	4.4	5.61	6.39	3.11	4.92	2.1	3.77	2.49	2.75		*	-	-
	HEMBA1000940	8.69	8.39	12.11	6.45	5.94	4.28	6.33	4.58	4.22	*	*	-	-
	HEMBA1000942	12.05	15.91	20.05	9.92	11.92	8.31	14.27	9.3	8.99				
	HEMBA1000943	2.61	3.51	9.04	0.06	1.63	0.43	1.65	0.02	0.85				
20	HEMBA1000946	5.48	9.79	16.74	3.82	4.51	6.06	3.38	0.73	4.11				
	HEMBA1000960	30.15	53.34	82.32	44.07	41.58	37.38	55.19	30.36	32.98				
	HEMBA1000962	10.91	13.68	14.99	4.87	9.87	8.15	6	5.38	7.85	*	**	-	-
	HEMBA1000968	9.18	5.88	12.53	7.34	5.67	5.5	4.92	3.16	5.55				
	HEMBA1000971	12.8	9.28	22.24	4.73	7.24	3.99	4.56	3.74	2.56		*	-	-
	HEMBA1000972	8.17	5.02	15.62	6.78	5.58	5.96	5.46	4.31	5.77				
25	HEMBA1000974	17.96	18.06	33.14	22.9	19.86	19.01	13.64	8.08	13.41				
	HEMBA1000975	8.54	6.18	15.36	5.78	4.48	4.06	6.6	5	4.55				
	HEMBA1000979	12.05	14.89	32.47	11.86	10.02	10.56	16.5	7.76	11.37				
	HEMBA1000981	31.09	24.35	60.14	12.11	16.96	23.49	26.22	14.59	14.47				
	HEMBA1000983	16.01	16.07	24.38	8.83	12.27	20.3	15.26	9.78	16.85				
	HEMBA1000985	7.28	3.65	6.98	4.91	4.64	4.99	4.05	3.11	1.91				
30	HEMBA1000986	13.51	10.48	26.88	15.8	12.5	15.39	12.22	6.19	7.06				
	HEMBA1000991	15.73	13.96	24.7	13.38	13.44	8.96	12.92	7.37	7.9				
	HEMBA1001007	6.2	4.4	10.1	3.64	3.96	2.18	2.52	1.45	2.54				
	HEMBA1001008	5.26	4.15	10.22	2.95	3.18	4.11	4.27	1.48	2.86				
	HEMBA1001009	2.98	2.47	7.99	2.44	3.53	2.07	2.05	0.9	2.84				
	HEMBA1001014	36.78	43.69	57.32	33.05	32.39	34.29	37.95	15.24	32.56				
35	HEMBA1001017	7.14	5.71	12.9	9.32	5.72	6.57	4.21	2.97	4.79				
	HEMBA1001019	6.35	3.7	5.48	7.22	3.14	5.53	3.87	2.27	2.61				
	HEMBA1001020	9.13	7.41	10.99	8.19	4.18	5.07	8.01	5.07	4.27				
	HEMBA1001021	4.2	4.32	9.05	3.87	3.59	5.86	6.3	1.95	6.15				
	HEMBA1001022	10.5	4.41	10.29	9.91	9.22	14.59	10.15	4.7	6.8				
	HEMBA1001024	1.82	2.83	5.27	3.68	2.95	3.77	2.92	1.3	2.29				
40	HEMBA1001026	3.74	3.71	5.2	2.99	4.11	4.69	3.01	1.9	3.66				
	HEMBA1001043	6.37	5.28	6.61	4.42	5.68	7.08	4.73	0.86	3.01				
	HEMBA1001051	120.57	138.21	211.05	111.88	82.79	99.92	82.72	88.42	94.95				
	HEMBA1001052	6.69	6.44	5.5	6.15	5.41	3.95	3.07	3.55	4.05	**		-	-
	HEMBA1001059	56.7	56.44	76.92	96.6	52.77	73	38.68	40.32	41.94	*		-	-
	HEMBA1001060	22.93	14.44	26.88	16.88	16.28	14.69	14.87	11.27	12.22				
45	HEMBA1001064	7.94	5.9	11.63	5.61	6.84	7.38	5.01	1.85	2.88				
	HEMBA1001071	2.97	5.22	8.35	8.63	6.39	5.39	3.26	1.85	3.81				
	HEMBA1001077	6.95	10.47	5.65	10.99	11.81	13.69	3.82	3.2	5.87				
	HEMBA1001078	13.55	16.29	18.17	15.7	24.22	16.62	14.25	7.88	7.1				
	HEMBA1001080	18.26	14.99	25.65	14.28	9.2	7.86	14.01	11.12	10.13				
	HEMBA1001084	10.12	12.02	19.64	11.43	8.23	10.4	8.52	5.91	8.47				
50	HEMBA1001085	12.67	14.13	17.46	10.37	7.16	7.36	9.72	8.19	7.2	*	*	-	-
	HEMBA1001088	3.47	2.77	6.21	3.04	2.22	2.64	4.71	4.47	2.67				
	HEMBA1001093	5.99	7.48	12.08	5.52	4.12	4.26	4.75	3.73	5.78				
	HEMBA1001094	3.87	3.67	7.3	1.83	2.98	1.32	1.79	1.61	3.04				
	HEMBA1001099	4.27	4.88	10.87	6.66	5.88	4.18	3.44	1.48	3.72				
	HEMBA1001104	3.23	5.58	9.6	7.66	21.55	10.79	5.83	1.68	4.13				
55	HEMBA1001109	55.09	49.61	96.04	54.26	41.61	45.47	44.91	34.62	57.09				
	HEMBA1001114	101.03	160.97	118.61	64.42	78.99	99.5	43.15	105.03	85.05				
	HEMBA1001121	8.11	7.04	9.73	5.44	4.04	4.32	4.43	2.6	4.72	*	*	-	-

Table 358

	HEMBA1001122	9.39	9.29	17.71	6.58	5.73	6.53	2.46	3.1	3.26	*	-
	HEMBA1001123	17.13	17.37	24.47	15.29	11.78	13.71	12.33	9.75	10.61	*	-
5	HEMBA1001133	8.92	6.97	12.93	3.69	4.11	4.57	3.05	2.9	3.3	*	-
	HEMBA1001137	6.57	7.37	12.88	4.24	4.79	2.86	4.1	2.06	3.89		
	HEMBA1001140	9.64	11.4	16.66	10.87	12.26	10.82	8.45	8.07	5.83		
	HEMBA1001144	75.62	79.41	130.35	64.7	57.88	71.91	43.23	38.45	52.04	*	-
	HEMBA1001145	228.88	419.26	297.93	34.88	83.53	106.81	28.23	79.02	93.39	*	-
10	HEMBA1001158	11.25	10.45	12.32	5.71	7.87	10.11	6.5	4.55	5.45	**	-
	HEMBA1001172	13.23	15.14	21.25	10.8	9.67	9.91	10.54	8.89	11.23		
	HEMBA1001174	4.77	4.96	13.93	3.36	4.72	5.71	5.53	3.53	3.57		
	HEMBA1001175	25.64	49.85	37.18	5.53	36.99	18.9	6.53	8.52	5.43	*	-
	HEMBA1001182	253.75	199.19	217.61	213.83	179.06	196.11	166.5	128.3	113.47	*	-
	HEMBA1001184	2.72	5.66	6.46	2.92	7.84	3.84	2.54	1.64	3.55		
15	HEMBA1001192	7.71	9.61	13.89	5.11	4.84	2.98	2.49	2.97	4.44	*	-
	HEMBA1001196	20.51	33.03	45	22.81	18.19	24.13	7.47	12.08	16.7		
	HEMBA1001197	377.82	621.74	482.95	613.89	355.35	492.48	223.5	509.73	494.09		
	HEMBA1001208	6.77	4.91	9.09	4.11	4.25	4.69	3.47	2.44	4.54		
	HEMBA1001213	162.45	150.13	151.86	224.78	129.48	188.61	135.18	97.08	115.8	*	-
	HEMBA1001214	10.4	15.18	18.46	6.51	7.45	6.56	4.99	3.77	6.34	*	-
20	HEMBA1001221	12.82	12.25	13.21	2.1	6.95	5.45	2.31	0.75	2.8	**	-
	HEMBA1001225	4.23	4.43	8.6	1.43	2.73	4.08	2.02	0.94	2.52		
	HEMBA1001226	43.15	51.42	64.65	33.28	48.87	38.83	29.67	18.32	24.38	*	-
	HEMBA1001228	5.8	4.52	8.07	5.69	4.51	3.32	3.32	1.37	1.24	*	-
	HEMBA1001229	171.43	141.71	227.65	215.79	153.09	225.88	105.81	85.9	109.68	*	-
	HEMBA1001235	51.44	62.4	68.51	46.01	34.3	36.55	26.86	20.23	22.59	*	-
25	HEMBA1001238	19.14	19.72	19.8	10.86	15.88	9.5	15.04	10.36	16.33	*	-
	HEMBA1001242	153.09	161.43	160.67	152.69	145.07	151.85	99.19	75.76	86.89	**	-
	HEMBA1001247	33.3	29.15	48.14	21.32	32.34	22.28	34.27	20.52	27.05		
	HEMBA1001253	159.45	91.8	142.61	116.02	138.28	127.87	95.67	74.41	74.86		
	HEMBA1001257	10.7	11.57	12.78	5.67	10.33	4.37	9.19	6.06	4.62	*	-
	HEMBA1001261	6.83	4.18	8.42	7.74	2.14	4.76	3.41	1.78	5.45		
30	HEMBA1001262	12	7.56	5.09	4.62	4.49	6.27	3.32	1.44	4.7		
	HEMBA1001265	15.44	18.41	25	9.71	8.97	12.14	13.41	14.3	11.72	*	-
	HEMBA1001266	22.75	26.99	30.66	16.84	17.03	12.35	18.86	10.28	14.84	*	-
	HEMBA1001269	62.54	134.76	5.56	0.22	1.58	0.07	24.28	23.59	16.64		
	HEMBA1001272	5.33	4.56	13.33	2.87	3.94	3.83	3.1	1.67	1.95		
	HEMBA1001279	26.1	31.13	42.25	28.49	33.02	28.73	22.53	17.36	24.84		
35	HEMBA1001281	43.22	55.66	55.89	31.39	34.2	26.87	21.08	11.24	15.62	*	-
	HEMBA1001286	42.89	33.78	59.69	41.46	36.64	48.02	50.11	34.66	41.6		
	HEMBA1001289	4.71	4.83	5.28	3.13	4.27	3.23	3.56	1.6	3.12	*	-
	HEMBA1001291	36.57	24.72	38.55	19.37	18.57	13.13	19.39	15.96	11.69	*	-
	HEMBA1001294	8.41	15.41	16.09	9.8	8.09	6.28	18.25	5.05	15.73		
	HEMBA1001296	7.97	20.06	12.99	5.33	6.56	3.52	5.19	2.03	4.63		
40	HEMBA1001297	10.62	19.22	19.19	4.41	7.4	5.61	6.49	1.83	3.17	*	-
	HEMBA1001299	34.22	39.68	53.21	25.14	29.23	20.66	39.68	22.86	32.79	*	-
	HEMBA1001302	25.32	40.78	38.96	17.94	26.15	22.11	18.04	11.91	7.95	*	-
	HEMBA1001303	10.97	8.86	13.92	4.53	5.04	4.42	4.71	4.03	7.45	*	-
	HEMBA1001306	14.82	11.94	17.26	5.51	7.45	6.38	3.83	5.28	4.41	**	-
	HEMBA1001308	44.73	35.49	88.39	29.14	49.52	28	40.25	28.31	38		
45	HEMBA1001310	8.14	6.04	8.8	2.67	3.81	3.08	5.37	3.64	2.99	**	-
	HEMBA1001312	42.22	39.35	44.87	10.33	40.14	18.42	38.81	18.56	13.38		
	HEMBA1001319	3.83	6.75	12.77	3	5.03	13.5	4.72	0.95	4.62		
	HEMBA1001322	10.16	10.91	17.38	3.57	7.15	4.09	5.93	2.59	3.36	*	-
	HEMBA1001323	41.14	36.93	47.79	17.38	18.24	15.31	13.85	10.42	3.9	**	-
	HEMBA1001326	38.26	32.16	36.43	4.89	17.62	29.01	7.49	3.64	9.8	**	-
50	HEMBA1001327	22.04	9.71	15.11	7.86	12.59	16.77	4.84	4.12	2.75	*	-
	HEMBA1001330	29.76	31.78	64.11	34.57	26.99	26.81	34.76	20.01	20.9		
	HEMBA1001348	8.77	6.35	12.87	5.62	7.19	5.23	5.41	4.95	2.78		
	HEMBA1001350	11.78	12.52	19.81	3.72	3.89	6.89	7.45	5.17	4.88	*	-
	HEMBA1001351	31.73	33.01	83.64	16.41	14.04	17.67	14.45	12.88	6.51		
	HEMBA1001352	16.11	10.31	24.58	3.9	5.27	4.13	8.48	3.75	2.44	*	-
55	HEMBA1001353	239.33	87.11	196.31	30.75	66.77	70.17	148.92	56.48	39.11		
	HEMBA1001358	74.35	56.7	93	21.23	34.67	61.64	20.12	9.88	14.9	**	-
	HEMBA1001361	9.19	10.7	19.27	11.26	10.32	15.03	5.68	3.47	4.41		

Table 359

	HEMBA1001364	5.59	5.71	8.25	5.34	8.32	6.23	4.19	2.87	3.41	*	-
	HEMBA1001375	10.82	8.04	9.96	6.56	6.52	8.55	3.93	8.03	4.02		
5	HEMBA1001377	30.09	30.45	47.44	34.01	31.38	34.79	26.34	19.08	22.43		
	HEMBA1001383	3.91	6.12	10.35	4.08	4.49	3.29	3.04	1.16	2.13		
	HEMBA1001387	4.6	4.17	9.82	4.35	3.61	5.27	5	2.3	4.29		
	HEMBA1001388	3.38	12.99	10.77	8.84	13.96	11.27	14.15	2.79	4.79		
	HEMBA1001390	16.62	20.96	41.58	20.9	20.32	29.35	22.75	17.7	27.56		
10	HEMBA1001391	2.64	5.63	6.55	6.35	4.1	4.57	3.4	1.38	3.14		
	HEMBA1001398	7.95	9	20.79	14.55	10.11	10.1	9.09	3.86	9.96		
	HEMBA1001405	12.88	15.37	29.38	17.27	15.08	16.39	13.42	7.68	15.76		
	HEMBA1001406	1.07	1.48	6.07	4.64	2.23	2.45	3.84	0.53	2.8		
	HEMBA1001407	26.07	42.46	69.39	34.3	28.94	28.07	26.15	15.14	21.96		
	HEMBA1001411	12.19	10.95	23.76	12.34	12.91	16.6	13.01	4.8	11.91		
15	HEMBA1001413	3.96	7.52	13.68	7.68	4.74	6.7	4.77	2.46	3.91		
	HEMBA1001414	10.32	10.99	22.49	13.09	11.95	9.01	7.42	9.57	11.87		
	HEMBA1001415	108.07	112.24	218.31	253.58	139.52	200.62	94.4	74.64	97.27		
	HEMBA1001416	5.94	4.6	7.89	5.06	3.57	4.15	3.74	1.73	3.21	*	-
	HEMBA1001432	3.3	3.49	7.34	4.93	5.95	7.57	4.22	3.23	2.6		
	HEMBA1001433	5.11	5.55	7.48	5.92	7.1	6.22	4.04	2.29	5.52		
20	HEMBA1001435	448.61	559.24	661.15	777.73	679.52	650.29	640.12	377.73	859.06		
	HEMBA1001442	5.84	10.08	7.28	7.83	12.04	8.46	5.85	1.96	2.4		
	HEMBA1001446	3.77	5.34	6.49	8.2	4.64	4.7	3.45	2.22	3.65		
	HEMBA1001450	87.92	103.44	150.5	232.41	124.8	175.34	89.47	74.72	92.31		
	HEMBA1001454	32.58	33.13	59.47	19.79	12.7	25.66	18.88	24.9	33.22		
	HEMBA1001455	4.27	6.3	7.42	3.13	5.27	4.96	6.16	1.51	6.96		
25	HEMBA1001459	13.66	26.28	34.13	12.19	9.69	14.19	9.18	11.22	13.6		
	HEMBA1001461	30.98	26.88	43.29	63.45	32.06	36.73	26.62	18.12	23.29		
	HEMBA1001462	9.43	9.05	11.64	4.2	7.04	5.63	4.19	2.77	3.22	*	**
	HEMBA1001463	1.15	4.7	4.74	4.99	6.6	4.02	4.68	1.57	3.46		
	HEMBA1001469	23.94	42.87	64.76	64.17	33.38	52.34	14.36	18.57	20.01		
	HEMBA1001473	7.37	9.89	11.35	4.59	3.3	4.44	2.71	5.14	2.51	*	*
30	HEMBA1001477	143.72	139.98	283.29	91.65	145.02	139.05	125.85	114.31	63.92		
	HEMBA1001478	3.38	2.99	11.83	2.63	2.55	3.35	2.27	2.13	2.08		
	HEMBA1001480	12.29	13.63	23.93	4.88	9.2	12.63	3.97	2.72	4.12	*	-
	HEMBA1001483	20.97	27.37	23.32	22.22	18.94	28.05	14.33	10.01	19.51	*	-
	HEMBA1001490	14.01	20.37	28.13	15.26	17.45	15.48	22.44	13.02	12.6		
	HEMBA1001495	29.87	31.18	55.68	75.52	52.85	69.44	21.73	15.8	24.63		
35	HEMBA1001497	50.34	63.13	114.17	128.19	117.69	137.5	43.07	37.4	51.44		
	HEMBA1001510	6.77	7.43	13.73	8.69	8.1	7.82	5.34	3.9	10.87		
	HEMBA1001515	4.96	2.98	9.2	1.95	4	3.02	1.96	0.89	7.49		
	HEMBA1001517	8.97	7.98	15.08	6.1	6.94	5.43	7.39	5.25	8.47		
	HEMBA1001522	12.78	16.29	21.22	10.39	13.01	11	10.54	9.25	10.66		
	HEMBA1001526	8.05	10.86	20.31	6.19	10.35	7.24	6.93	4.75	7.32		
40	HEMBA1001533	10.67	13.52	23.12	12.09	16.84	9.55	9.42	6.16	11.58		
	HEMBA1001547	5.91	8.31	10.54	8.17	5.66	9.57	6.23	2.5	7.38		
	HEMBA1001552	2.97	4.72	5.75	6.36	5.56	2.49	2.68	1	5.09		
	HEMBA1001553	11.17	10.19	22.05	10.98	12.27	11.05	5.91	7.82	10.68		
	HEMBA1001557	7.49	2.45	11.09	3.83	4.84	5.27	3.14	6.97	8.01		
	HEMBA1001563	6.6	2.01	15.37	5.55	6.29	6.53	4.15	2	6.53		
45	HEMBA1001566	4.27	3.01	8.62	2.13	3.6	3.87	2.2	1.62	3.88		
	HEMBA1001569	9.15	15.35	27.87	11.41	11.78	14.08	8.02	5.27	11.03		
	HEMBA1001570	10.89	22.06	19.57	12.99	13.03	16.53	9.14	4.13	3.81	*	-
	HEMBA1001579	95.92	121.26	222.36	134.48	102.06	70.96	25.6	43.38	73.16		
	HEMBA1001581	4.11	4.25	7.71	3.25	2.45	2.33	0.91	1.64	3.55		
	HEMBA1001582	12.19	16.67	20.04	15.87	10.82	11.89	13.98	8.69	21.33		
50	HEMBA1001585	6.81	4.99	13.1	7.76	5	7.16	4.04	1.85	5.57		
	HEMBA1001589	7.95	8.96	19.02	7.86	6.17	6	7.81	5.42	8.45		
	HEMBA1001595	152.72	179.08	178.84	145.86	142.24	141.98	126.66	83.83	110.77	*	*
	HEMBA1001604	23.66	24.89	37.02	23.72	21.32	19.26	15.97	14.33	15.78	*	-
	HEMBA1001608	43.55	20.96	66.71	67.7	43.63	57.55	24.58	18.07	23.43		
	HEMBA1001615	5.42	4.63	6.98	6.61	4.72	4.09	3.11	2.02	10.18		
55	HEMBA1001620	30.69	48.66	53.49	25.04	17.81	22.67	7.35	9.47	10.42	*	**
	HEMBA1001621	8.82	12.26	20.39	18.14	12.47	10.32	10.67	8.68	14.11		
	HEMBA1001635	3.29	3.32	8.82	2.2	2.68	3.13	2.05	0.94	1.44		

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	HEMBA1001636	3.01	3.66	7.63	2.63	2.16	1.96	2	2.43	2.09			
	HEMBA1001640	29.8	43.06	50.77	23.27	24.57	21.36	34.37	24.57	21.57	*	-	
5	HEMBA1001647	5.45	3.94	16.28	4.05	6.97	2.61	5.21	2.15	4.19			
	HEMBA1001651	40.26	49.2	70.61	64.68	55.88	51.2	30.59	17.33	15.12	*	-	
	HEMBA1001655	10.17	9.88	20.1	6.79	14.34	13.87	15	5.01	12.4			
	HEMBA1001658	5.48	21.34	12.68	3.21	27.79	21.94	17.32	4.91	4.48			
	HEMBA1001661	1.92	2.27	3.66	1.72	2.22	1.93	2.04	0.71	3.46			
	HEMBA1001665	5.27	5.54	9.55	3.17	2.96	2.46	2.94	1.87	2.02	*	*	- -
10	HEMBA1001670	14.59	18.93	22.5	10.01	11.18	7.78	13.23	9.01	14.55	*	-	
	HEMBA1001672	5.67	6.19	14.07	4.38	5.16	2.99	5.11	2.78	4.53			
	HEMBA1001673	67.5	83.13	100.8	79.52	76.6	62.66	79.54	46.76	80.49			
	HEMBA1001675	11.65	14.39	26.02	11.92	12.54	11.44	8.96	6.24	12.74			
	HEMBA1001676	5.94	6.55	16.33	9.03	9.2	9.7	5.97	3.49	7.17			
15	HEMBA1001678	408.84	460.84	545.99	212.4	385.11	245.37	243.82	358.42	324.52	*	*	- -
	HEMBA1001680	17.81	21.9	34.13	4.77	16.15	9.85	5.24	7.39	4.29	*	-	
	HEMBA1001681	4.07	7.09	7.63	4.19	6.03	3.95	5.56	3.95	9.27			
	HEMBA1001684	9.98	10.79	18.76	5.52	7.17	3.85	8.63	7.5	7.69			
	HEMBA1001695	6.3	10.78	12.26	4.59	5.86	5.01	6.15	3.07	8.56			
	HEMBA1001702	4.21	4.98	12.28	2.87	3.73	2.48	2.67	0.5	1.76			
20	HEMBA1001709	2.14	4.26	13.24	2.55	2.4	2.49	3	0.8	2.49			
	HEMBA1001711	4.46	2.9	7.77	4.65	5.15	6.37	2.22	1.03	3.22			
	HEMBA1001712	17.3	21.73	24.38	4.68	4.43	7.93	6.13	3.94	7.49	**	**	- -
	HEMBA1001714	5.44	5.05	12.26	3.87	6.98	3.98	4.35	1.76	2.27			
	HEMBA1001717	12.02	13.24	20.14	10.04	12.58	8.86	8.97	5.33	8.75			
	HEMBA1001718	6.01	7.09	16.45	6.91	7.4	6.4	6.45	5.23	4.35			
25	HEMBA1001723	4.38	5.84	13.91	3.89	3.74	3.51	3.82	2.36	1.25			
	HEMBA1001731	2.72	5.88	12.37	2.09	2.33	1.98	2.59	1.24	1.73			
	HEMBA1001734	3.48	4.86	15.18	4.34	3.76	3.13	3.75	1.03	2.79			
	HEMBA1001736	7.38	10.86	24.38	12.76	10.32	13.2	4.98	2.9	5.27			
	HEMBA1001741	15.06	22.96	34.81	18.57	17.99	31.53	19.64	14.22	21.03			
	HEMBA1001744	3.63	4.77	7.03	5.75	5.45	4.88	3.08	0.38	1.67			
30	HEMBA1001745	6.61	5.99	11.87	4.17	5.23	3.45	2.53	2.9	1.77	*	-	
	HEMBA1001746	10	14.3	20.05	11.55	8.04	11.63	7.31	4.66	10.54			
	HEMBA1001761	4.09	4.47	15.81	2.95	5.47	4.97	4.55	2.51	3.77			
	HEMBA1001762	12.27	16.22	31.71	11.79	12.77	9.07	10.3	5.04	7.64			
	HEMBA1001781	15.21	11.25	22.91	6.13	9.86	7.74	12.65	6.92	10.68			
	HEMBA1001784	7.14	8.4	14.02	11.89	8.86	32.45	4.84	4.18	5.94			
35	HEMBA1001791	5.49	5.04	11.37	7.91	5.03	6.87	4.96	3.16	6.54			
	HEMBA1001794	20.29	19.03	24.02	20.07	12.65	17.58	18.71	4.14	12.87			
	HEMBA1001800	3.21	4.6	6.87	7.34	5.09	5.03	5.14	1.64	4.39			
	HEMBA1001803	13.17	17	29.4	25.23	15.99	17.41	14	9.49	14.18			
	HEMBA1001804	10.28	12.82	18.21	18.52	13.37	6.76	5.06	3.75	9.33			
	HEMBA1001808	1.39	1.46	0.57	2.77	3.18	1.86	0.98	1.2	0.86	*	+	
40	HEMBA1001809	10.03	14.07	29.16	27.06	14.98	19.9	10.22	6.76	12.88			
	HEMBA1001811	4.85	4.27	3.18	10.29	3.63	4.31	3.6	2.84	5.25			
	HEMBA1001815	12.35	11.27	24.93	14.76	10.57	16.04	11.75	6.51	11.06			
	HEMBA1001816	15.52	16.02	31.22	15.84	13.09	17.05	15.48	10.68	15.2			
	HEMBA1001819	6.04	14.01	18.63	8.04	9.05	17.69	7.85	3.75	9.93			
	HEMBA1001820	1.8	2.22	6.75	3.5	2.81	3.45	1.98	0.63	2.02			
45	HEMBA1001822	10	12.84	23.21	14.57	16.12	12.64	12.36	6.85	15.78			
	HEMBA1001824	5.2	8.63	7.51	6.46	8.51	5.78	4.67	0.98	4.7			
	HEMBA1001835	9.56	9.62	14.11	4.64	5.39	6.11	3.44	4.66	3.04	*	**	- -
	HEMBA1001844	8.02	10.52	19.05	12.42	10.73	9.57	5.22	6.54	4.99			
	HEMBA1001847	5.48	6.03	7.01	5.38	4.93	4.88	3.96	3.19	3.69	**	-	
	HEMBA1001849	6.93	9.14	14.78	5.03	7.86	7.21	7.8	8.87	10.07			
50	HEMBA1001850	16.31	17.09	25.61	18.6	20.16	20.58	11.51	7.47	10.97	*	-	
	HEMBA1001861	2.36	3.42	4.47	4.07	3.37	3.99	2	1.11	3.64			
	HEMBA1001862	13.85	31.74	17.1	16.22	16.82	16.11	10.11	2.6	10.67			
	HEMBA1001864	2.79	3.87	7.65	5.32	5.64	4.4	3.29	2.25	6.43			
	HEMBA1001866	5.87	7.28	17.71	11.53	8.34	6.62	3.42	4.81	5.52			
	HEMBA1001869	12.96	19.53	27.66	23.68	16.72	23.14	5.91	10.06	12.62			
55	HEMBA1001871	3.56	6.35	8.61	4.54	2.2	3.49	3.21	1.17	2.75			
	HEMBA1001876	4.6	3.93	8.22	5.16	4.46	4.33	3.76	4.15	6.11			
	HEMBA1001878	8.8	14.72	27.92	7.18	13.52	10.62	6.43	4.37	4.82			

Table 361

	HEMBA1001879	23.8	24.57	36.17	27.25	30.71	21.12	18.92	12.59	21.51			
	HEMBA1001884	22.79	25.41	39.57	18.36	21.7	20.15	24.74	18.16	27.02			
5	HEMBA1001886	2.49	3.21	10.85	4.21	4.2	3.06	3.99	2.94	2.81			
	HEMBA1001888	5.93	5.79	13.13	8.79	5.21	8.71	5.32	6.52	7.9			
	HEMBA1001890	12.55	17.2	16.26	7.93	7.84	9.91	5.34	7.04	9.79	*	*	-
	HEMBA1001896	8.62	13.4	18.92	9.94	9.97	13.19	7.37	7.12	11.57			
	HEMBA1001899	9.63	9.32	14.65	9.07	9.12	9.82	4.74	3.78	7.78			
	HEMBA1001904	17.69	9.43	25.81	8.49	15.82	16.23	7.42	3.21	4			
10	HEMBA1001910	13.84	17.03	18.88	10.76	16.22	11.5	15.72	11.44	11.3			
	HEMBA1001911	84.18	136.96	104.54	60.48	92.99	36.82	38.97	44.93	16.51	*		-
	HEMBA1001912	8.8	18.15	15.1	11.38	13.1	11.76	6.02	5.45	6.48	*		-
	HEMBA1001913	63.5	67.85	178.77	91.97	76.48	71.89	38.1	40.9	79.58			
	HEMBA1001915	9.95	12.39	24.42	17.53	14.5	13	8.17	4.57	10.88			
	HEMBA1001918	5.57	6.46	12.5	8.11	6.81	8.09	4.3	2.18	7.19			
15	HEMBA1001921	8.68	9.91	12.62	8.57	8.25	7.86	5.28	3.66	4.78	**		-
	HEMBA1001931	9.24	10.47	21.38	7.16	7.58	6.86	8.41	6.87	7.96			
	HEMBA1001939	3.59	7.32	15.17	1.25	16.55	5.08	4.84	5.03	14.82			
	HEMBA1001940	11.2	9.93	21.45	9.87	12.2	10.55	7.02	5.09	7.03			
	HEMBA1001942	22.25	36.8	27.34	8.22	35.32	31.27	17.26	9.8	12.44	*		-
20	HEMBA1001944	14.23	17.39	30.07	21.25	14.66	13.47	4.56	8.32	14.97			
	HEMBA1001945	8.53	9.04	18.07	9.58	9.66	6.81	6.7	4.7	10.21			
	HEMBA1001950	35.24	36.06	25.81	22.39	20.56	21.76	31.55	22.6	14.77	*		-
	HEMBA1001951	39.37	38.17	52.67	44.58	33.39	34.05	41.69	23.81	45.03			
	HEMBA1001958	3.68	3.88	9.13	1.87	2.36	1.68	2.36	1.43	3.59			
	HEMBA1001960	11.92	13.79	24.84	7.91	13.38	11.06	7.97	3.56	9.09			
25	HEMBA1001962	10.82	11.31	28.75	9.3	13.76	9.37	10.95	7.24	13.69			
	HEMBA1001964	11.99	14.1	28.18	9.47	13.95	12.22	12.21	4.77	10.5			
	HEMBA1001967	33.16	31.11	63.39	22.3	13.19	20.77	8.29	10.21	24.27			
	HEMBA1001979	6.77	6.74	6.61	3.38	4.61	6.79	4.27	2.37	4.75	*	*	-
	HEMBA1001987	6.84	5.64	7.7	5.03	3.79	3.32	4.73	5.25	2.63	*		-
	HEMBA1001991	4.14	2.8	6.6	1.78	2.7	1.18	2.19	1.73	1.57			
30	HEMBA1002003	3.19	3.64	8.31	2.58	2.51	1.13	4.14	2.93	2.53			
	HEMBA1002005	21.43	25.67	43.64	22.86	20.88	16.44	24.76	11.27	20.55			
	HEMBA1002008	15.2	19.08	39.6	14.05	18.61	13.62	20.77	11.98	21.03			
	HEMBA1002018	4.58	11.59	12.53	3.51	5.86	20.49	4.43	1.81	2.74			
	HEMBA1002022	29.07	36.45	75.11	52.83	42.93	48.33	30.25	25.12	55.78			
	HEMBA1002029	19.99	24.25	30.34	10.7	17.32	16.65	10.55	13.15	11.59	*		-
35	HEMBA1002030	11.06	12.89	19.22	8.24	7.3	5.76	8	6.82	6.24	*	*	-
	HEMBA1002035	3.07	17.04	7.87	2.25	5.11	2.16	4.64	3.69	6.06			
	HEMBA1002037	95.17	141.19	140.82	59.83	84.82	73.74	61.45	42.2	28.14	*	*	-
	HEMBA1002038	11.96	19.11	18.49	6.44	9.02	6.74	4.63	2.27	2.59	*	**	-
	HEMBA1002039	6.42	7.41	13.49	2.37	5.91	2.48	3.27	1.37	3.16	*		-
	HEMBA1002042	3.25	8.61	11.52	6.6	6.65	6.58	7.97	0.75	4.67			
40	HEMBA1002043	13.24	16.58	22.47	5.13	6.87	6.08	5.01	5.72	8.43	*	*	-
	HEMBA1002048	25.65	31.58	36.46	5.14	12.63	17.17	11.27	12.56	24.5	*	*	-
	HEMBA1002049	431.22	564.03	858.02	234.02	525.06	482.28	304.41	585.23	233.29			
	HEMBA1002053	66.35	61.58	114.43	104.42	98.85	104.79	56.5	40.65	69.44			
	HEMBA1002055	19.16	20.77	33.11	22.38	16.8	17.16	15.07	11.5	15.77			
	HEMBA1002056	5.26	6.55	10.96	2.52	2.93	4.72	5.3	2.16	5.03			
45	HEMBA1002061	3.02	4.19	9.86	2.45	3.45	0.92	2.37	0	1.82			
	HEMBA1002080	2.59	8.96	20.11	3.27	8.34	5.7	6.09	2.76	4.82			
	HEMBA1002084	7.01	3.85	10.52	5.96	3.47	4.97	2.69	1.31	2.02			
	HEMBA1002085	3.68	5.88	10.92	2.9	5.24	7.31	3.65	1.95	5			
	HEMBA1002092	18.94	17.76	38.17	14.49	14.47	17.01	14.19	7.25	10.23			
	HEMBA1002098	8.74	16.29	15.2	3.59	8.82	8.02	9.31	14.32	5.83			
50	HEMBA1002100	13.69	10.18	19.02	11.56	6.49	4.52	8.34	7.69	7.11			
	HEMBA1002101	12.62	14.09	31.93	14.79	12.76	11.05	16.17	8.68	13.96			
	HEMBA1002102	4.18	7.54	13.28	4.1	4.71	4.56	3.77	3.14	3.09			
	HEMBA1002105	5.07	7.15	15.22	5.77	3.71	9.62	4.21	1.98	2.79			
	HEMBA1002107	7.22	7.4	21.27	9.53	10.18	12.18	2.67	2.93	5.58			
	HEMBA1002113	5.14	7.17	14.68	10.73	7.63	8.56	6.5	2.35	7.99			
55	HEMBA1002119	24.1	26.96	60	38.03	31.14	26.41	31.91	16.47	21.72			
	HEMBA1002125	4.31	5.62	9.66	11.65	3.83	5.15	2.02	2.4	2.97			
	HEMBA1002131	2612	1876.5	3959.7	1306.5	2879.6	1519.6	1255.8	1936.4	1651.4			

Table 362

	HEMBA1002133	29.03	35.39	76.13	107.6	70.61	84.67	29.03	14.5	31.23		
	HEMBA1002139	11.59	23.7	52.84	28.04	21.84	20.31	32.1	12.89	25.76		
5	HEMBA1002141	3.72	5.77	10.55	5.21	5.75	3.18	3.83	1.34	5.31		
	HEMBA1002144	2.85	4.6	6.42	4.94	2.2	5.21	1.49	2.58	2.66		
	HEMBA1002147	10.27	15.44	23.81	11.25	8.38	13.35	8.76	6.54	9.55		
	HEMBA1002150	1.33	1.23	3.53	2.46	2.28	2.8	1.93	0.73	2.03		
	HEMBA1002151	6.03	4.63	11.41	5.99	5.56	6.68	5.34	2.78	4.91		
	HEMBA1002153	0.77	2.83	4.03	3.46	4.19	3.78	2.71	1.39	3.61		
10	HEMBA1002156	2.06	3.91	4.83	5.6	4.46	2.69	2.87	0.76	2.49		
	HEMBA1002160	56.44	32.19	84.15	108.2	70.78	79.86	43.2	16.4	44.96		
	HEMBA1002161	44.7	21.27	41.93	61.65	56.83	51.89	26.74	12.83	24.21		
	HEMBA1002162	89.86	103.46	226.68	313.25	143.99	221.76	91.22	73.96	98.59		
	HEMBA1002163	40.99	33.35	79.59	79.2	53.49	69.59	30.86	22.17	36.21		
	HEMBA1002164	5.75	8.38	13.54	8.04	3.83	5.52	3.45	2.03	3.62		
15	HEMBA1002166	15.02	15.38	25.99	20.34	17.99	15.76	15	11.24	18.28		
	HEMBA1002167	11.24	16.13	23.3	10.71	13.78	13.32	12.46	7.17	15.43		
	HEMBA1002173	2.74	4.74	7.08	7.8	4.98	8.26	4.32	0.11	6.96		
	HEMBA1002177	3.19	7.92	6.73	9.46	13.68	11.32	3.6	0.89	5.89	*	+
	HEMBA1002178	3.07	3.14	5.24	4.35	5.65	4.54	2.7	1.64	3.18		
	HEMBA1002179	4.9	4.72	9.91	6.66	4.93	4.53	2.62	2.86	3.55		
20	HEMBA1002185	24.67	32.27	51.89	14.08	21.43	18.77	8.38	11.95	12.92	*	-
	HEMBA1002188	5.88	6.14	7.11	2.97	4.39	3.33	2.27	4.54	2.68	**	*
	HEMBA1002189	69.59	81.69	157.25	233.85	141.07	152.77	75.89	48.73	66.24		
	HEMBA1002191	4.08	3	7.66	6.05	7	4.24	3.01	1.76	4.2		
	HEMBA1002192	5.95	7	11.91	7.01	6.79	6.52	4.64	2.39	5.33		
25	HEMBA1002195	4.46	6.6	10.03	6.4	6.23	6.42	6.4	2.77	4.74		
	HEMBA1002196	11.48	14.42	16.69	14.62	12.56	12.05	7.65	1.78	5.06	*	-
	HEMBA1002199	17.19	29.45	44.34	8.12	15.7	10.6	4.22	6.56	8.91	*	-
	HEMBA1002204	12.36	17.29	25.36	18.54	15.65	13.06	6.95	7.55	12.67		
	HEMBA1002208	4.42	3.1	8.67	2.76	2.3	3.61	1.67	2.17	2.81		
	HEMBA1002212	8.54	9.41	18.06	5.8	6.49	9.16	8.07	6.31	7.72		
30	HEMBA1002215	3.77	4.75	11.1	3.82	3.64	4.93	3.19	2.31	3.82		
	HEMBA1002217	3.21	2.97	8.05	1.88	2.5	3.26	2.77	1.7	3.42		
	HEMBA1002220	40.07	58.29	38.41	33.44	37.1	26.5	27.12	21.87	26.71	*	-
	HEMBA1002226	3.86	6.37	9.01	5.94	8.12	6.13	6.11	1.94	2.28		
	HEMBA1002227	29.2	48.92	80.06	21.26	24.93	28.49	9.06	21.04	35.76		
	HEMBA1002229	33.53	65.16	51.1	12.99	38.46	30.19	10.92	21.02	13.32	*	-
35	HEMBA1002237	5.24	7.25	13.43	6.25	5.49	6.14	5.27	3.9	7.13		
	HEMBA1002239	4.63	2.53	7.61	2.56	2.45	2.52	2.39	1.83	5.54		
	HEMBA1002241	106.58	86.21	101.41	191.32	99.49	119.15	95.67	52.74	66.24	*	**
	HEMBA1002253	12.22	17.16	20.51	2.71	7.33	6.42	3.87	2.39	2.33	*	*
	HEMBA1002257	7.54	10.24	15.29	4.58	6.87	7.36	4.9	4.18	3.85		
	HEMBA1002259	13.5	22.26	29.8	14.68	19.62	16.23	17.99	11.27	18.91		
40	HEMBA1002262	15.09	23.24	29.3	18.72	15.42	11.55	9.03	9.95	14.69		
	HEMBA1002265	14.18	19.86	21.44	12.15	13.48	12.48	8.23	10.18	13.41	*	-
	HEMBA1002267	27.68	15.47	50.07	10.16	19.76	26.78	8.51	9.81	8.8		
	HEMBA1002270	6.74	5	13	3.57	4.76	3.79	3.06	1.88	3.1		
	HEMBA1002286	3.26	3.45	8.41	1.32	1.98	2.17	2.49	0.44	3.13		
	HEMBA1002290	13.88	14.35	29.79	17.54	14.92	16.25	8.98	7.54	11.64		
45	HEMBA1002302	2.59	3.21	9.4	1.67	2.25	2.2	2.59	2.03	2.91		
	HEMBA1002304	28.75	42.22	44.71	47.37	56.93	39.52	32.89	19.02	22.8		
	HEMBA1002307	11.61	12.1	29.02	16.8	17.62	14.8	7.63	7.75	11.14		
	HEMBA1002316	59.64	53.59	76.81	100.13	70.41	86.41	40.44	34.11	39.43	*	-
	HEMBA1002319	5.85	5.03	12.11	6.62	5.15	5.86	4.45	4.18	4.84		
	HEMBA1002320	5.15	6.41	11.19	4.43	3.26	5.68	2.72	1.07	1.82	*	*
50	HEMBA1002321	26.14	32.72	45.81	15.36	15.91	12.15	25.74	14.29	26.13	*	-
	HEMBA1002328	3.49	3.33	9.66	1.53	2.94	1.89	1.67	1.15	3.51		
	HEMBA1002333	14.03	17.53	33.87	10.39	17.53	10.54	14.85	12.2	18.17		
	HEMBA1002337	74.1	90.11	104.64	39.01	88.83	67.57	65.51	46.31	39.48	*	-
	HEMBA1002339	7.99	5.95	12.61	11.75	8.3	7.98	3.81	2.17	4.39		
	HEMBA1002341	10.07	14.65	15.74	8.32	6.89	8.79	4.57	2.09	3.76	*	**
55	HEMBA1002348	59.9	42.49	67.67	22.81	39.26	47.94	42.75	47.55	14.2		
	HEMBA1002349	3.79	4.77	8.57	3.9	2.41	2.17	3.1	1.47	1.4		
	HEMBA1002353	16.84	19.17	38.76	16.44	19.61	18.36	31.34	14.04	19.17		

Table 363

	HEMBA1002356	36	42.3	70.07	29.6	29.36	25.6	38.93	22.92	26.48			
	HEMBA1002357	5.52	13.1	13.45	6.21	11.96	5.72	6.55	2.43	6.78			
5	HEMBA1002360	7.18	14.99	31.54	16.74	12.78	10.39	10.06	6.73	9.23			
	HEMBA1002363	7.21	6.56	15.23	7.32	10.07	12.95	6.94	4.08	5.41			
	HEMBA1002365	5.13	6.37	6.27	3.06	3.21	2.92	4.54	1.5	1.04	**	*	-
	HEMBA1002370	2.68	3.2	4.12	1.48	1.53	1.16	1.82	1.08	0.59	*	*	-
	HEMBA1002374	7.98	8.73	12.15	4.74	5.3	4.18	4.71	3.04	5.14	*	*	-
	HEMBA1002376	3.93	7.64	11.22	5.3	5.08	2.77	3.34	1	2.5			
10	HEMBA1002377	9.59	9.89	16.96	5.63	7.09	6.15	6.12	1.21	4.87		*	-
	HEMBA1002380	10.33	16.4	28.08	14.11	13.73	11.4	15.31	7.9	14.99			
	HEMBA1002381	4.05	9.29	15.58	7.37	6.4	6.25	6.86	1.71	6.19			
	HEMBA1002384	8.47	11.56	16.49	7.99	8.37	10.32	10.3	5.34	12.08			
	HEMBA1002389	11.42	20.29	29.05	5.75	14.68	8.45	8.49	15.83	6.08			
15	HEMBA1002396	12.69	16.26	27.27	7.41	9.5	6.56	5.14	3.17	3.81	*		-
	HEMBA1002402	11.74	16.83	21.99	13.15	10.97	7.11	8.38	8.96	10.5			
	HEMBA1002417	16.84	19.38	28.25	14.12	13.6	10.71	18.74	11.52	12.94			
	HEMBA1002419	5.76	8.38	11.36	2.24	4.5	1.91	3.6	1.74	2.93	*	*	-
	HEMBA1002420	19.24	23.07	51.09	26.34	25.11	18.31	20.11	12.19	18.92			
	HEMBA1002421	18.39	32.76	48.68	28.36	38.24	25	28.96	7.94	14.32			
20	HEMBA1002423	22.61	32.68	44.06	7.09	7.86	5.55	4.56	5.5	6.54	*	*	-
	HEMBA1002424	10.97	10.88	26.72	15.1	10.87	9.61	12.1	6.14	11.48			
	HEMBA1002426	7.39	16.83	33.68	10.19	19.75	11.23	14.09	9.36	9.51			
	HEMBA1002430	3.4	2.99	7.25	1.05	5.01	3.49	1.89	3.82	1.55			
	HEMBA1002439	16.88	14.68	38.41	5.15	12.09	6.57	10.43	3.04	5.71			
	HEMBA1002441	6.85	11.02	20	8.08	6.54	5.94	8.36	4.52	6.62			
25	HEMBA1002454	12.57	18.57	41.83	19.84	16.12	15.91	15.68	8.28	16.15			
	HEMBA1002458	18.76	29.12	42.05	23.99	29.98	19.78	21.68	9.8	15.93			
	HEMBA1002460	17.05	22.65	60.16	30.55	31.36	38.17	25.74	12.29	25.18			
	HEMBA1002462	4.29	4.96	6.67	4.04	2.82	5.54	6.09	4.59	1.34			
	HEMBA1002465	18.46	17.14	33.42	10.69	9.15	14.44	4.41	4.25	2.08	*		-
	HEMBA1002469	5.68	18.77	19	7.83	8.55	8.09	9.48	5.61	6.29			
30	HEMBA1002475	4.8	4.95	7.67	3.53	3.61	2.82	2.16	0.66	3.66	*		-
	HEMBA1002477	14.5	19.14	47.19	10.6	19.29	17.91	11.51	6.53	9.54			
	HEMBA1002480	3.04	4.91	11.31	4.99	4.91	2.26	3.45	1.28	2.5			
	HEMBA1002481	3.73	5.8	10.36	6.68	9.38	9.35	6.55	0.82	5.73			
	HEMBA1002486	14.96	20.73	36.85	17.9	13.84	17.9	9.8	9.17	15.34			
	HEMBA1002490	32.89	43.68	75.36	48.87	29.68	38.22	19.18	16.64	20.65			
35	HEMBA1002495	43.66	58.23	82.55	111.1	32.51	41.26	76.83	29.1	14.88			
	HEMBA1002498	3.78	6.46	9.54	6.71	5.27	12.7	10.64	3.53	6.2			
	HEMBA1002501	7.77	5.26	15.06	10.61	8.44	10.8	6.66	2.76	7.39			
	HEMBA1002503	1.3	3.76	4.26	11.14	4.16	3.06	2.94	0.74	2.46			
	HEMBA1002504	11.32	6.35	15.09	5.12	7.76	6.01	3.02	1.3	4.4	*		-
	HEMBA1002508	5.06	9.32	4.01	3.71	7.02	5.17	4.27	2.18	3.39			
40	HEMBA1002513	9.71	15.43	17.71	11.5	8.94	8.42	3.65	5.7	5.29	*		-
	HEMBA1002515	22.59	29.58	33.08	19.66	17.58	7.29	3.31	4.58	5.25	**		-
	HEMBA1002524	2.52	5.5	6.81	5.24	5.07	5.47	3.51	2.04	6.31			
	HEMBA1002538	4.86	8.27	13.28	5.54	6.86	8.78	7.76	3.44	3.36			
	HEMBA1002542	14.29	22.48	34.17	23.25	22.99	20.23	26.21	13.64	24.16			
	HEMBA1002544	80.29	71.81	142.33	191.63	103.72	120.69	75.35	42.62	73.64			
45	HEMBA1002546	16.49	22.78	27.12	14.78	15.43	17.06	9.62	3.52	9.44	*		-
	HEMBA1002547	3.95	4.98	8.23	6.73	9.06	6.15	8.5	2.36	7.03			
	HEMBA1002550	49.15	78.71	90.52	40.75	20.92	26.29	11.49	22.91	24.84	*	*	-
	HEMBA1002551	21.39	26.41	43.07	27.63	15.98	20.86	15.81	13.41	19.29			
	HEMBA1002552	2.51	5.57	9.92	2.51	4.26	4.71	1.72	3.19	4.1			
	HEMBA1002555	22.2	20.07	42.05	23.19	22.23	22.76	15.94	12.91	13.98			
50	HEMBA1002558	12.09	15.97	19.47	12.44	11.51	11.85	16.99	12.78	19.34			
	HEMBA1002561	5.12	5.08	10.95	9.59	4.94	7.59	3.52	2.9	5.93			
	HEMBA1002562	11.02	16.11	24.74	19.26	26.78	27.85	11.51	7.07	19.83			
	HEMBA1002568	196.94	317.85	248.99	300.72	297.51	250.18	199.37	60.64	136.04			
	HEMBA1002569	23.5	41.31	56.08	12.56	22.81	12.46	7.29	13.02	18.03			
	HEMBA1002570	30.8	40.14	52.73	26.65	25.92	32.98	19.03	21.81	22.76	*		-
55	HEMBA1002574	18.81	26.29	36.64	14.11	18.09	18.3	12.06	11.37	15.9			
	HEMBA1002583	7.94	6.71	16.38	5.31	5.66	5.07	2.73	4.44	3.12			
	HEMBA1002587	2.94	4.41	12.22	7.72	5.53	9.69	4.6	2.49	5.42			



Table 364

	HEMBA1002590	5.95	11.3	17.91	3.86	9.68	7.63	4.92	3.2	3.29			
	HEMBA1002592	24.56	35.63	62.38	31.85	31.39	28.3	31.44	17.58	25.5			
5	HEMBA1002595	18.13	24.94	28.1	20.67	22.43	16.85	23.31	9.38	10.88			
	HEMBA1002609	10.62	12.63	20.23	14.42	14.63	14.25	5.32	5.93	14.35			
	HEMBA1002617	4.27	5.73	7.4	1.57	2.4	3.96	1.42	3.15	4.02			
	HEMBA1002619	2.85	2.62	7.5	3.1	2.95	3.67	1.94	0.73	2.61			
	HEMBA1002621	8.59	8.17	23.61	10.11	9.98	16.3	7.86	5.98	9.09			
10	HEMBA1002624	27.35	35.73	38.2	18.75	33.76	30.42	15.63	13.42	13.94	**	-	
	HEMBA1002628	9.91	18.29	22.67	1.48	9.73	6.58	2.84	2.68	1.86	*	-	
	HEMBA1002629	17.6	28.89	36.07	15.14	20.64	15.47	19.33	12.69	24.63	*	-	
	HEMBA1002632	12.9	25.94	21.19	10.8	16.54	18.64	7.96	5.15	6.22			
	HEMBA1002645	10.16	17.89	28.87	12.29	14.08	14.33	9.35	8.1	11.96			
	HEMBA1002651	13.26	18.44	26.72	15.43	10.74	15.26	12.68	8.84	17.98			
15	HEMBA1002652	38.73	48.42	65.53	46.16	37.25	33.78	28.26	20.1	36.36			
	HEMBA1002659	9.03	11.88	19.16	8.75	10.05	12.88	11.02	6.8	9.75			
	HEMBA1002661	5.06	3.99	9.25	2.67	2.42	2.71	2.5	0.54	3.81			
	HEMBA1002666	4.98	2.76	10.31	1.02	2.15	2.47	1.95	1.39	2.97			
	HEMBA1002667	66.26	92.17	95.25	40.2	49.75	38.64	17.08	15.46	18.87	*	**	-
	HEMBA1002673	10.24	11.61	24.1	10.91	20.39	11.76	14.29	6.19	10.4			
20	HEMBA1002678	13.62	19.9	33.62	20.45	17.4	13.57	11.46	10.78	12.98			
	HEMBA1002679	13.69	14.71	16.04	4.7	9.65	9.85	3.39	2.88	4.57	*	**	-
	HEMBA1002688	5.6	5.12	9.48	4.59	5.44	5.04	4.69	4.1	9.84			
	HEMBA1002696	59.06	73.44	43.41	32.21	38.96	30.65	22.83	22.73	43.71			
	HEMBA1002703	7.17	12.58	16.11	7.07	6.09	6.51	6.44	2.28	5.09			
	HEMBA1002706	6.13	6.22	16.32	2.59	4.89	3.24	4.44	2.11	3.85			
25	HEMBA1002712	11.08	15.22	21.38	7.53	9.92	6.72	6.23	2.15	5.09	*	-	
	HEMBA1002715	7.25	9.24	15.63	3.34	13.16	4.85	8.59	3.19	5.46			
	HEMBA1002716	10.24	5.79	8.57	7.72	6.63	11.75	6.68	8.82	8.25			
	HEMBA1002718	5.54	9.62	8.18	5.1	4.05	3.87	4.38	2.74	1.77	*	-	
	HEMBA1002728	12.44	14.25	13.51	6.78	9.73	5.54	5.16	3.78	4.32	*	**	-
	HEMBA1002730	18.89	21.85	36.97	19.48	14.69	13.56	21.24	13.64	21.33			
30	HEMBA1002734	18.2	30.15	26.54	25.61	18.78	20.96	17.72	11.44	17.14			
	HEMBA1002742	3.87	2.34	11.09	2.03	2.86	2.81	1.76	0.66	1.41			
	HEMBA1002746	22.55	32.65	52.23	26.89	25.86	22.2	22.76	13.04	18.94			
	HEMBA1002748	9.65	15.62	22.06	9.53	12.94	6.47	8.64	2.48	4.44			
	HEMBA1002750	4.66	4.65	9.25	7.27	4.67	4.79	3.27	2.62	3.14			
	HEMBA1002755	6.97	7.74	9.25	6.37	7.77	4.16	3.95	4.22	4.36	**	-	
35	HEMBA1002759	16.7	17.27	27.62	16.79	11.68	13.5	9.91	9.05	10.68	*	-	
	HEMBA1002763	47.58	57.94	56.78	54.23	36.74	38.37	36.64	19.12	21.65	*	-	
	HEMBA1002767	8.72	14.41	17.03	5.04	11.17	4.96	8.31	3.05	8.44			
	HEMBA1002768	5.52	5.94	12.79	2.88	4.3	2.49	2.51	1.17	1.65			
	HEMBA1002769	17.19	27.21	15.86	8.55	10.93	3.03	6.22	1.99	5.25	*	*	-
	HEMBA1002770	2.13	4.12	10.85	3.83	4.73	3.88	2.44	1.5	3.81			
40	HEMBA1002777	6.28	5.97	10	5.84	6.03	4.58	3.3	3.36	7.09			
	HEMBA1002779	4.32	3.05	9.05	3.43	3.09	3.54	2.97	2.09	4.26			
	HEMBA1002780	18.15	7.73	29.43	3.93	22.04	8.61	11.74	14.31	4.26			
	HEMBA1002790	44.22	50.48	73.09	31.77	35.83	33.38	43.74	34.78	30.04			
	HEMBA1002794	7.76	9.01	14.22	4.88	6.33	4.1	3.98	2.38	3.09	*	-	
	HEMBA1002798	58.19	53	86.62	94.91	76.86	71.68	49.35	25.85	43.83			
45	HEMBA1002801	3.51	8.44	16.4	3.59	4.66	6.72	3.9	1.17	4.1			
	HEMBA1002810	3.05	9.57	15.59	8.92	5.81	6.43	5.04	3.55	5.63			
	HEMBA1002816	33.54	55.39	45.57	5.42	16.08	37.06	10.38	10.74	17.79	**	-	
	HEMBA1002818	13.01	14.09	20.64	7.78	6.78	5.49	5.04	2.96	3.82	*	**	-
	HEMBA1002820	27.01	29.21	56.88	35.9	30.38	30.6	30.02	21.79	27.81			
	HEMBA1002826	19.2	24.63	59.75	28.13	24.2	21.9	24.8	13.89	24.13			
50	HEMBA1002833	63.25	54.77	137.72	30.62	26.06	40.67	37.5	33.73	24.96			
	HEMBA1002850	32.24	50.44	106.97	13.72	14.84	20.17	21.65	20.43	7.04			
	HEMBA1002862	2.91	4.02	13.2	2.77	4.61	2.19	2.67	1.11	1.52			
	HEMBA1002863	5.54	4.99	10.17	2.83	5.36	5.71	5.41	0.6	2.81			
	HEMBA1002867	12.64	16.67	40.23	22.98	17.46	25	12.79	7.67	12.96			
	HEMBA1002876	33.33	40.68	56.24	16.95	25.21	41.71	19.36	18.11	7.35	*	-	
55	HEMBA1002886	38.07	46.59	100.23	134.31	130.1	87.32	31.47	23.92	40.5			
	HEMBA1002896	373.7	87.77	442.56	153.27	289.24	233.48	153.73	231.71	129.4			
	HEMBA1002913	5.91	13.06	17.5	7.91	16.67	18.64	16.24	3.53	12.2			

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	HEMBA1002921	10.08	17.69	26.78	4.57	11.52	17.13	10.57	6.89	8.36			
	HEMBA1002924	16.52	23.06	41.44	17.55	21.51	18.51	16.69	6.29	12.01			
5	HEMBA1002934	7.43	7.93	15.24	8.33	19.71	10.41	9.2	4.34	7.83			
	HEMBA1002935	44.38	58.85	52.49	15.89	32.69	26.1	15.32	13.88	12.84	*	**	-
	HEMBA1002937	2.13	5.21	6.49	6.16	3.25	2.49	3.22	1.79	2.68			
	HEMBA1002939	6.4	9.23	9.9	6.39	7.51	3.18	2.69	1.8	1.53		**	-
	HEMBA1002944	6.74	7.31	12.98	7.18	6.53	7.34	7.96	2.7	9.59			
10	HEMBA1002951	2.29	3.34	4.29	3.26	3.2	3.99	3	1.79	2.41			
	HEMBA1002954	17.42	19.44	25.7	12.87	16.68	13.48	13.76	7.82	14.9			
	HEMBA1002962	8.79	11.09	12.46	11.77	11.02	6.43	11.04	6.23	10.79			
	HEMBA1002968	7.03	12.43	15.52	4.99	4.92	6.17	4.89	4.54	3.33	*		-
	HEMBA1002970	3.97	3.94	8.85	9.45	5.39	4.2	3.04	1.94	3.66			
	HEMBA1002971	46.35	65.62	65.66	55.83	32.32	29.43	18.21	22.18	16.03		**	-
15	HEMBA1002973	19.1	22.88	32.02	18.54	14.79	14.79	14.19	10.32	16.42			
	HEMBA1002978	9.61	14.49	12.56	9.49	10.35	10.49	8.97	6.63	9.32			
	HEMBA1002981	7.62	7.65	10.48	7.25	7.54	7.91	5.93	4.75	6.33			
	HEMBA1002985	117.94	141.29	115.79	100.57	91.73	67.47	36.07	32.99	67.86	*	**	-
	HEMBA1002986	1.09	4.19	2.41	1.9	4.92	2.49	2.41	1.95	2.68			
	HEMBA1002988	6.76	12.45	10.76	6.53	13.58	5.88	8.35	4.66	5.88			
20	HEMBA1002992	6.35	10.06	11.88	10.23	8.86	4.79	4.31	25.89	6.31			
	HEMBA1002995	4.3	8.89	7.73	5.51	4.55	4.85	3.59	3.01	4.66			
	HEMBA1002997	107.63	114.87	183.64	177.35	156.59	181.54	82.75	91.36	112.69			
	HEMBA1002999	53.34	68.01	72.24	37.39	47.67	41.25	62.98	43.59	63.81	*		-
	HEMBA1003004	3.64	4.33	7.42	2.58	3.67	3.65	3	1.57	3.06			
	HEMBA1003006	4.28	5.05	7.7	1.79	6.77	4.05	4.37	2.61	3.52			
25	HEMBA1003008	27.15	36.55	38.8	26.92	32.63	23.56	33.58	25.15	30.26			
	HEMBA1003021	5.81	12.5	13.45	11.13	6.12	5.84	7.32	6.94	6.02			
	HEMBA1003027	18.79	26.5	31.66	21.25	18.71	19.18	16.11	14.87	19.02			
	HEMBA1003029	19.01	29.05	31.26	23.38	17.83	18.43	16.34	15.3	19.09			
	HEMBA1003031	23.27	32.76	35.52	18.12	20.06	19.05	22.57	22.89	27.58	*		-
	HEMBA1003032	10.51	18.48	23.57	10.46	10.87	8.93	13.71	10.94	13.4			
30	HEMBA1003033	3.28	3.5	9.21	2.58	2.99	3.45	2.32	2.32	3.69			
	HEMBA1003034	32.22	43.17	44.46	25.3	23.69	20.88	30.34	23.98	27.83	*	*	-
	HEMBA1003035	6.89	6.34	9.49	7.01	5.99	4.57	6.73	1.95	2.1			
	HEMBA1003037	3.15	4.76	8.43	6.95	3.5	6.33	1.17	2.19	4.48			
	HEMBA1003041	5.81	4.77	6.88	6.46	7.11	3.98	3.65	3.49	6.68			
	HEMBA1003046	3.59	5.57	7.67	2.55	3.97	2.74	1.99	1	3.62			
35	HEMBA1003047	2.75	3.6	7.28	2.24	3.39	2.22	1.7	2.72	4.34			
	HEMBA1003048	7.72	9.91	17.38	5.16	6.98	5.24	7.18	5.24	6.81			
	HEMBA1003064	7.42	7.15	11.39	6.45	5.86	2.65	4.01	3.53	5.26	*		-
	HEMBA1003067	3.5	4.14	10.69	1.88	3.75	2.7	1.84	2.09	2.56			
	HEMBA1003071	4.3	6.5	8.99	2.07	3.4	1.57	3.49	0.09	2.65	*		-
	HEMBA1003072	22.65	30.56	72.67	40.85	32.84	36.51	17.64	22.4	33.19			
40	HEMBA1003076	10.41	7.13	12.54	12.87	5.59	14.57	5.56	3.38	7.99			
	HEMBA1003077	57.77	42.56	38.04	15.22	22.46	42.9	9.06	21.41	25.7	*		-
	HEMBA1003078	5.9	3.99	8.44	5.05	5.47	3.08	3.19	1.13	4			
	HEMBA1003079	2.67	1.28	11.95	1.19	1.44	0	1.26	1.15	2.5			
	HEMBA1003083	17.29	19.57	26.48	12.28	16.41	11.4	17.96	11.77	14.23			
	HEMBA1003086	66.37	81.42	75.05	81.77	61.06	81.5	45.88	45.17	41.59	**		-
45	HEMBA1003090	27.88	31.13	33.36	17.15	38.66	20.27	13.44	24.06	7.13	*		-
	HEMBA1003094	7.62	15.14	35.58	19.46	14.45	10.58	6.94	6.32	13.5			
	HEMBA1003096	5.15	5.97	7.99	4.67	5.25	3.62	2.44	1.23	5.06			
	HEMBA1003098	51.24	56.94	73.88	44.19	37.83	35.41	49.21	42.96	49.32	*		-
	HEMBA1003101	55.72	62.33	39.5	28.21	27.13	36.8	19.35	33.07	15.18	*	*	-
	HEMBA1003109	21.19	29.16	38.82	18.38	20.48	14.86	17.89	17.36	21.07			
50	HEMBA1003114	16.2	22.18	27.85	11.32	13.05	11.32	15.03	12.24	12.98	*		-
	HEMBA1003117	4.55	5.29	16.23	3.16	6.98	2.06	3.55	1.47	2.05			
	HEMBA1003120	26.44	23.65	42.74	11.15	27.45	17.66	13.62	6.31	12.11	*		-
	HEMBA1003129	13.18	14.01	38.23	23.62	19.83	17.41	9	7.3	18.68			
	HEMBA1003133	18.25	22.53	34.22	24.55	19.61	15.34	21.94	16.17	21.16			
	HEMBA1003136	16.39	19.51	25.59	18.11	18.16	15.75	14.64	13.22	14.96			
55	HEMBA1003142	14.56	16.27	15.48	9.65	8.16	8.79	8.14	5.26	6.82	**	**	-
	HEMBA1003148	16.81	26.84	29.42	16.45	15.92	11.14	21.43	11.51	11.59			
	HEMBA1003151	8.82	10.43	18.65	5.42	8.75	3.56	10.89	7.34	8.14			

Table 366

	HEMBA1003152	4.25	6.9	16.54	3.43	9.18	3.49	6.82	2.75	2.37			
	HEMBA1003157	16.47	20.65	36.14	14.57	15.21	12.8	18.89	12.37	10.25			
5	HEMBA1003166	6.07	8.14	15.45	9.26	7.78	7.15	6.88	3	7.14			
	HEMBA1003171	4.76	6.01	1.83	0.22	9.4	0.95	4.99	3.3	4.74			
	HEMBA1003175	9.06	9.36	15.39	5.94	5.41	4.09	8.31	5.54	6.76	*	-	
	HEMBA1003179	11.74	19.14	23.08	11.43	19.69	16.88	15.24	11.13	8.75			
	HEMBA1003186	32.34	34.21	53.13	30.02	30.6	23.62	32.72	27.67	23.79			
10	HEMBA1003196	4.93	5.75	11.29	1.52	4.36	1.61	2.88	1.66	1.27			
	HEMBA1003197	11.79	16.34	26.33	10.88	17.37	11.43	13.65	9.71	13.56			
	HEMBA1003199	23.1	49.93	40.51	25.63	28.94	20.25	30.98	8.01	23.38			
	HEMBA1003202	23.9	28.7	33.49	4.92	13.85	16.67	6.88	7.46	15.28	*	**	- -
	HEMBA1003204	4.47	10.56	14.07	5.38	6.97	3.66	4.1	2.93	5.45			
	HEMBA1003210	26.93	30.85	39.03	16.12	18.97	10.78	20.75	18.2	19.07	*	*	- -
15	HEMBA1003212	25.47	38.89	40.06	19.34	20.63	15.78	34.72	24.84	21.07	*	-	
	HEMBA1003218	4.32	4.85	11.19	2.63	4.58	1.07	3.74	6.58	2.3			
	HEMBA1003220	35.02	49.9	56.61	20.36	27.56	20.54	37.25	33.59	30.02	*	-	
	HEMBA1003222	6.38	11.47	27.57	6.14	9.88	5.85	9.63	5.71	6.41			
	HEMBA1003225	1.99	5.89	11.4	3.67	2.98	2	2.78	0.36	1.82			
	HEMBA1003229	4.11	5.35	10.53	5.06	6.91	5.05	3.62	3.37	4.28			
20	HEMBA1003230	19	22.89	41.86	21.05	18.18	18.78	15.9	9.68	15.54			
	HEMBA1003235	6.36	6.82	18.89	3.6	5.78	3.31	5.14	2.94	2.76			
	HEMBA1003236	28.57	38.02	51.11	22.25	24.92	17.63	25.41	23	19.94			
	HEMBA1003250	3.88	5.03	10.29	3.12	4.49	3.35	3.78	2.8	3.87			
	HEMBA1003252	10.38	11.26	18.86	6.09	9.53	8.62	8.03	4.87	3.9			
	HEMBA1003257	4.81	5.23	14.11	3.29	4.4	2.15	4.08	0.86	2.62			
25	HEMBA1003268	4.15	9.87	10.08	10.51	3.68	3.28	8.7	2.22	2.32			
	HEMBA1003273	11.8	16.03	28.72	15.07	19.11	17.4	12.91	12.48	21.18			
	HEMBA1003276	149.48	149.2	143.91	64.58	44.3	74.17	103.96	79.83	39.01	**	*	- -
	HEMBA1003277	46.25	23.14	67.56	22.07	19.01	38.9	14.72	11.37	3.34			
	HEMBA1003278	4.71	4.24	12.6	4.3	4.28	2.48	2.75	2.48	1.06			
	HEMBA1003280	129.77	109.77	149.42	22.66	42.91	45.72	29.75	44.29	19.43	**	**	- -
30	HEMBA1003281	66.35	33.44	113.06	20.36	31.97	38.12	40.97	35.41	13.12			
	HEMBA1003284	4.17	19.37	13.16	7.85	6.12	2.69	7.14	1.71	3.34			
	HEMBA1003286	19.63	12.62	36.72	8.93	14.12	12.7	52.4	15.77	36.62			
	HEMBA1003291	72.44	65.02	121.3	168.07	81.81	87.09	38.11	45.46	43.73			
	HEMBA1003294	2.81	2.31	6.5	6.68	2.5	2.72	2.16	1.36	1.58			
	HEMBA1003296	44.35	42.6	76.86	89.38	53.17	64.95	32.4	28.59	38.37			
35	HEMBA1003304	9.89	11.83	11.34	8.37	7.94	10.02	7.8	7.09	8.26	**	-	
	HEMBA1003306	13.02	19.68	19.63	24.93	17.19	18.48	10.47	8.08	13.83			
	HEMBA1003309	1.78	3.09	6.44	4.38	2.65	4.86	2.49	0.95	2.26			
	HEMBA1003314	2.38	3.32	2.13	4.26	4.38	3.35	2.15	1.3	2.04	*	+	-
	HEMBA1003315	4.7	9	9.09	4.13	2.95	4.64	2.23	3.29	3.07	*	*	-
	HEMBA1003322	21.51	21.29	36.71	38.62	23.41	31.81	14.65	15.44	16.23			
40	HEMBA1003326	6.02	5.69	11.31	6.59	5.79	5.51	2.11	1.05	2.65	*	-	
	HEMBA1003327	7.54	6.06	15.43	8.47	7.53	8.8	4.99	4.52	3.75			
	HEMBA1003328	105.65	106.38	147.91	165.04	127.51	111.83	74.7	76.39	78.34	*	-	
	HEMBA1003330	6.01	12.33	12.91	7.65	8.96	7.41	6.19	2.7	6.56			
	HEMBA1003348	3.04	4.46	6.33	4.48	9.58	12.27	5.11	0.11	2.09			
	HEMBA1003369	4.61	6.54	9.12	7.83	6.84	2.91	5.15	1.7	5.2			
45	HEMBA1003370	3.59	5.98	8.58	5.67	3.43	4.27	2.86	5.19	3.68			
	HEMBA1003373	11.8	17.95	18.19	5.05	9.3	7.7	3.82	6.22	4.16	*	**	- -
	HEMBA1003376	3.97	3.38	4.86	3.82	1.97	2.14	1.54	0.79	1.25	**	-	
	HEMBA1003380	1.93	2.67	5.1	1.31	0.26	1.37	0.83	1.72	0.69			
	HEMBA1003384	26.49	38.34	57.87	29.22	29.1	27.24	18.27	17.42	21.24			
	HEMBA1003387	16.13	19.1	24.1	17.73	14.37	13.92	9.34	7.52	11.3	*	-	
50	HEMBA1003392	2.68	3.97	8.74	2.76	4.49	2.32	2.44	0.39	3.04			
	HEMBA1003395	2.69	3.42	9.32	1.54	4.93	3.86	3.02	1.02	1.64			
	HEMBA1003399	20.63	29.8	52.54	29.45	22.45	24.07	12.86	13.2	21.21			
	HEMBA1003400	3.56	5.58	6.33	3.88	4.46	4.23	1.87	2.25	1.87	*	-	
	HEMBA1003402	38.86	90.8	85.59	22.6	36.87	47.3	19.41	16.83	28.09	*	-	
	HEMBA1003403	4.18	3.19	7.45	2.51	2.47	2.16	1.4	2.51	3.27			
55	HEMBA1003408	25.83	33.63	38.04	42.18	33.38	41.52	23.7	19.86	28.4			
	HEMBA1003412	5.21	6.25	13.71	2.82	5	4.22	2.53	1.53	2.45			
	HEMBA1003417	21.02	35.52	34.24	13.8	14.17	10.79	5.28	6.88	9.43	*	**	- -

Table 367

	HEMBA1003418	9.46	10.25	16.29	13.88	11.67	7.88	6.52	7.48	6.95		
5	HEMBA1003420	15.13	21.37	34.54	8.98	7.12	8.99	3.93	4.32	8.36	*	-
	HEMBA1003425	3.65	4.02	7.55	3.03	3.24	2.46	1.29	1.12	2.83		
	HEMBA1003433	12.41	15.45	35.09	18.37	16.85	15.26	10.85	5.12	17.58		
	HEMBA1003440	22.95	34.38	33.51	20.78	28.45	21.36	23.78	22.34	28.46		
	HEMBA1003442	12.86	16.85	24.45	11.09	13.33	10.29	12.08	9.47	11.31		
	HEMBA1003447	27.49	33.89	33.23	17.4	23.73	18.49	24	17.15	19.81	*	*
10	HEMBA1003453	4.92	6.64	13.34	4.01	5.69	5.13	2.36	4.48	3.86		
	HEMBA1003461	31.42	55.4	52.29	25.16	39.67	29.85	35.26	26.74	37.73		
	HEMBA1003463	20.03	30.11	90.85	47.21	1.41	0.3	30.58	24.08	33.93		
	HEMBA1003465	4.42	6.66	9.68	7.8	5.17	6.44	3.4	2.84	6.1		
	HEMBA1003480	8.18	9.01	15.32	7.58	7.38	7.85	10.22	6.26	8.1		
	HEMBA1003485	8.87	6.95	9.95	4.15	3.42	4.03	5.45	1.61	3.1	**	*
15	HEMBA1003487	40.56	64.18	72.24	34.53	33.37	41.02	45.43	44.42	46.48		
	HEMBA1003492	47.07	69.63	47.91	15.87	60.76	43.2	54.01	24.37	34.94		
	HEMBA1003494	8.97	13.82	17.09	5.4	7.03	7.86	9.14	5.83	9.54		
	HEMBA1003497	27.59	34.3	36.93	14.93	24.2	20.37	27.68	19.83	25.35	*	-
	HEMBA1003503	17.58	24.95	1.06	0.82	1.26	0.04	6.53	10.32	21.23		
20	HEMBA1003511	10.13	12.6	23.58	12.03	11.2	10.45	9.65	8.73	14.36		
	HEMBA1003528	10.75	13.6	9.55	5.22	4.34	5.54	2.88	3.04	2.97	**	**
	HEMBA1003530	6.02	6.59	12.41	4.68	4.85	4.75	5.24	2.55	3.96		
	HEMBA1003531	12.73	22.2	30.65	9.86	14.37	9.03	13.96	8.06	18.14		
	HEMBA1003532	13.65	14.91	22.65	9.4	21.22	7.2	8.43	8.83	11.91		
	HEMBA1003538	10.23	12.68	27.62	8.9	13.63	10.34	9.68	5.53	8.3		
	HEMBA1003545	4.35	9.29	13.49	7.12	6.86	6.1	7.44	2.65	6.35		
25	HEMBA1003546	6.53	3.47	17.38	20.26	8.26	12.59	2.96	5.15	4.61		
	HEMBA1003548	2.71	6.58	8.78	3.2	9.19	3.14	6.24	4.03	2.98		
	HEMBA1003553	4	4.81	7.29	3.53	3.84	2.73	2.82	2.01	2.64	*	-
	HEMBA1003555	8.02	14.32	16.54	7.4	9.1	7.1	7.78	7.09	7.03		
	HEMBA1003556	5	8.35	8.92	2.85	4.91	3.37	2.9	2.25	2.94	*	-
	HEMBA1003560	11.54	14.47	20.06	8.38	13.16	7.52	7.48	5.19	5.3	*	-
30	HEMBA1003565	12.47	6.48	14.4	4.78	7.63	5.19	7.77	3.47	4.1		
	HEMBA1003568	167.82	373.84	257.14	82.85	193.26	96.08	64.68	26.85	13.07	*	-
	HEMBA1003569	19.02	23.29	63.64	40.15	29.03	28.36	20	16.6	26.95		
	HEMBA1003571	8.12	11.43	9.83	5.26	10.52	5.78	8.95	5.27	5.01		
	HEMBA1003579	22.13	20.38	39.63	17.94	15.09	12.56	17.53	15.68	17.94		
	HEMBA1003580	18.63	22.77	31.1	30.35	20	21.57	12.72	8.11	11.25	*	-
35	HEMBA1003581	4.54	7.44	11.51	2.94	2.83	4.01	3.4	1.33	1.8		
	HEMBA1003591	9.77	30.24	25.57	6.75	16.55	5.72	11.87	5.17	9.69		
	HEMBA1003595	11.6	18.67	39.48	13.28	20.4	12.94	13.52	5.6	8.35		
	HEMBA1003597	34.44	63.26	65.19	37.08	35.21	30.06	23.33	8.38	16.41	*	-
	HEMBA1003598	2.25	2.74	3.02	2.41	2.07	1.24	1.39	0.6	1.38	*	-
	HEMBA1003600	21.91	26.66	48.26	21.72	21.86	19.48	19.9	18.88	27.46		
40	HEMBA1003602	5.44	4.97	13.36	4.53	6.21	5.48	3.61	3.19	3.61		
	HEMBA1003604	4.52	2.99	9.05	3.91	3.29	1.56	2.58	2.5	3.04		
	HEMBA1003610	13.16	15.85	27.61	10.3	9.81	5.68	10.32	8.77	8.07		
	HEMBA1003615	14.12	19.51	37.31	8.32	15.31	10.64	25.53	7.2	9.53		
	HEMBA1003617	2.15	10.76	12.38	1.63	5.11	1.57	4.87	0.26	2.23		
	HEMBA1003620	1.75	4.53	12.78	1.34	3.78	1.52	1.5	0.27	0.68		
45	HEMBA1003621	12.05	16.03	37.29	21.96	16.06	15.37	10.98	5.36	14.36		
	HEMBA1003622	7.66	5.59	10	3.27	5.47	4.78	6.97	4.55	2.99		
	HEMBA1003630	43.11	47.17	86.26	32.33	46.01	44.24	29.63	21.05	20.55		
	HEMBA1003637	920.66	472.86	680.3	365.52	904.5	411.7	621.11	976.32	238.58		
	HEMBA1003640	62.65	69.86	125.99	45.58	48.68	42	65.31	45.48	45.21		
	HEMBA1003645	15.97	22.75	34.7	19.9	17.55	14.87	21.4	9.64	18.1		
50	HEMBA1003646	6.76	13.27	28.86	11.35	10.28	4.41	12.2	6.62	10.03		
	HEMBA1003647	68.54	91.82	142.01	91.35	74.78	80.66	83.06	37.92	60.33		
	HEMBA1003656	41.62	46.94	78.5	39.66	28.08	37.31	18.6	12.53	17.55	*	-
	HEMBA1003662	9.43	10.68	20.41	19.54	13.98	13.03	9.65	4.93	11.88		
	HEMBA1003666	8.44	8.9	21.02	18.11	19.64	14.87	11.75	6.74	12.93		
	HEMBA1003667	27	32.49	46.33	29.7	40.13	34.43	25.82	21.77	25.87		
55	HEMBA1003670	16.71	15.12	35.71	10.11	19.12	14.79	10.97	18.94	10.06		
	HEMBA1003674	3.06	3.93	11.38	12.14	7.69	5.61	4.08	1.48	5.42		
	HEMBA1003677	3.62	4.3	9.92	2.94	5.26	2.08	4.03	0.72	1.84		

Table 368

	HEMBA1003679	15.99	25.43	34.72	23.29	23.03	14.07	32.67	15.26	20.68			
	HEMBA1003680	2.36	1.32	3.39	2.39	1.66	4.26	2	1.23	1.59			
5	HEMBA1003684	27.44	32.04	37.17	24.58	15.64	21.48	12.03	9.61	13.69	*	**	-
	HEMBA1003690	26.36	32.22	54.74	28.94	29.04	32.33	34.36	26.69	39.53			
	HEMBA1003692	6.49	10.11	9.34	7.04	5.15	6.04	7.51	6.23	5.84			
	HEMBA1003702	8.56	9.3	12.43	12.4	14.68	13.17	6.17	5.02	7.69			
	HEMBA1003711	8.11	10.45	15.16	11.96	9.29	6.3	7.03	5.46	7.91			
	HEMBA1003714	6.44	11.03	12.83	2.97	13.46	9.98	7.86	7.19	9.67			
10	HEMBA1003715	14.81	13.59	14.56	12.43	13.78	10.5	10.14	8.94	12.29	*		-
	HEMBA1003717	42.45	55.77	82.27	41.74	41.39	40.14	43.46	40.44	41.87			
	HEMBA1003720	6.21	6.28	13.24	9.93	12.72	5.69	6.86	5.05	6.12			
	HEMBA1003725	3.95	3.77	7.26	6.08	3.65	3.36	2.76	2.23	2.52			
	HEMBA1003728	4.28	12.26	8.88	10.99	2.88	4.38	6.4	1.69	3.67			
	HEMBA1003729	12.13	13.18	16.13	8.92	13.67	11.13	18.08	6.56	14.8			
15	HEMBA1003732	30.17	53.31	40.17	33.85	38.01	30.07	19.05	11.75	17.73	*		-
	HEMBA1003733	3.45	4.52	4.35	2.89	6.7	2.94	3.18	1.76	2.64	*		-
	HEMBA1003742	9.01	9.99	10.98	9.56	10.71	5.69	9.3	5.6	9.68			
	HEMBA1003743	9.87	14.77	20.42	19.53	13.74	11.37	9.02	7.5	9.36			
	HEMBA1003758	14.27	20.31	26.23	15.6	15.1	13.01	12.22	13.09	13.08			
20	HEMBA1003760	19.21	17.1	29.51	6.01	14.54	12.36	3.4	6.9	5.12	*		-
	HEMBA1003764	14.01	17.88	25.76	13.37	20.5	16.53	15.36	15.5	19.31			
	HEMBA1003769	38.51	54.43	53.66	30.93	34.09	32.37	42.08	31.8	46.8	*		-
	HEMBA1003773	6.19	9.28	8.37	4.69	7.62	4.92	2.95	1.6	4.58	*		-
	HEMBA1003783	2.33	2.73	7.18	6	7.98	9.31	5.24	2.04	3.66			
	HEMBA1003784	24.68	20.11	23.17	22.69	20.46	14.65	16.36	8.3	11.94	*		-
	HEMBA1003794	35.77	59.53	74.01	32.36	32.73	29.52	23.99	30.47	35.64			
25	HEMBA1003799	28.51	43.08	44.43	24.39	25.46	22.11	20.76	21.74	26.31	*	*	-
	HEMBA1003803	6.9	7.98	12.5	2.71	3.98	5.61	1.91	2.94	2.14	*		-
	HEMBA1003804	12.17	15.5	24.58	5.01	10.25	5.91	7.51	11.06	8.61			
	HEMBA1003805	15.63	21.11	29.95	13.7	15.15	11.89	15.1	12.06	15.76			
	HEMBA1003807	12.24	15.49	18.72	15.37	14.25	10.11	18.36	12.3	19.08			
30	HEMBA1003810	4.78	6.92	11.21	4.53	9.91	7.45	6.79	2.53	4.42			
	HEMBA1003827	10.51	13.97	18.38	12.97	15	8.61	18.16	7.58	9.11			
	HEMBA1003836	4.91	7.17	10.85	4.73	8.8	6.53	3.27	4.61	5.48			
	HEMBA1003838	48.74	66.87	76.01	40.91	58.53	48.34	31.6	26.6	30.51	*		-
	HEMBA1003843	23.09	39.55	55.11	24.97	26.61	27.21	27.17	12.95	30.84			
	HEMBA1003846	18.74	19.56	28.45	26.4	19.75	21.25	14.77	12.94	15.9			
35	HEMBA1003856	31.17	48.34	48.82	28.74	30.87	25.87	49.83	42.07	42.91			
	HEMBA1003857	3.66	4.84	10.52	2.38	4.43	1.85	3.66	2.4	2.28			
	HEMBA1003864	24.35	38.16	29.59	24.03	32.07	18.61	15.17	4.79	6.89	*		-
	HEMBA1003866	15.55	24.7	24.92	21.6	24.17	13.88	22.15	14.95	14.16			
	HEMBA1003868	3.42	4.24	4.55	5.4	4.56	2.52	1.88	2.32	3.07	*		-
	HEMBA1003879	54.55	71.41	99.07	52.85	60.23	59.91	38.15	32.08	50.85			
40	HEMBA1003880	26.75	40.67	50.47	32.31	30.57	23.71	28.74	17.94	31.69			
	HEMBA1003884	3.51	2.7	10.4	2.34	3.19	1.65	5.36	1.65	2.02			
	HEMBA1003885	15.83	16.07	23.65	9.67	12.61	9.91	13.22	10.04	13.72	*		-
	HEMBA1003887	8.92	10.53	15.63	3.65	12.51	2.64	7.43	4.94	3.2			
	HEMBA1003890	5.77	11.6	13.5	3.76	5.14	4.95	4.38	2.51	3.42	*		-
	HEMBA1003893	2.5	2.24	6.97	3.71	6.34	3.91	2.06	0.55	2.76			
45	HEMBA1003896	13.16	13.74	38.07	17.77	20.7	14.83	10.45	11	13.75			
	HEMBA1003902	6.09	5.71	13.87	4.58	5.68	4.39	3.52	2.56	5.08			
	HEMBA1003904	41	55.7	67.32	43.67	30.73	35.35	31.08	26.57	32.22	*		-
	HEMBA1003908	27.42	42.25	49.6	27.37	22.92	19.91	28.26	21.38	25.22			
	HEMBA1003926	35.54	56.96	89.19	56.48	59.31	44	48.79	37.72	50.83			
	HEMBA1003937	14.37	14.68	20.38	10.43	17.34	12.15	14.47	8.13	15.59			
50	HEMBA1003939	3.4	3.02	10.99	1.88	5.36	0.25	1.12	0.35	2.25			
	HEMBA1003940	6.76	11.65	10.45	4.59	10.56	5.86	9.9	2.16	3.94			
	HEMBA1003941	31.48	46.87	93.42	56.75	59.75	51.31	23.68	24.05	38.11			
	HEMBA1003942	3.19	4.4	9.44	4.64	4.07	4.72	1.95	2.11	3.24			
	HEMBA1003945	59.01	80.97	80.84	37.7	37.04	46.98	37.87	33.83	28.54	*	**	-
	HEMBA1003949	12.02	16.53	20.22	10.36	8.89	9.69	11.57	6.85	10.8			
55	HEMBA1003950	27.53	47.63	43.7	25.53	28.11	14.15	20.64	11.67	12.95	*		-
	HEMBA1003953	10.33	12.12	25.01	8.15	9.43	6.53	13.65	9.93	7.98			
	HEMBA1003958	4.65	6.88	15.41	6.73	7.93	3.72	5.9	3.43	4.74			

Table 369

	HEMBA1003959	14.89	19.53	30.66	18.5	16.34	12.43	19.48	10.78	14.94			
	HEMBA1003960	6.1	5.31	11.07	8.55	9.98	6.62	4.38	4.38	3.84			
5	HEMBA1003966	4.32	4.36	6.33	4.53	3.74	1.94	2.49	2.11	0.85	*	-	
	HEMBA1003967	11.38	13.34	19.36	11.07	6.9	6.77	8.93	7.19	5.9	*	-	
	HEMBA1003968	52.83	102.28	87.2	14.25	26.41	16.31	15.76	9.02	11.36	*	**	-
	HEMBA1003974	4.37	4.4	7.25	2.02	4.53	1.13	3.82	0.89	2.56			
	HEMBA1003976	15.15	20.18	27.02	12.74	18.84	11.73	18.38	14.83	18			
10	HEMBA1003977	8.76	9.42	22.28	9.64	11.17	3.97	8.14	5.18	9.28			
	HEMBA1003978	9.01	16.51	20.07	10.86	6.71	7.75	11.84	5.73	13.48			
	HEMBA1003981	68.06	77.17	117.23	62.61	51.44	47.41	51.47	46.06	74.31			
	HEMBA1003982	5.4	13.31	18.21	3.94	11.62	6.14	3.92	4.82	3.97			
	HEMBA1003985	7.59	8.14	15.01	6.55	7.27	6.74	5.12	5.29	7.02			
	HEMBA1003987	10.14	14.01	20.78	6.87	9.2	5.37	6.58	6.5	8.96			
15	HEMBA1003989	10.11	15.44	20.52	5.53	5.4	4.86	8.66	4.07	5.03	*	*	-
	HEMBA1004000	2.93	4.96	11.45	2.25	2.97	1.76	2.52	0.75	2.54			
	HEMBA1004006	18.54	20.18	42.2	18.19	19.39	15.33	18.84	12.3	17.01			
	HEMBA1004007	19.65	39.73	40.28	26.62	20.72	17.41	38.95	21.37	27.19			
	HEMBA1004010	67.05	91.68	2.46	0.19	0.95	0.35	50.08	44.9	72.79			
	HEMBA1004011	10.54	11.89	17.43	5.17	7.46	5.81	5.72	5.31	4.01	*	*	-
20	HEMBA1004012	20.42	22.3	36.75	7.27	17.23	8.75	11.84	7.16	6.96	*	*	-
	HEMBA1004015	4.26	3.69	8.92	3.2	3.73	2.56	1.97	1.37	3.1			
	HEMBA1004024	7.24	8.25	20.14	4.09	6.96	4.29	7.49	2.93	4.36			
	HEMBA1004029	3.05	5.65	11.19	0.74	1.77	1.68	2.55	0.21	0.47			
	HEMBA1004038	30.88	38.16	65.02	18.09	23.34	18.57	34.1	18.52	13.77			
	HEMBA1004042	0.37	2.38	5.48	0.32	1.77	1.14	0.62	0	0.22			
25	HEMBA1004045	20.4	33.53	50.23	28.78	29.43	29.29	14.02	11.2	16.1			
	HEMBA1004048	37.85	38.8	52.99	50.26	40.74	37.18	34.52	20.41	13.02			
	HEMBA1004049	21.46	22.41	47.43	24.15	22.42	24.41	19.84	20.47	15.98			
	HEMBA1004051	9.9	8.46	21.25	12.84	10.63	10.43	12.39	7.87	8.34			
	HEMBA1004053	15.29	25.2	37.82	19.98	13.35	13.99	21.18	11.93	18.89			
	HEMBA1004055	5.25	11.05	5.64	0.16	1.02	0	9.11	3.17	5.22	*	-	
30	HEMBA1004056	2.41	5.85	10.01	3.45	3.17	2.37	4.07	0.71	2.14			
	HEMBA1004060	6.43	8.34	15.71	14.49	7.75	6	14.41	5.93	6.72			
	HEMBA1004061	7.43	8.52	15.21	11.54	9.65	13.29	5.83	3.71	5.22			
	HEMBA1004067	8.97	11.51	14.78	16.09	9.22	11.3	7.43	5.81	9.07			
	HEMBA1004071	2.92	2.4	5.93	4.14	2.31	3.09	3.1	0.97	2.2			
	HEMBA1004074	126.78	177.45	131.41	229.36	160.88	89.6	187.87	113.1	134.85			
35	HEMBA1004078	20.55	20.84	34.63	28.09	31.27	21.15	16.53	16.06	27.35			
	HEMBA1004085	20.65	31.8	30.03	32.27	21.47	13.85	11.87	12.81	9.59	*	-	
	HEMBA1004086	2.06	3.76	5.23	2.03	3.33	2.95	2.57	0.6	1.89			
	HEMBA1004097	1.94	3.31	1.59	1.13	4.7	3.06	2.83	1.2	1.23			
	HEMBA1004100	14.77	24.96	29.01	20.87	18.7	13.96	10.94	12.24	15.57			
	HEMBA1004103	7.32	13.02	15.94	12.18	10.65	9.17	7.19	6.37	7.49			
40	HEMBA1004110	19.03	26.3	37.33	22.14	20.14	20.02	18.64	15.91	19.14			
	HEMBA1004111	24.42	41.97	41.29	22.57	21.56	20.91	28.72	16.68	19.6			
	HEMBA1004124	10.47	10.61	15.29	11.7	10.51	11.56	7.45	6.39	9.02			
	HEMBA1004130	6.32	9.6	13.12	7.07	7.66	3.98	10.02	6.52	8.94			
	HEMBA1004131	11.62	15.68	22.49	12.3	15.58	10.2	7.69	8.91	12.88			
	HEMBA1004132	1.7	3.66	8.07	2.75	4.82	2.5	5.8	1.43	6.28			
45	HEMBA1004133	61.09	100.97	106.22	48.94	25.58	18.64	11.83	36.24	13.37	*	*	-
	HEMBA1004138	8.15	8.84	9.84	8.72	6.31	5.94	4.18	4.48	5.03	**	-	
	HEMBA1004143	6.39	11.32	13.28	4.24	5.74	4.33	4.63	4.09	3.58	*	-	
	HEMBA1004146	12.23	19.23	24.6	16.14	12.69	10.61	14.04	14.11	16.75			
	HEMBA1004148	5.02	6.85	14.92	7.36	6.63	8.78	2.34	5.06	6.01			
	HEMBA1004149	13.01	27.48	21.59	12.24	21.36	25.46	6.33	6.45	12.24			
50	HEMBA1004150	162.3	225.69	242.62	246.24	265.35	201.29	161.22	151.68	209.57			
	HEMBA1004154	54.95	73.81	77.08	67.59	61.25	43.45	53.14	36.47	45.98	*	-	
	HEMBA1004164	27.89	39.95	75.25	53.13	38	41.78	27.04	21.48	32.66			
	HEMBA1004168	27.29	41.16	48.5	30.28	31.63	25.87	20.87	19.25	25.4			
	HEMBA1004199	11.53	17.04	30.46	12.77	16.45	14.72	15.81	10.26	14.34			
	HEMBA1004200	10.21	15.6	23.4	12.76	12.18	11.22	9.51	9.03	10.57			
55	HEMBA1004201	27.51	39.39	51.71	29.35	27.61	28.68	24.64	21.71	24.17			
	HEMBA1004202	18.3	30.46	37.1	17.92	20.38	16.33	20.83	15.59	21.86			
	HEMBA1004203	11.35	16.48	25.18	12.27	10.37	8.08	12.69	8.41	9.37			

Table 370

	HEMBA1004207	5.23	7	7.18	5.06	6.93	4.27	6.27	2.78	3.75				
	HEMBA1004210	4.96	5.53	8.99	5.1	8.24	7.88	8.78	4.25	6.82				
5	HEMBA1004225	11.76	16.11	15.08	1.96	9.21	5.85	1.74	2.95	4.57	*	**	-	-
	HEMBA1004227	5.13	5	14.56	6.73	5.83	3.8	3.56	2.92	3.47				
	HEMBA1004235	55.87	67.36	100.86	60.82	63.74	64.98	56.93	44.28	61.25				
	HEMBA1004237	63.06	67.44	67.86	54.44	56.68	54.92	61.37	42.55	49.6	**		-	
	HEMBA1004238	5.4	9.74	19.37	3.19	7.79	5.08	4.55	3.62	5.8				
10	HEMBA1004241	58.53	94.19	86.84	45.42	61.25	30.71	41.3	31.18	35.09	*		-	
	HEMBA1004242	95.96	94.64	132.52	129.29	124.32	88.47	86.26	40.26	43.03				
	HEMBA1004243	7.18	9.59	11.11	5.01	7.55	7.79	4.07	6.19	8.9				
	HEMBA1004246	3.92	5.45	6.92	3.64	1.73	7.61	2.23	1.7	3.01	*		-	
	HEMBA1004247	36.08	39.65	23.46	13.27	21.43	17.87	8.15	9.3	7.87	*	**	-	-
	HEMBA1004248	60.7	102.92	68.75	40.08	49.28	54.01	55.12	49.8	49.38				
15	HEMBA1004250	6.46	7.1	17.92	5.92	8.57	3.92	3.52	3.06	5.66	*		-	
	HEMBA1004252	9.76	13.49	18.16	5.3	8	5.39	8.18	4.43	8.93	*		-	
	HEMBA1004260	3.71	7.97	10.5	2.84	9.75	1.75	6.82	1.55	1.83				
	HEMBA1004264	4.86	4.92	5.04	3.34	5.85	4	4.03	2.37	1.97	*		-	
	HEMBA1004267	14.31	26.05	30.36	19.35	16.25	13.91	15.22	15.98	20.33	**	**	-	-
	HEMBA1004272	7.23	8.73	9.64	3.95	3.4	3.74	3.02	1.81	2.67				
20	HEMBA1004274	3.8	4.23	13.32	4.59	3.82	2.88	5.15	2.11	5.65				
	HEMBA1004275	6.92	5.28	11.01	3.44	3.27	3.1	4.62	3.75	4.56				
	HEMBA1004276	53.98	104.51	88.12	40.54	57.2	47.57	40.16	23.52	29.44	*		-	
	HEMBA1004279	3.9	4.4	11.72	1.47	4.01	1.18	2.34	1.51	2.01				
	HEMBA1004284	15.6	17.68	32.1	11.85	15.45	12.29	19.44	11.68	15.92				
	HEMBA1004286	1.1	4.52	5.35	1.91	3.11	0	3.7	0.1	2.34				
25	HEMBA1004289	4.33	10.31	14.89	4.93	9.21	6.85	5.43	4.43	9.27				
	HEMBA1004293	14.22	23.33	31.53	19.23	14.77	12.78	16.77	15.46	15.6				
	HEMBA1004295	5.99	9.65	12.39	6.69	4.97	4.03	6.51	6.63	6.32				
	HEMBA1004302	27.72	69.78	67.78	35.38	30.81	31.86	31.74	25.34	24.05				
	HEMBA1004306	22.59	41.69	39.11	30.27	34.77	20.17	21.64	11.35	18.3				
	HEMBA1004312	8.29	12	23.23	5.76	9.79	3.74	7.73	4.58	8.66				
30	HEMBA1004314	17.03	23.79	39.64	14.71	20.95	13.02	20.7	16.59	24.72				
	HEMBA1004321	2.16	4.06	8.11	3.21	4	1.12	2.54	0	3.38				
	HEMBA1004323	4.43	3.01	0.68	0.1	10.07	1.6	2.71	1.11	0.96				
	HEMBA1004327	3.2	5.57	7.13	3.58	3.76	2.03	3.61	2.13	4.27				
	HEMBA1004329	47.09	53.32	108.52	56.12	44.95	40.88	71.49	47.58	48.41				
	HEMBA1004330	7.28	14.18	16.85	8.09	8.07	7.74	11.04	9.62	5.53				
35	HEMBA1004334	6.28	6.86	13.5	5.07	6.47	3.23	5.33	2.42	4.72				
	HEMBA1004335	2.77	3.49	11.65	1.67	3.64	0.75	1.36	0.2	2				
	HEMBA1004341	4.79	7.07	13.59	3.55	3.83	2.11	5.23	1.8	5.75				
	HEMBA1004344	5.88	15.53	22.36	10.54	9.43	7.32	16.14	4.47	6.61				
	HEMBA1004347	8.48	17.07	21.37	11.69	14.36	7.58	5.26	6.18	12.85				
	HEMBA1004349	19.03	22.2	39.78	17.07	23.84	11.42	16.44	11.72	16.17				
40	HEMBA1004352	30.35	31.05	54.47	23.2	27.22	18.91	26.94	20.35	19.47	*		-	
	HEMBA1004353	65.35	90.37	111.41	40.12	57.25	44.69	62.88	49.41	51.19		*	-	
	HEMBA1004354	31.04	48.91	55.45	29.8	26.92	23.18	26.7	16	25				
	HEMBA1004356	36.8	69.45	87.9	42.77	38.63	30.42	48.78	31.27	34.28				
	HEMBA1004360	21.37	39.1	60.88	24.3	25.32	19.97	35.28	18.19	17.1				
	HEMBA1004366	3.36	19.8	13.89	9.13	8.25	3.58	5.88	3.78	6.29				
45	HEMBA1004372	25.71	35.24	61.82	27.78	27.66	28.9	23.52	16.32	31.11				
	HEMBA1004377	57.43	64.54	125.12	52.77	52.36	39.76	63.76	39.09	45.41				
	HEMBA1004389	26.6	23.69	56.36	35.4	23.53	18.76	21.22	13.56	17.27				
	HEMBA1004391	15.02	20.13	38.52	17.1	15.91	14.1	20.59	16.16	16.69				
	HEMBA1004393	6.23	8.43	14.77	10.01	2.68	5.81	6.08	4.76	4.24				
	HEMBA1004394	6.59	9.68	22.73	7.13	7.36	4.87	8.86	2.4	3.32				
50	HEMBA1004396	6.98	7.79	21.04	5.3	10.85	6.63	4.46	2.99	4.78				
	HEMBA1004401	25.42	37.64	61.19	35.6	34.11	30.34	50.39	18.9	33.72				
	HEMBA1004405	12.61	20.04	37.41	22.75	14.99	14.73	15.19	9.3	13.54				
	HEMBA1004408	33.43	47.3	70.7	34.73	36.57	32.16	33.47	25.45	21.56				
	HEMBA1004414	11.75	12.41	34.08	20.66	20.73	15.48	9.96	9.26	12.21				
	HEMBA1004429	11.38	11.1	25.62	16.77	12.96	11.07	10.66	8.23	8.04				
55	HEMBA1004433	4.53	4.23	9.92	6.93	6.74	8.36	4.52	0.98	3.02				
	HEMBA1004440	12.02	23.81	31.06	19.67	29.44	19.7	15.12	10.66	15.31				
	HEMBA1004444	18.31	24.79	46.54	21.84	22.35	18.04	25.64	13.85	21.08				

Table 371

	HEMBA1004446	1.03	3.03	4.89	2.99	6.41	1.96	3.37	0.17	1.81		
	HEMBA1004451	47.91	49.66	86.71	31.61	23.94	40.91	29.4	25.22	31.73		
5	HEMBA1004452	7.95	9.5	12.93	8.01	5.07	6.5	4.65	4.16	4.59	*	-
	HEMBA1004454	21.61	21.48	36.91	22.76	21.2	22.64	20.66	13.58	20.72		
	HEMBA1004460	3.23	5	9.05	6.23	2.51	4.45	3.96	1.85	1.76		
	HEMBA1004461	9.82	11.87	18.26	13.46	12.46	12.25	11.75	5.13	11.97		
	HEMBA1004468	5.97	8.24	11.49	13.09	9.63	6.4	4.93	3.14	5.27		
10	HEMBA1004479	7.22	6.26	11.32	4.91	8.01	9.21	5.84	3.77	4.35		
	HEMBA1004482	5.37	8.99	11.74	7.23	3.06	5.24	4.77	2.99	3.49		
	HEMBA1004491	7.67	10.41	13.9	11.84	11.35	7.74	9.41	6.84	7.99		
	HEMBA1004499	7.91	12.25	21.91	14.4	10.84	11.41	12.99	9.9	12.88		
	HEMBA1004502	28.69	31.67	44.53	24.39	21.51	21.75	15.45	9.07	14.65	*	-
	HEMBA1004505	9.98	9.29	16.72	11.78	9.95	10.23	12.78	4.69	8.35		
15	HEMBA1004506	10.31	10.67	16.69	10.45	12.56	11.51	11.7	4.59	11.13		
	HEMBA1004507	21.1	25.48	30.3	21.45	19.73	18.7	29.74	17.59	32.44		
	HEMBA1004509	2.41	4.16	3.19	4.33	6.97	5.13	3.86	1.09	3.24		
	HEMBA1004523	16.14	17.44	35.11	23.55	14.39	18.02	17.09	11.42	16.4		
	HEMBA1004528	10.51	13.24	19.75	9.57	16.03	13.29	6.5	10.38	8.52		
20	HEMBA1004534	15.22	16.88	30.37	16.94	14.03	18.54	14.2	7.84	17.61		
	HEMBA1004536	6.18	6.2	10.88	7.97	5.18	6.58	4.33	4.17	3.26		
	HEMBA1004538	9.62	8.85	16.21	10.28	7.48	8.38	4.46	3.25	4.87	*	-
	HEMBA1004542	7.28	10.06	13.56	7.76	7.83	8.12	4.06	4.75	6.69		
	HEMBA1004552	3.25	4.65	8.61	4.79	5	6.2	4.33	0.53	3.64		
	HEMBA1004554	8.19	11.95	16.92	9.57	13.98	10.14	9	4.19	10.81		
	HEMBA1004558	12.36	17.94	21.39	13.09	11.7	13.96	9.64	9.22	10.83		
25	HEMBA1004560	4.66	8.68	10.86	4.85	5.89	4.95	2.86	5.27	5.83		
	HEMBA1004564	9.73	17.48	27.36	16.06	14.28	12.2	13.33	10.15	10.66		
	HEMBA1004566	3.56	3.98	12.25	2.36	4.04	2.92	3.05	2.38	2.63		
	HEMBA1004573	4.48	3.98	12.03	4.58	4.29	4.64	2.63	3.89	4.83		
	HEMBA1004576	18.09	17.62	32.93	24.33	34.17	25.83	17	11.99	13.66		
	HEMBA1004577	3.54	7.83	16.24	7.08	11.02	14.75	9.75	3.87	4.69		
30	HEMBA1004586	4.65	5.81	14.36	5.07	7.86	5.89	6.37	2	4.74		
	HEMBA1004596	284.44	249.12	425.92	413.25	261.05	315.49	139.33	269.7	335.01		
	HEMBA1004604	11.58	13.47	19.78	11.02	11.29	12.05	9.52	8.82	11.26		
	HEMBA1004607	44.74	50.81	86.88	51.55	56.7	51.72	48.7	32.51	56.83		
	HEMBA1004610	6.05	7.49	14.69	9.25	6.9	7.29	6.72	4.7	9.16		
	HEMBA1004617	12.1	9.56	20.48	8.02	10.16	8.41	9.52	5.32	9.98		
35	HEMBA1004622	5.16	6.28	10.24	4.13	6.32	4.27	7.06	2.49	4.07		
	HEMBA1004626	5.67	7.39	15	4.2	9.2	4.95	4.59	5.59	4.31		
	HEMBA1004629	13.02	21.22	41.46	19.54	21.07	18.99	20.74	13.12	14.82		
	HEMBA1004631	73.82	82.05	86.06	51.43	26.56	15.5	10.72	28.9	42.6	*	**
	HEMBA1004632	24.68	42.63	52.95	37.34	39.22	29.39	26.96	22.05	34.67		
	HEMBA1004633	38.98	38.11	53.52	17.86	40.68	39.12	15.84	33.55	35.48		
40	HEMBA1004636	16.64	14.75	24.41	11.5	12.22	12.63	6.1	4.97	7.02	*	-
	HEMBA1004637	10.33	12.11	26.18	5.02	9.26	11.39	12.44	6.08	12.85		
	HEMBA1004638	17.07	21.26	52.09	19.97	27.34	24.5	24.76	14.24	22.8		
	HEMBA1004645	41.39	65.54	74.75	36.73	58.32	57.87	35.72	21.96	40.06		
	HEMBA1004656	33.89	50.4	80.19	35.73	46.51	37.77	45.77	32.71	37.95		
	HEMBA1004657	8.65	8.21	14.8	8.65	5.01	4.76	2.7	2.34	16.46		
45	HEMBA1004666	18.27	17.29	28.67	14.15	16.19	11.73	13.41	11.89	17.32		
	HEMBA1004669	9.31	10.17	13.58	7.96	6.32	5.8	4.8	3.37	4.51	*	**
	HEMBA1004670	6.26	8.23	12.51	5.31	4.65	7.13	5.07	1.93	2.73	*	-
	HEMBA1004672	7.49	5.42	13.8	6.32	5.91	7.14	7.17	3.42	6.19		
	HEMBA1004689	18.06	37.4	36.02	13.85	14.84	13.32	10.59	5.45	12.39	*	-
	HEMBA1004690	8.71	10.59	14.84	3.74	5.26	4.9	4.08	1.25	4.02	*	*
50	HEMBA1004693	54.63	51.62	109.86	81.26	86.47	81.99	74.06	35.68	58.9		
	HEMBA1004697	107.99	90.54	174.23	129.1	114.25	71.95	45.98	67.21	100.42		
	HEMBA1004702	17.82	20.4	33.62	24.43	14.82	19.64	15.1	13.79	12.53		
	HEMBA1004704	4.12	4.28	3.95	3.01	2.64	2.5	2.6	1.84	1.67	**	**
	HEMBA1004705	8.53	8.58	10.66	4.87	5.69	4.53	7.25	3.35	5.23	**	*
	HEMBA1004706	4.44	4.15	10.51	3.36	3.58	2.66	4.3	1.58	2.61		
55	HEMBA1004709	17.24	19.06	37.36	23.46	18.59	23.59	17.98	10.66	14.19		
	HEMBA1004711	162.08	157.26	293.47	260.03	204.86	251.04	138.17	104.82	96.04		
	HEMBA1004723	8.81	12.37	23.58	15.07	18	14.65	13.5	4.03	7.35		



Table 372

	HEMBA1004725	8.16	9.51	14.17	11.97	14.28	12.46	9.22	7.11	10.71			
	HEMBA1004730	9.5	30.77	15.01	11.4	24.39	8.96	5.69	6.95	7.79			
5	HEMBA1004733	4.35	1.94	6.11	2.44	2.1	1.31	3.15	0.66	3.23			
	HEMBA1004734	6.35	4.56	8.84	3.47	5.46	3.65	7.89	2.85	5.88			
	HEMBA1004736	16.7	24.9	39.79	8.08	17.63	7.89	15.58	8.45	13.06			
	HEMBA1004748	7.15	9.02	16.19	2.15	7.19	3.48	6.72	4.3	8.2			
	HEMBA1004749	24.36	23.03	33.63	4.23	9.92	4.61	5.83	2.01	3.6	**	**	-
	HEMBA1004751	2.98	5.64	15.55	3.81	7.93	4.03	5.96	2.05	2.94			
10	HEMBA1004752	114.05	106.99	178.16	68.94	72.11	86.46	30.58	32.81	51.61		*	-
	HEMBA1004753	63.77	72.42	98.61	28.89	47.7	46.76	41.95	35	54.38	*	*	-
	HEMBA1004755	14.23	13.71	21.59	11.51	11.62	10.29	10.53	11.28	11.46			
	HEMBA1004756	8	8.06	13.16	9.58	10.37	12.14	11.47	5.24	11.51			
	HEMBA1004758	28.52	33.28	46.67	20.49	28.34	19.64	31.58	21.06	23.78			
15	HEMBA1004763	5.55	6.08	11.46	2.37	10.09	17.67	15.26	61.35	5.43			
	HEMBA1004768	3.64	9.18	17.67	4.3	5.33	4.44	3.13	1.14	2.86			
	HEMBA1004770	3.52	3.97	15.56	4.59	3.64	3.31	3.4	1.61	4.49			
	HEMBA1004771	9.14	8.57	13.33	7.83	4.73	6.17	4.13	3.12	6.19	*		-
	HEMBA1004775	4.31	4.72	7.01	2.54	3.11	3.68	4.57	1.14	2.99			
	HEMBA1004776	24.15	24.27	34.07	11	13.72	16.67	11.79	13.87	5.14	*	*	-
	HEMBA1004778	7.73	3.98	15.13	3.29	12.02	3.24	6.23	3.84	2.81			
20	HEMBA1004784	24.44	36.5	43.33	23.54	19.27	15.1	33.56	28.4	19.49			
	HEMBA1004785	13.67	18.37	27.67	13.73	15.71	13.71	15.09	7.19	15.39			
	HEMBA1004789	4.14	8.07	13.1	2.66	4.24	5.12	10.75	3.53	4.53			
	HEMBA1004795	7.33	8.35	20.46	14.48	8.52	7.53	6.22	3.52	6.52			
	HEMBA1004797	7.1	4.75	10.25	8.19	4.85	5.24	4.01	3.13	5.6			
25	HEMBA1004803	8.6	9.94	11.36	7.93	6.31	7.52	6.11	2.35	5.54	*	*	-
	HEMBA1004806	3.19	2.79	8.69	6.88	5.26	4.11	3.33	0.92	0.9			
	HEMBA1004807	4.03	3.35	11.54	5.63	6	7.16	2.01	2.6	2.3			
	HEMBA1004816	15.48	10.97	19.39	6.27	7.54	6.26	5.63	8.15	5.23	*	*	-
	HEMBA1004820	7.87	10.12	20.63	12.23	11.52	10.1	9.12	3.16	8.37			
	HEMBA1004833	4.21	6.73	18.25	5.9	8.04	9.77	5.85	1.98	3.49			
30	HEMBA1004847	3.02	6.46	11.24	4.65	7.78	8.66	8.67	2.5	5.11			
	HEMBA1004850	4.4	5.74	10.78	6.32	4.58	7.77	3.54	4.67	2.65			
	HEMBA1004863	17.31	15.86	32.11	21.23	15.33	16.21	14.88	9.41	17.84			
	HEMBA1004864	17.46	20.24	32.03	15.36	13.18	16.06	19.67	7.45	13.87			
	HEMBA1004865	113.3	61.73	148.7	148.79	88.87	115.94	64.71	39.42	63.09			
	HEMBA1004880	8.83	11.17	12.28	9.73	8.92	10.05	5.47	2.68	3.9	**		-
35	HEMBA1004882	141.61	124.12	179	131.9	123.22	118.49	123.09	86.3	152.75			
	HEMBA1004885	7.94	7.93	12.26	7.41	11.08	9.32	5.37	3.13	5.59	*		-
	HEMBA1004889	35.77	44.93	60.57	51.03	25.98	30.7	17.41	45.83	36.11			
	HEMBA1004900	52.96	49.82	61.95	21.61	27.4	15.4	7.06	13.28	12.57	**	**	-
	HEMBA1004909	14.18	13.16	28.88	16.89	11.25	13.43	12.38	9.23	13.02			
	HEMBA1004918	6.03	4.11	8.13	4.43	3.46	3.67	3.79	1.63	1.47			
40	HEMBA1004923	9.64	9.9	14.09	8.35	13.9	10.52	5.58	4.15	7.26	*		-
	HEMBA1004929	3.15	3.03	7.44	3.03	3.95	3.22	2.76	0.8	3.27			
	HEMBA1004930	4.7	7.7	9.9	4.33	7.94	6.01	5.83	3.66	7.33			
	HEMBA1004933	48.9	58.84	65.65	52.38	60.44	49.38	52.85	24.83	54.95			
	HEMBA1004934	3.85	4.55	8.24	5.31	3.47	5.34	6.35	6.72	5.35			
	HEMBA1004937	12.55	13.42	25.29	16.02	10.93	15.03	11.34	9.36	13.16			
45	HEMBA1004943	6.33	9.2	8.01	2.75	3.28	2.19	4.11	2.61	3.13	**	**	-
	HEMBA1004944	19.58	19.31	31.82	17.17	17.7	18.72	15.62	10.66	19.2			
	HEMBA1004946	12.19	9.84	23.87	11.5	9.34	11.54	7.67	6.35	7.52			
	HEMBA1004952	5.52	5.6	7.61	2.28	4.07	4.82	1.95	1.52	2.27	**		-
	HEMBA1004954	95.41	161.15	61.32	125.56	130.49	124.27	79.29	36.2	131.05			
	HEMBA1004956	3.34	5.15	10.1	3.76	7.59	6.47	4.82	2.29	4.38			
50	HEMBA1004960	18.1	21	43	23.94	15.38	19.28	12.99	14.78	18.5			
	HEMBA1004971	17.31	26.71	28.24	5.08	6.02	5.94	4.63	4.75	6.7	**	**	-
	HEMBA1004972	122.03	238.04	172.22	44.53	137.98	72.83	61.38	80.13	88.64	*		-
	HEMBA1004973	3.44	2.83	7.72	3.58	1.82	6.46	2.6	2.06	3.24			
	HEMBA1004977	14	10.09	24.08	10.99	9.73	9.85	6.91	5.11	5.98			
	HEMBA1004978	11.81	9.75	18.48	9.66	9.26	8.27	8.68	4.77	8.65			
55	HEMBA1004980	6.76	8.63	15.4	3.58	6.32	6.19	5.45	3.4	4.05			
	HEMBA1004982	6.24	8	15.9	4.68	8.72	7.61	5.71	2.32	4.42			
	HEMBA1004983	27.66	31.4	50.17	31.75	22.28	27.83	26.75	25.03	37.28			

Table 373

	HEMBA1004995	13.04	8.58	10.13	7.12	8.06	6.92	2.73	3.68	5.31	*	*	-
	HEMBA1005004	4.77	5.36	6.34	4.11	3.26	3.94	3.94	3.84	5.52	*	-	-
5	HEMBA1005008	57.09	40.78	98.86	67.53	69.03	54.32	23.5	39.71	21.46			
	HEMBA1005009	1057.6	723.08	1508	886.08	1346.5	1172.9	1256.5	763.02	961.92			
	HEMBA1005019	4.41	3.37	12.38	2.48	5.05	3.17	5.8	3.17	5.15			
	HEMBA1005021	20.78	39.68	34.72	6.67	27.86	14.2	11.45	16.23	4.97	*	-	-
	HEMBA1005029	70.74	90.66	114.47	109.76	103.35	90.04	59.53	40.06	53.52	*	-	-
	HEMBA1005035	18.47	18.85	35.14	26.8	19.92	22.3	9.64	15.48	14.58			
10	HEMBA1005036	6.46	8.45	12.94	4.31	7.1	4.1	3.99	2.47	4.91			
	HEMBA1005039	30.97	34.92	39.63	34.24	27.86	28.36	12.93	8.11	16.92	**	-	-
	HEMBA1005047	8.28	10.14	13.81	4.91	5.09	5.36	2.77	2.57	2.31	*	**	-
	HEMBA1005050	3.68	2.17	10.81	2.45	2.33	1.31	2.32	1.28	0.56			
	HEMBA1005062	4.16	12.91	14.13	4.05	8.34	22.08	6.52	3.12	5.74			
	HEMBA1005066	10.67	14.99	36.8	11.75	15.95	10.56	12.8	8.39	12.44			
15	HEMBA1005067	4.44	5.11	10.87	2.4	4.78	3.11	2.95	0.22	2.1			
	HEMBA1005070	52.72	54.64	132.49	164.51	146.19	162.23	48.46	33.29	55.3	*	+	-
	HEMBA1005075	3.89	4.62	7.08	4.3	4.86	3.7	4.12	2.52	4.18			
	HEMBA1005078	9.47	16.56	13.83	7.13	9.41	6.63	4.44	6.27	3.76	*	-	-
	HEMBA1005079	31.02	35.09	45.38	24.46	22.17	19.63	32.37	21.21	24.67	*	-	-
20	HEMBA1005083	6.87	5.26	12.68	2.37	3.44	3.16	3.82	1.83	4.73			
	HEMBA1005084	14.72	21.03	25.93	7.18	18.88	15.76	10.99	5.75	6.49	*	-	-
	HEMBA1005088	4.46	4.67	12.93	1.85	3.81	2.49	3.1	1.87	2.53			
	HEMBA1005089	4.71	9.88	14.88	4.89	6.06	3.51	4.1	0.92	1.92			
	HEMBA1005090	25.03	17.55	31.81	18.25	14.13	11.76	5.18	6.32	11.92	*	-	-
	HEMBA1005096	5.89	3.91	4.65	4.65	2.95	3.34	2.39	2.2	2.94	*	-	-
25	HEMBA1005101	39.08	41.35	50.86	29.48	23.15	20.02	33.26	32.78	29.58	**	-	-
	HEMBA1005107	40	41.43	50.54	29.82	24.91	24.18	41.74	30.86	33.12	**	-	-
	HEMBA1005113	113.11	107.38	156.04	92.91	86.12	76.09	106.26	47.64	78.36			
	HEMBA1005123	10.25	18.19	27.19	10.94	11.91	8.06	14	8.52	9.01			
	HEMBA1005133	17.82	23.43	41.02	14.36	24.16	22.06	27.83	16.74	25.23			
	HEMBA1005135	5.59	8.93	15.2	4.63	7.32	4.29	4.52	1.48	2.68			
30	HEMBA1005145	4.53	2.71	8.45	5.36	4.35	4.23	3.05	2.29	4.35			
	HEMBA1005149	378.91	317.95	317.16	22.18	181	208.94	102.53	216.46	124.98	*	**	-
	HEMBA1005152	6.82	9.2	10.54	4.39	6.2	1.79	3.59	2.97	2.92	*	**	-
	HEMBA1005159	7.43	8	10.73	4.97	6.07	2.08	4.16	3.29	1.57	*	-	-
	HEMBA1005172	7.45	10.34	13.12	4.47	4.62	4.49	4.3	1.57	2.99	*	*	-
	HEMBA1005185	22.87	28.13	43.59	20.68	26.1	16.31	27.6	18.57	18.78			
35	HEMBA1005186	8.26	12.01	22.97	7.71	9.71	6.32	6.15	2.19	5.11			
	HEMBA1005195	21.01	45.46	54.34	19.83	21.77	13.25	11.91	3.42	10.22	*	-	-
	HEMBA1005201	30.23	25.81	53.48	38.66	31.34	27.12	18.26	15.51	22.99			
	HEMBA1005202	5.59	7.98	9.58	3.99	3.6	4.2	6.81	2.2	7.96	*	-	-
	HEMBA1005204	16.46	12.78	28.18	11.48	14.05	9.97	14.37	10.45	14.76			
	HEMBA1005206	23.26	6.89	27.27	4.57	14.1	5.14	8.86	8.11	3.99			
40	HEMBA1005219	46.02	33.86	64.57	13.22	55.15	17.76	33.33	34.4	11.24			
	HEMBA1005223	6.35	5.89	13.54	0.44	2.75	4.32	3.73	1.82	1.78			
	HEMBA1005229	6.79	9.67	19.26	5.01	5.11	5.18	4.75	0.62	2.59			
	HEMBA1005230	211.84	132.19	314.59	37.27	92.19	87.58	104.99	40.98	12.2	*	-	-
	HEMBA1005232	5.02	3.23	8	4.94	3.86	4.85	3.42	2.21	2.54			
	HEMBA1005238	4.01	4.87	12.04	12.05	4.27	6.06	2.73	1.86	3.31			
45	HEMBA1005241	4.78	4.02	12.24	4.12	3.03	3.52	2.77	1.9	3.08			
	HEMBA1005244	7.96	6.13	14.8	5.66	6.64	4.51	3.63	3.58	2.47			
	HEMBA1005246	144.3	160.26	353.25	249	171.68	181.26	165.76	91.77	157.68			
	HEMBA1005251	11.91	8.98	32.78	5.64	10.3	10.41	18.87	11.34	4.1			
	HEMBA1005252	12.15	18.12	37.6	17.48	16.35	13.11	14.26	8.12	11.62			
	HEMBA1005267	41.28	35.46	59.97	65.43	48.12	53.65	34.92	15.48	29.09			
50	HEMBA1005274	146.06	122.53	200.33	113.76	78.58	123.13	106.12	96.92	123.47			
	HEMBA1005275	50.96	52.4	71.8	62.52	44.67	45.43	64.52	35.24	52.21			
	HEMBA1005288	36.19	33.62	70.75	88.7	68.37	56.26	25.84	20.1	22.79			
	HEMBA1005293	11.95	9.22	34.15	19.57	13.03	24.04	13.57	18.82	7.5			
	HEMBA1005296	17.02	8.96	24.16	11.91	18.13	12.63	5.55	16.37	7.9			
	HEMBA1005301	7.64	4.4	12.18	6.44	7.08	7.49	6.66	3.04	4.73			
55	HEMBA1005304	3.18	4.74	9.81	5.51	5.89	5.14	6.35	2.58	2.92			
	HEMBA1005305	4.23	5.99	12.03	5.04	5.33	5.38	6.54	0.53	2.54			
	HEMBA1005311	11.53	9.17	14.37	12.69	6.17	11	10.14	6.62	9.41			

Table 374

	HEMBA1005313	33.27	32.37	38.89	32.29	19.06	24.67	17.8	16.01	18.82		**	-
	HEMBA1005314	24.58	33.06	42.65	21.87	11.43	15.5	9.92	9.33	8.85	*	*	-
5	HEMBA1005315	12.58	12.96	19.94	17.38	10.31	13.36	9.94	6.48	5.8	*	*	-
	HEMBA1005317	4.9	4.68	7.03	6.55	5.75	6.41	3.83	2.01	4.66			
	HEMBA1005318	2.91	3.45	4.86	4.07	3.07	4.69	2.08	0.38	2.27			
	HEMBA1005324	11.54	12.46	27.19	15.78	17.61	18.74	11.73	1.86	14.23			
	HEMBA1005331	43.61	41.81	60.5	40.68	48.26	41.6	45.76	21.6	43.46			
10	HEMBA1005337	20.3	20.66	34.16	18.47	13.27	15.91	13.2	7.95	13.16	*	*	-
	HEMBA1005338	37.76	51.08	62.83	38.86	14.3	16.63	9.18	11.59	18.35	**	**	-
	HEMBA1005344	58.27	53.4	127.13	158.88	86.48	122.88	43.73	24.53	36.87			
	HEMBA1005353	291.67	197.22	329.41	381.89	358.33	324.87	364.08	232.83	294.3			
	HEMBA1005359	3.54	4.47	8.65	4.81	7.38	8.25	4.29	2.88	3.92			
	HEMBA1005362	14.29	12.72	20.99	11.94	11.74	13.92	13.73	6.82	10.98			
15	HEMBA1005364	3.08	8.57	11.19	9.32	9.41	5.54	6.78	3.23	3.82			
	HEMBA1005367	9.52	14.36	9.74	11.62	16.31	12.41	12.24	9.27	3.86			
	HEMBA1005372	309.34	404.59	430.49	84.13	123.69	78.11	25.56	68.19	97.12	**	**	-
	HEMBA1005374	36.56	51.63	69.8	44.44	39.19	38.53	36.51	36.03	34.64			
	HEMBA1005379	33.5	27	43.36	22.13	30.25	17.05	21.18	29.05	27.22			
	HEMBA1005382	15.49	19.66	32.8	16.35	15.89	24.51	20.76	15.49	21.41			
20	HEMBA1005384	6.36	8.47	15.31	11.14	12.78	12.49	8.42	6.41	12.29			
	HEMBA1005386	7.43	7.3	12.47	6.27	5.44	7.51	3.39	1.08	4.63	*	*	-
	HEMBA1005389	18.61	20.29	18.71	13.6	21.69	22.09	19.9	13.97	9.2			
	HEMBA1005394	12.89	8.67	16.27	12.3	14.5	11.32	10.11	3.58	3.69			
	HEMBA1005403	4.34	4.47	10.77	7.65	8.37	7.4	6.03	4.21	5.27			
	HEMBA1005408	5.14	5.28	8.12	4.84	5.38	6.7	5.4	4.72	1.33			
25	HEMBA1005410	147.8	198.98	244.61	96.9	175.54	169.68	68.34	63.45	81.73	*	*	-
	HEMBA1005411	3.94	4.86	10.62	4.18	2.45	4.02	1.07	3.25	2.19			
	HEMBA1005423	7.19	6.73	19.41	6.38	7.84	8.58	6.14	3.21	5.83			
	HEMBA1005426	95.36	92.66	185.58	213.51	144.79	175.18	76.93	45.72	96.01			
	HEMBA1005427	3.18	3.68	9.55	2.9	4.08	4.42	2.98	1.86	3.96			
	HEMBA1005430	38.92	50.77	66.51	41.28	49.27	33.43	51.65	28.88	24.29			
30	HEMBA1005438	85.73	96.52	156.38	59.22	45.51	57.38	12.76	14.31	32.68	*	*	-
	HEMBA1005443	15.2	22.18	31.05	12.38	21.42	15.9	15.18	10.34	15.89			
	HEMBA1005447	7.4	8.91	13.83	6.04	6.83	6.51	4.71	3.18	4.95	*	*	-
	HEMBA1005449	188.67	185.78	227.88	315.2	205.18	189.94	184.99	92.08	155.69			
	HEMBA1005452	87.1	82.51	97.54	153.23	76.5	106.72	73.14	41.42	77.58			
	HEMBA1005454	4.07	5.62	12.12	2.12	9.94	2.42	3.66	2.56	2.8			
35	HEMBA1005468	3.12	5.06	12.85	2.9	5.78	4.72	3.8	1.69	1.54			
	HEMBA1005469	4.06	5.82	14.74	4.56	9.66	7.3	4.34	3.61	3.19			
	HEMBA1005472	48.84	68.93	98.37	43.92	45.45	42.16	48.44	44.29	63.31			
	HEMBA1005474	3.81	5.4	6.23	3.61	6.81	3.03	3.23	2.83	4.47			
	HEMBA1005475	18.35	13.18	29.74	13.69	11.52	8.61	14	8.86	16.92			
	HEMBA1005489	11.24	6.84	19.41	11.32	8.2	10.15	7.69	4.76	6.72			
40	HEMBA1005497	3.55	3.84	13.2	3.87	5.02	4.47	2.68	1.54	6.08			
	HEMBA1005500	9.06	12.27	15.75	5.67	8.54	10.09	5.5	7.58	6.57	*	*	-
	HEMBA1005506	66.72	77.27	99.37	69.96	83.48	86.85	48.45	36.29	43.04	*	*	-
	HEMBA1005508	10.52	16.74	23.57	15.52	16.57	19.17	24.35	7.4	7.32			
	HEMBA1005511	106.43	145.35	110.4	50.22	49.21	46.23	5.8	10.19	8.56	**	**	-
	HEMBA1005513	13.22	13.61	12.43	5.61	8.6	9.42	6.36	6.5	6.97	*	*	-
45	HEMBA1005517	8.83	13.8	21.17	12.19	9.09	9.65	12.06	10.72	8.14			
	HEMBA1005518	6.15	6.12	10.29	3.31	2.65	3.34	2.82	2.51	2.48	*	*	-
	HEMBA1005520	4.72	5.27	15.66	1.8	9.96	5.07	11.44	4.1	6.1			
	HEMBA1005522	7.43	6.22	15.1	2.69	4.51	4.56	4.2	1.89	5.13			
	HEMBA1005526	12.95	11.98	23.79	6.97	14.67	6.23	7.41	3.51	8.41			
	HEMBA1005528	20.88	31.78	47.82	17.24	26.35	20.12	19.44	10.67	18.86			
50	HEMBA1005530	155.03	123.7	313.84	376.32	270.85	265.42	127.01	98.49	126.67			
	HEMBA1005538	4.22	2.81	4.67	3.91	2.23	1.75	0.82	1.49	1.34	*	*	-
	HEMBA1005539	7.37	8.42	11.33	9.56	8.07	5.43	6.22	7.08	3.71			
	HEMBA1005545	6.67	6.11	9.83	3.2	2.97	2.68	4.51	2.07	2.36	*	*	-
	HEMBA1005548	9.67	16.77	17.36	7.24	13.44	14.5	10.18	7.2	5.13			
	HEMBA1005552	51.47	60.33	76.88	44.85	67.33	45.49	61.05	38.5	41.19			
55	HEMBA1005558	1303.4	1695.5	2079.7	1863.4	2100.7	1420	1688.2	1099.2	644.47			
	HEMBA1005568	18.05	24.94	43.8	19.93	30.36	19.35	24.29	10.08	5.54			
	HEMBA1005570	9.18	10.68	10.58	5.69	4.61	5.33	3.91	1.39	3.62	**	**	-

Table 375

	HEMBA1005576	3.76	5.34	5.63	3.54	6.15	2.3	3.82	3.83	3.35			
	HEMBA1005577	3.45	4.03	5.12	2.3	2.95	1.9	2.63	1.06	1.56	*	*	-
5	HEMBA1005581	17.34	15.11	23.24	3.89	10.6	7.1	4.64	4.62	3.74	*	**	-
	HEMBA1005582	240.9	356.29	365.46	317.4	608.67	346.15	243.13	155.96	316.09			
	HEMBA1005583	56.28	75.41	54.74	36.66	53.45	30.25	44.93	12.37	20.67		*	-
	HEMBA1005588	48.19	61.31	71.13	27.32	36.77	18.93	99.81	56.7	45.14	*		-
	HEMBA1005593	8.46	13.58	28.24	14.33	10.97	7.86	11.3	3.59	6.67			
	HEMBA1005595	5.4	4.89	14.77	3.77	3.53	5.64	3.73	2.81	4.24			
10	HEMBA1005597	4.61	6.07	5.65	4.04	20.76	7.93	6.41	5.62	16.69			
	HEMBA1005606	10.57	19.2	23.77	3.86	10.94	4.17	5.54	1.39	3.32		*	-
	HEMBA1005609	15.17	18.03	17.77	3.19	7.05	3.09	3.33	3.84	3.16	**	**	-
	HEMBA1005616	3.29	3.65	8.89	1.88	4.28	2.06	3.75	2.04	3.26			
	HEMBA1005621	2.8	5.27	13.13	1.63	2.71	2.81	4.45	1.3	2.19			
15	HEMBA1005627	26.17	45.68	60.66	11.35	32.13	15.73	25.61	10.31	7.55			
	HEMBA1005628	4.16	6.62	18.11	5.71	6.97	5.93	6.45	1.4	3.09			
	HEMBA1005631	2.97	2.99	6.58	2.7	2.52	4.68	1.93	1.12	1.83			
	HEMBA1005632	8.75	7.76	13.3	5.6	4.94	4.75	6.21	2.5	5.1	*		-
	HEMBA1005634	13.26	27.71	36.18	8.65	7.52	11.69	10.2	6.61	5.28			
	HEMBA1005662	5.49	5.63	8.59	1.07	4.9	3.69	4.47	3.62	2.83			
20	HEMBA1005666	4.1	8.92	17.42	4.51	5.05	7.36	8.37	3.56	4.18			
	HEMBA1005670	19.65	25.57	58.84	10.77	25.74	28.55	25.33	19.21	13.78			
	HEMBA1005671	3.25	3.78	12.05	4.13	4.03	2.36	2.63	0.58	1.59			
	HEMBA1005679	30.48	23.92	60.53	11.99	24.03	21.81	34.62	12.99	24.28			
	HEMBA1005680	5.31	5.25	11.55	7.98	6.67	8.25	4.31	2.95	4.88			
	HEMBA1005685	10.54	10.31	19.75	6.25	14.08	11.58	12.25	7.49	2.77			
25	HEMBA1005698	3.05	4.09	5.98	5.75	3.35	4.26	2.89	1.71	1.85			
	HEMBA1005699	81.55	73.56	131.24	173.55	121.01	131.74	58.39	29.63	52.24			
	HEMBA1005703	8.7	6.7	19.33	15.32	12.15	10.29	11.29	5.53	9.29			
	HEMBA1005705	10.69	16.62	28.52	12.65	15.48	9.89	13.24	7.86	8.73			
	HEMBA1005712	14.41	9.07	21.89	4.52	12.06	8.24	12.54	7.16	9.37			
	HEMBA1005717	9.58	15.11	28.28	15.34	17.37	16.39	10.48	4.92	9.53			
30	HEMBA1005718	14.72	17.46	32.28	23.31	13	19.82	12.33	8.89	13.45			
	HEMBA1005721	7.61	8.19	16.43	10.15	9	9.16	5.24	3.31	7.52			
	HEMBA1005722	8.96	8.38	15.56	10.88	5.15	8.22	6.16	2.61	4.2			
	HEMBA1005724	3.21	3.63	9.19	3.08	3.41	4.96	4.32	2.79	3.41			
	HEMBA1005732	26.35	14.39	37.65	46.13	33.11	35.41	27.65	13.58	24.67			
	HEMBA1005737	10.7	10.58	19.74	12.96	11.14	14.53	14.77	5.18	11.46			
35	HEMBA1005742	24.19	21.22	31.29	17.65	22.38	19.25	19.89	11.57	20.16			
	HEMBA1005746	16.18	18.76	28.18	19.8	21.24	20.22	17.64	16.51	21.84			
	HEMBA1005747	4.59	6.97	9.33	5.84	4.66	4.23	3.4	2.42	2.9	*		-
	HEMBA1005749	4.06	4.65	5.89	4.59	4.51	2.42	4.14	4.65	3.14			
	HEMBA1005755	6.51	5.76	10.77	4.34	2.96	3.2	3.26	2.6	1.41	*		-
	HEMBA1005760	8.14	6.09	21.23	11.82	15.12	18.05	5.99	3.99	9.09			
40	HEMBA1005765	16.17	18.36	30.68	12.16	17.74	19.5	18.91	12.07	18.52			
	HEMBA1005766	4.59	6.7	11.4	6.4	6.48	7.14	3.63	2.36	6.46			
	HEMBA1005780	66.74	88.34	50.49	70.57	83.73	79.9	51.01	23.87	50.17			
	HEMBA1005795	12.49	13.53	22.26	21.04	27.08	17.3	17.89	8.53	16.93			
	HEMBA1005809	27.58	28.57	37.75	10.82	11.75	10.76	7.41	20.02	13.83	**	*	-
	HEMBA1005813	11.01	13.12	21.07	10.05	5.62	7.48	3.75	4.75	2.72		*	-
45	HEMBA1005815	13.88	21.46	26.3	18.7	15.38	15.54	15.88	14.09	23.04			
	HEMBA1005822	2.32	4.46	5.72	1.33	1.78	1.99	1.83	4.15	2.65			
	HEMBA1005829	11.63	17.29	26.15	14.23	14.49	18.69	18.12	8.68	16.12			
	HEMBA1005833	7.51	11.08	19.55	8.36	9.46	9.74	7.13	4.47	9.24			
	HEMBA1005834	2.53	4.28	9.15	2.39	5.2	3.43	3.05	1.57	2.22			
	HEMBA1005844	5.49	8.18	12.47	6.96	9.74	5.87	6.18	2.19	5.4			
50	HEMBA1005852	9.05	12.52	17.23	5.22	7.99	5.59	7.73	5.09	7.72			
	HEMBA1005853	12.09	27.26	20.62	6.51	8.22	6.09	4.4	8.87	5.67	*	*	-
	HEMBA1005878	16.48	26.29	29.76	6.78	14.33	12.64	11.87	13.79	15.64	*		-
	HEMBA1005883	10.6	8.45	21.85	5.18	5.86	5.16	3.04	2.55	2.52			
	HEMBA1005884	18.4	17.45	38.78	13.72	28.17	26.47	16.14	9.17	16.98			
	HEMBA1005891	14.35	23.5	29.7	12.96	17.06	15.29	15.47	12.21	17.4			
55	HEMBA1005894	20.76	25	45.44	20.3	23.59	18.03	21.15	9.72	19.92			
	HEMBA1005898	6.21	7.33	9.72	7.72	7.66	5.64	3.86	1.59	3.36	*		-
	HEMBA1005902	52.63	54.98	95.93	140.97	103.88	141.36	40.77	40.69	57.15	*	+	

Table 376

	HEMBA1005907	11.51	24.95	21.68	5.18	12.96	7.51	14.52	20.83	32.4			
	HEMBA1005909	12.54	10.65	15.16	9.37	9.7	8.92	5.33	5.2	5.61	**	-	
5	HEMBA1005911	4.25	2.94	8.69	4.53	4.07	3.47	3.19	0.81	2.14			
	HEMBA1005912	35.05	30.41	48.44	55.56	35.89	54.16	35.55	16.99	36.27			
	HEMBA1005913	8.07	12.66	17.16	3.35	11.55	8.12	4.56	4.08	5.57	*	-	
	HEMBA1005921	8.39	17.95	29.27	13.5	18.47	18.42	20.02	11.79	13.13			
	HEMBA1005922	10.23	12.69	22.71	8.62	19.47	16.43	10.1	8.02	9.98			
	HEMBA1005929	14.03	14.99	35	19.43	15.07	16.06	12.42	10.95	15.92			
10	HEMBA1005931	6.92	7.45	8.96	7.96	7.11	4.38	5.8	5.53	5.56	*	-	
	HEMBA1005934	9.15	11.61	14.52	6.47	9.42	7.17	6.06	6.07	3.78	*	-	
	HEMBA1005945	13.18	17.17	24.76	14.61	10.38	10.87	14.78	9.7	14.04			
	HEMBA1005962	8.03	8.91	21.61	8.95	9.17	9.16	8.64	3.56	9.28			
	HEMBA1005963	7.03	8.04	15.69	2.68	5.58	6.69	5.62	2.88	7			
	HEMBA1005990	1.77	6.11	10.33	2.7	4.79	2.9	2.4	1.78	3.08			
15	HEMBA1005991	64.98	101.38	91.59	21.08	89.91	49.01	45.05	21.27	28.13	*	-	
	HEMBA1005999	10.77	8.18	14.85	9.74	9.96	11.62	9.75	7.35	11.3			
	HEMBA1006002	4.73	10.03	9.92	4.44	5.47	3.19	2.29	3.3	1.96	*	-	
	HEMBA1006005	11.33	12.26	21.89	15.72	14.29	10.03	11.77	7.68	11.25			
	HEMBA1006011	7.74	6.02	9.99	4.17	3.85	3.65	4.89	1.78	2.14	*	*	-
20	HEMBA1006013	15.75	24.43	27.02	14.33	11.65	10.41	12.44	6.76	8.78	*	*	-
	HEMBA1006016	12.67	16.72	32.68	4.67	8.33	5.18	11.34	2.62	5.66			
	HEMBA1006019	39.35	43.51	94.43	41.01	47.95	33.8	48.65	20.74	35.48			
	HEMBA1006021	100.18	64.95	186.84	161.47	154.88	173.68	76.07	51.55	67.34			
	HEMBA1006022	4.41	4.65	8.97	5.98	4.93	5.29	5.93	2.38	6.8			
	HEMBA1006031	54.5	55.09	63.41	23.75	30.34	33.23	14.55	24.74	14.18	**	**	-
25	HEMBA1006035	26.81	26.57	28.41	13.64	17.75	10.2	23.49	16.85	24.27	**	-	
	HEMBA1006036	30.41	35.58	51.17	28.85	21.84	21.47	22.61	12.69	16.92	*	*	-
	HEMBA1006042	14.78	15.89	30.2	21.62	13.62	17.35	12.05	7.06	10.83			
	HEMBA1006044	6.37	6.38	15.67	2.89	5.13	3.3	5.6	2.77	4.16			
	HEMBA1006045	5.05	5.98	16.26	5.37	6.51	3.98	4.26	3.34	4.33			
	HEMBA1006048	5.66	8.21	17.12	5.57	7.7	7.23	7.81	2.07	6.93			
30	HEMBA1006053	9.91	12.14	22.17	11.19	10.11	10.25	6.6	4.29	8.53			
	HEMBA1006055	18.11	16.89	29.58	15.19	13.98	12.78	12.35	11.58	12.66			
	HEMBA1006058	12.02	10.46	14.6	9.27	7.95	6.43	9.22	7.8	6.16	*	*	-
	HEMBA1006063	115.82	107.87	141.14	161.05	129.88	130.01	94.43	64.84	83.98	*	*	-
	HEMBA1006067	14.46	16.19	18.97	8.28	13.91	5.01	10.46	4.28	4.98	*	*	-
	HEMBA1006081	3.95	8.3	15.7	2.09	6.94	3.38	3.92	1.35	3.37			
35	HEMBA1006089	4.09	6.69	17.6	2.93	4.85	1.66	3.54	1.57	3.85			
	HEMBA1006090	16.61	33.98	39.21	14.19	23.81	18.25	18.94	5.99	5.67			
	HEMBA1006091	6.4	6.94	10.5	5.04	5.34	5.02	4.02	3.3	3.85	*	*	-
	HEMBA1006093	24.23	35.95	33.59	5.11	7.76	13.97	5.79	10.1	7.62	**	**	-
	HEMBA1006099	23.7	22.12	46.77	18.77	21.87	13.39	21.06	17.59	21.54			
	HEMBA1006100	15.19	17.46	28.4	13.14	14.55	10.6	18.9	11.15	17.08			
40	HEMBA1006108	9.23	5.57	12.26	4.66	7.02	4.99	4.59	2.55	4.37			
	HEMBA1006114	6.24	4.2	16.8	2.53	7.16	4.48	5.37	0.85	3.06			
	HEMBA1006121	4.96	7.47	17.94	3.37	6.22	2.88	5.11	1.02	2.9			
	HEMBA1006124	23.37	10.77	43.63	10.18	13.13	12.16	9.91	5.78	5.28			
	HEMBA1006125	5.3	5.09	9.35	4.55	4.9	6.58	2.71	1.37	4.21			
	HEMBA1006130	81.41	100.18	218.91	239.88	178.96	190.17	100.6	68.45	89.08			
45	HEMBA1006138	16.78	21.47	42.54	20.91	18.85	14.71	18.67	11.93	13.92			
	HEMBA1006142	6.25	5.14	9.74	3.49	5.53	4.08	2.75	2.92	2.44	*	-	
	HEMBA1006150	20.94	16.77	47.47	16.05	12.94	20.13	22.73	16.22	18.83			
	HEMBA1006151	3.81	3.62	12.07	4.06	2.71	3.79	4.85	1.6	3.25			
	HEMBA1006155	51.87	36.97	81.85	14.8	33.19	24.55	29.86	21.38	8.77			
	HEMBA1006158	7.8	6.18	16.28	4	7.84	5.44	10.27	1.55	3.09			
50	HEMBA1006164	7.41	4.45	10.51	11.19	6.62	6.2	5.41	2.39	2.71			
	HEMBA1006171	11.38	13.76	11.95	10	9.74	12.84	7.5	4.2	3.45	**	-	
	HEMBA1006173	5.77	5.17	5.55	5.75	11.01	7.35	5.28	2.14	3.83			
	HEMBA1006176	10.21	6.39	20.68	12.36	13.62	14.28	6.26	8.81	6.76			
	HEMBA1006182	6.52	8.53	12.82	8.56	9.55	11.37	5.71	3.32	5.23			
	HEMBA1006197	4.36	5.59	8.45	4.07	4.78	4.63	3.18	1.47	2.61	*	-	
55	HEMBA1006198	6.83	8.29	18.43	9.27	9.93	14.63	6.95	4.93	6.04			
	HEMBA1006213	46.5	59.16	87.76	45.37	52.9	41.61	64.69	38.82	49.81			
	HEMBA1006217	77.53	104.19	150.86	44.45	56.82	81.63	56.2	53.63	65.92			

Table 377

	HEMBA1006226	60.66	89.4	128.3	98.59	21.45	56.73	34.83	42.34	47.3		
	HEMBA1006235	7.29	6.42	9.51	4.4	5.83	6.34	4	1.9	2.78	*	-
5	HEMBA1006248	8.59	14.3	12.76	17.84	10.1	10.62	14.29	11.1	13.06		
	HEMBA1006251	15.98	24.11	24.67	22.82	19.08	21.09	16.03	3.32	8.44		
	HEMBA1006252	6.29	11.35	24.58	17.83	5.75	7.22	9.32	6.16	9.75		
	HEMBA1006253	6.65	9.14	20.63	14.78	17.19	22.49	8.79	1.77	6.4		
	HEMBA1006259	11.81	21.15	28.91	16.9	10.94	16.19	15.68	14.83	17.05		
10	HEMBA1006261	25.45	37.82	48.94	33.85	29.71	14.07	18.76	15.97	24.68		
	HEMBA1006268	4.53	5.62	11.14	5.03	3.83	5.91	4.8	2.63	2.52		
	HEMBA1006271	27.87	48.98	84.46	39.21	39.6	40.82	30.74	14.23	28.33		
	HEMBA1006272	3.48	5.09	12.53	3.82	7.27	10.33	8.77	2.68	5.16		
	HEMBA1006273	4.26	5.62	9.16	7.22	6.74	6.25	4.33	1.91	3.78		
	HEMBA1006276	8	7.56	13.01	10.92	8.88	11.33	8.59	5.55	8.36		
15	HEMBA1006278	3.56	6.86	4.87	4.56	7.03	4.18	3.68	1.91	2.81		
	HEMBA1006283	21.61	22.15	38.14	17.11	13.97	13.64	11.04	8.54	8.53	*	-
	HEMBA1006284	9.77	12.43	9.21	7.3	6.48	8.66	4.11	16.95	4.13		
	HEMBA1006291	7.57	5.98	8.47	4.12	5.97	5.86	4.51	2.35	4.32	*	-
	HEMBA1006292	28.37	23.25	41.05	49.83	29.24	37.1	21.69	20.86	21.95		
	HEMBA1006293	3.75	5.49	8.43	3.08	2.38	10.01	0.91	2.39	2.11	*	-
20	HEMBA1006299	20.83	28.58	31.92	37.12	28.94	29.71	18.96	13.53	20.58		
	HEMBA1006309	12.21	13.85	16.63	10.12	12.48	15.92	14.59	3.8	13.91		
	HEMBA1006310	10.98	14.98	14.35	11.71	17.38	10.36	10.75	8.47	4.15		
	HEMBA1006311	7.24	7.64	16.35	13.11	5.74	8	7.15	4.03	4.85		
	HEMBA1006313	3.22	8.11	10.2	4.45	3.61	3.07	2.82	2.44	2.58		
	HEMBA1006316	7.65	12.92	15.52	10.38	5.11	11.89	7.9	6.94	9.74		
25	HEMBA1006328	21.63	21.11	38.33	32.37	21.64	26.1	17.68	13.27	19.36		
	HEMBA1006334	3.37	3.68	14.62	4.58	3.28	2.72	2.89	4.86	1.73		
	HEMBA1006335	17.68	32.85	46.47	23.14	32.25	24.21	26.2	15.13	17.28		
	HEMBA1006344	55.44	64.87	82.83	51.59	45.13	40.79	32.94	23.43	27.33	**	-
	HEMBA1006347	7.7	7.61	11.32	7.96	6.93	5.21	8.91	1.81	2.49		
	HEMBA1006349	5.12	7.39	13.08	11.96	7.92	10.21	7.73	3.41	9.88		
30	HEMBA1006352	4.71	5.44	5.8	3.17	4.05	6.34	3.53	2.18	6.11		
	HEMBA1006357	21.84	30.15	32.51	16.24	19.4	20.03	17.68	17.67	25.75	*	-
	HEMBA1006358	9.29	7.19	14.9	8.1	8.4	7.37	7.12	3.93	6.97		
	HEMBA1006359	5.5	5.93	13.36	4.55	6.66	5.77	4.91	2.59	3.15		
	HEMBA1006360	4.46	4.17	9.74	2.49	4.18	4.08	2.89	1.16	2.66		
	HEMBA1006364	4.83	5.25	14.76	2.78	4.9	3.21	2.71	2.21	3.79		
35	HEMBA1006377	80.85	114.32	105.84	75.76	102.36	58.33	93.99	60.04	78.87		
	HEMBA1006380	20.03	20.23	49.46	23.06	19.66	23.19	14.68	15.28	25.75		
	HEMBA1006381	21.8	26.78	34.04	28.98	18.12	16.56	28.76	15.54	19.65		
	HEMBA1006385	26.15	27.47	48.23	21.69	21.93	26.5	17.06	11.15	26.66		
	HEMBA1006390	66.76	79.54	86.03	47.23	63.78	61.2	79.04	51.69	65.97		
	HEMBA1006391	9.83	7.54	21.2	5.37	10.85	8.66	7.1	4.25	6.66		
40	HEMBA1006398	7.74	10.16	17.94	6.15	8.15	10.18	5.31	3.87	6.36		
	HEMBA1006405	17.21	30.3	36.97	11.67	17.28	9.3	9.52	5.99	10.52	*	-
	HEMBA1006410	12.29	24.19	20.82	11.01	22.54	19.08	10.32	24.08	7.5		
	HEMBA1006416	13.77	16.34	35.1	20.2	19.08	14.96	13.83	12.25	17.9		
	HEMBA1006418	14.88	14.23	12.55	8.74	10.37	7.82	5.57	12.05	3.94	**	-
	HEMBA1006419	30.32	26.38	45.23	21.57	20.76	20.5	35.29	23.16	35.95		
45	HEMBA1006421	6.94	7.3	14.62	4.48	5.03	4.44	5.76	2.74	5.79		
	HEMBA1006424	6.59	5.16	10.86	2.39	3.13	4.03	3.8	3.29	5.21		
	HEMBA1006426	16.94	21.77	35.51	13.82	15.6	11.92	15.06	10.89	16.55		
	HEMBA1006430	21.51	23.1	52.14	21.8	26.01	14.55	25.55	15.62	24.71		
	HEMBA1006438	7.39	9.88	27.72	9.7	12.86	10.02	7.77	3.89	8.06		
	HEMBA1006445	5.97	4.62	11.24	6.9	4.18	5.84	3.07	2.65	7.57		
50	HEMBA1006446	10.44	29.9	25.23	12.03	4.68	7.84	2.86	8.87	4.65		
	HEMBA1006456	20.27	20.9	27.71	19.85	19.2	23.69	16.72	10.9	15.13	*	-
	HEMBA1006461	10.85	13.87	19.86	8.91	8.16	8.85	10.75	7.35	8.75		
	HEMBA1006467	2.98	4.33	9.77	4.94	3.17	2.56	4.06	1.76	2.14		
	HEMBA1006470	34.3	38.7	56.67	41.16	36.04	29.19	28.2	24.42	29.45		
	HEMBA1006471	8.92	14.85	23.43	12.81	12.27	40.2	16.21	5.14	6.51		
55	HEMBA1006474	80.88	55.42	113.87	93.82	77.51	77.92	59.58	47.32	61.33		
	HEMBA1006476	124.18	125.67	311.61	282.54	252.79	111.47	88.12	112.31	128.83		
	HEMBA1006482	750.18	800.51	717.99	555.6	740.67	596.85	785.76	753.48	372.51		

Table 378

	HEMBA1006483	10.38	11.79	17.97	10.54	8.06	5.41	9.39	6.26	10.8			
	HEMBA1006485	14.11	21.34	22.05	9.66	9.42	6.66	9.41	4.35	6.34	*	*	-
5	HEMBA1006486	25.6	38.65	46.49	15.25	21.42	18.99	28.29	12.46	17.42	*		-
	HEMBA1006489	4.69	5.66	11.99	2.16	3.64	2.6	4.74	2.19	2.49			
	HEMBA1006492	21.26	21.32	31.79	8.11	21.1	11.99	16.25	6.33	8.98		*	-
	HEMBA1006494	3.73	5.82	13.17	4.37	5.86	3.22	4.57	1.78	4.99			
	HEMBA1006497	9.48	5.39	9.72	6.41	4.7	6.22	4.84	2.41	5.11			
	HEMBA1006501	70.71	74.3	109	137.89	121.18	132.43	56.47	47.55	54.22	*		+
10	HEMBA1006502	26	37.84	37.28	17.65	19.66	21.79	14.53	13.47	14.09	*	**	-
	HEMBA1006507	74.35	71.35	93.56	76.72	76.19	89.01	54.44	45.62	81.01			
	HEMBA1006517	10.15	13.34	25.2	8.05	9.91	8.2	9.98	8.78	9.53			
	HEMBA1006521	4.71	7.89	15.55	2.17	4.99	3.48	4.73	1.47	4.08			
	HEMBA1006529	20.44	40.14	54.85	11.1	18.97	9.04	8.44	3.17	5.16	*		-
	HEMBA1006530	2.11	3.93	16.06	3.3	3.94	2.97	2.36	0.8	2.85			
15	HEMBA1006535	4.76	6.35	8.43	4.93	4.07	4.99	1.52	1.3	3.36	*		-
	HEMBA1006536	7.73	9.35	15.74	6.97	6.8	8.19	6.06	4.78	7.71			
	HEMBA1006540	4.89	5.07	10.1	3.8	4.1	3.21	4.5	0.57	2.57			
	HEMBA1006544	9.55	9.44	12.65	5.51	6.6	3.64	6.81	6.28	5.66	*	*	-
	HEMBA1006546	13.83	18.34	35.37	18.49	13.07	8.02	20.42	13.65	12.24			
	HEMBA1006549	3.69	4.64	10.47	3.5	3.22	3.38	4.38	1.91	2.6			
20	HEMBA1006559	5.63	7.78	15.93	4.1	5.24	3.33	4.33	1.27	1.6			
	HEMBA1006562	4.46	7.73	13.41	4.81	4.36	7.66	6.04	1.8	5.11			
	HEMBA1006566	1.97	2.79	6.04	4.85	3.75	3.09	2.63	0.98	3.24			
	HEMBA1006569	9.03	13.38	17.77	8.08	5.02	11.82	6.18	3.56	5.28	*		-
	HEMBA1006572	4.01	5.33	6.28	3.85	4.61	4.82	3.06	1.11	1.97	*		-
	HEMBA1006579	48.81	48.67	106.01	77.85	58.85	72	32.03	38.94	29.18			
25	HEMBA1006583	21.83	28.38	52.62	37.84	32.54	33.86	32.6	18.06	30.33			
	HEMBA1006595	9.39	11.2	24.82	12.48	12.13	12.39	11.97	4.53	9.41			
	HEMBA1006597	10.74	17.9	34.13	14.71	18.52	13.99	17.64	9.01	20.29			
	HEMBA1006606	9.14	17.8	25.4	12.84	13.75	11.34	17.49	5.73	12.78			
	HEMBA1006612	16.16	16.45	27.36	16.16	10.37	13.84	7.68	7.75	9.58	*		-
30	HEMBA1006617	8.08	9.55	19.24	13.65	9.22	10.71	8.25	4.71	9.91			
	HEMBA1006624	62.58	66.3	115.43	55.71	47.06	62.71	45.87	24.82	44.31			
	HEMBA1006631	23.12	25.87	43.15	23.48	22.27	20.06	24.55	15.53	27.45			
	HEMBA1006635	7.91	10.88	14.85	9.02	10.78	9.39	11.43	5.66	11.05			
	HEMBA1006639	10.04	12.39	17.07	18.66	19.19	12.58	8.27	4.47	14.67			
	HEMBA1006643	1.84	4.34	3.2	4.98	3.53	3.26	2.93	0.82	1.75			
35	HEMBA1006648	15.53	17.03	27.49	19.15	15.29	16.67	5.29	8.82	12.26			
	HEMBA1006652	26.71	34.75	50.3	32.97	21.76	18.68	16.24	13.51	23.67			
	HEMBA1006653	7.56	6.61	17.15	7.18	4.77	7.22	2.33	2.95	3.74			
	HEMBA1006658	19.91	14.88	49.21	18.71	18.4	21.38	11.54	8.35	7.4			
	HEMBA1006659	58.61	60.76	125.49	159.5	103.52	108.54	57.82	49.19	67.43			
	HEMBA1006665	2.46	4.7	11.42	4.57	4.2	3.45	4.37	1.96	4.61			
40	HEMBA1006666	3.78	4.89	6.54	3.83	3.74	5.58	5.07	2.85	4.33			
	HEMBA1006671	29.88	46.04	31.81	11.03	10.78	7.48	20.4	8.57	17.2	**	*	-
	HEMBA1006674	17.95	21.64	48.41	21.77	17.05	22.65	20.34	20.43	18.22			
	HEMBA1006676	8.33	14.71	17.2	11.8	6.88	5.97	6.74	4.48	6.11		*	-
	HEMBA1006682	5.28	7.81	6.48	5.22	3.34	3.44	5.44	2.35	3.91			
	HEMBA1006688	8.06	7.99	15.76	5.58	7.11	7.53	6.82	4.86	5.53			
45	HEMBA1006695	11.68	16.81	23.72	8.98	10.42	13.13	10.55	9	11.41			
	HEMBA1006696	12.25	15.75	12.83	8.51	9.6	6.76	4.49	2.19	4.51	*	**	-
	HEMBA1006702	6.88	9.14	9.5	5.54	6.34	5.86	4.33	1.73	4.63	*	*	-
	HEMBA1006707	12.13	15.02	19.11	19.48	16.83	14.64	14.25	5.63	13.01			
	HEMBA1006708	7.17	12.19	21.37	12.13	8.06	8.49	3.77	4.26	7.59			
	HEMBA1006709	13.09	19.04	28.5	14.85	14.05	15.86	11.87	11.01	16.42			
50	HEMBA1006717	5.25	5.26	12.53	4.74	4.01	3.68	7.38	2.38	6.67			
	HEMBA1006724	12.11	8.3	19.78	5.53	10.32	5.8	9.44	6.24	6.16			
	HEMBA1006731	7.48	7.6	18.92	6.67	8.76	6.75	5.19	3.77	3.96			
	HEMBA1006737	6.06	6.19	10.33	4.37	4.14	4.69	4.38	0.91	4.4			
	HEMBA1006742	8.98	8.7	24.13	7.5	9.95	8.07	10.84	6.04	17.08			
	HEMBA1006743	14.91	22.66	22.54	17.15	17.28	14.05	13.93	8.87	7.89	*		-
55	HEMBA1006744	17.72	19.61	39.58	28.17	20.27	23.33	18.16	15.95	23.07			
	HEMBA1006749	4.84	4.51	4.65	3.84	2.79	5.06	3.99	2.53	5.17			
	HEMBA1006752	74.49	114.01	106.5	80.8	62.77	63.46	56.97	93.88	63.11			

Table 379

	HEMBA1006754	10.3	5.77	11.65	6.17	5.72	5.75	6.13	5.01	8.39			
	HEMBA1006758	7.27	4.9	12.62	10.94	5.09	5.73	5.5	2.15	4.84			
5	HEMBA1006767	5.55	6.53	9.74	2.73	5.09	3.33	3.97	3.29	3.02	*		-
	HEMBA1006770	10.91	18.24	23.01	9.34	17.17	9.49	6.46	5.37	4.52	*		-
	HEMBA1006779	21.14	29.08	46.61	19.18	32.07	21.74	27.02	14.11	23.35			
	HEMBA1006780	31.66	41.91	71.99	39.02	25.6	33.44	20.75	21.87	35.28			
	HEMBA1006789	11.15	8.92	10.14	6.24	5.48	5.24	3.29	3.78	6.02	**	**	-
10	HEMBA1006795	13.29	18.12	23.2	10.87	8.5	11.23	14.12	7.4	15.69			
	HEMBA1006796	8.15	7.65	12.79	2.99	3.39	3.14	3.97	0.85	2.9	*	*	-
	HEMBA1006805	10.17	13.14	20.22	7.25	5.84	4.86	8.13	5.47	7.83	*		-
	HEMBA1006807	358.41	425.1	450.14	425.56	524.37	388.31	479.65	356.88	266.31			
	HEMBA1006813	3.32	4.75	8.38	0.01	2.65	1.47	2.36	0.6	1.87			
	HEMBA1006819	11.44	14.72	25.12	8.56	18.43	11.48	10.78	2.32	9.36			
15	HEMBA1006821	15.76	14.89	42.37	23.12	22.95	19.27	10.56	11	21.11			
	HEMBA1006824	31.97	30.86	49.16	24.26	23.62	19.71	31.05	26.34	34.02			
	HEMBA1006832	259.36	308.26	291.59	339.91	237.21	321.61	326.22	280.59	176.89			
	HEMBA1006834	46.64	65.27	67.81	62.09	43.11	55.61	73	47.8	42.25			
	HEMBA1006835	8.46	14.27	21.58	9.55	10.78	10.45	9.6	6.1	8.18			
	HEMBA1006843	18.15	18.91	28.2	12.23	21.78	20.94	21.53	7.17	5.58			
20	HEMBA1006849	26.18	26.08	44.03	23.34	31.15	21.57	33.36	14.9	24.69			
	HEMBA1006850	16.77	33.56	37.75	10.59	18.63	8	9.03	3.5	6.56	*		-
	HEMBA1006861	14.67	13.53	34.61	20.34	16.15	19.04	12.38	6.63	17.89			
	HEMBA1006865	39.2	38.77	61.65	71.58	60.52	57.06	33.27	28.86	36.65			
	HEMBA1006867	18.5	15.53	22.34	9.22	8.88	9.34	9.42	6.3	3	**	**	-
	HEMBA1006873	17.71	23.93	26.16	14.12	11.71	14.57	15.58	7.18	17.11	*		-
25	HEMBA1006877	7.4	13.49	15.12	6.73	6.6	3.67	5.7	2.95	4.47	*		-
	HEMBA1006878	10.48	14.11	25.64	11.23	13.75	11.88	9.01	2.84	7.36			
	HEMBA1006879	12.94	16.27	24.73	12.26	12.67	8.96	12.1	3.4	9.76			
	HEMBA1006884	16.51	27.4	33.59	6.17	20.26	51.39	18.62	5.59	4.55			
	HEMBA1006885	29.88	29.68	41.54	20.77	25.78	20.37	13.71	10.53	21.42	*		-
	HEMBA1006886	94.54	114.96	86.8	8.15	45.42	40.45	16.06	32.92	14.53	**	**	-
30	HEMBA1006889	11.07	12.36	15.21	4.3	6.85	5.29	4.87	2.48	1.64	**	**	-
	HEMBA1006896	72.84	75.71	95.1	25.42	32.71	26.4	32.9	16.88	9.13	**	**	-
	HEMBA1006900	25.47	32.8	47.12	42.47	30.76	32.5	22.96	11.97	13.31			
	HEMBA1006902	4.95	12.4	20.5	3.65	6.21	3.85	6.17	0.96	2.8			
	HEMBA1006912	17.87	28.61	49.99	20.94	22.1	17.02	26.3	12.33	21.55			
	HEMBA1006914	76.35	138.05	152.36	81.86	82.01	60.45	85.41	43.28	74.2			
35	HEMBA1006916	15.23	15.18	19.35	6.9	10.02	9.36	4.27	4.91	5.74	**	**	-
	HEMBA1006921	5.69	9.45	11.27	4.84	7.39	7.2	5.96	4.4	4.47			
	HEMBA1006926	14.39	14.83	25.68	4.9	10.25	8.6	7.17	9.16	6.2	*		-
	HEMBA1006927	8.1	6.16	12.12	3.55	6.9	3.55	4.27	4.44	3.56			
	HEMBA1006929	20.15	20.6	39.98	22.07	23.94	22.4	25.87	18.49	21.97			
	HEMBA1006936	9.54	10.99	23.15	1.82	9.22	9.34	13.47	4.19	5.58			
40	HEMBA1006938	3.12	8.25	12.19	4.54	5.27	8.96	3.85	0.26	1.77			
	HEMBA1006941	38.07	33.9	81.07	14.16	37.03	19.11	37.54	10.57	9.16			
	HEMBA1006942	17.04	18.44	31.05	13.54	11.67	15.34	9.95	7.49	11.08			
	HEMBA1006945	67.94	90.41	117.96	45.68	44.82	62.84	58.07	38.55	55.06			
	HEMBA1006949	5.04	6.37	14.93	11.38	7.05	7.71	7.34	3.55	6.74			
	HEMBA1006952	4.19	5.26	9.54	3.87	5.23	3.34	4.22	1.4	1.92			
45	HEMBA1006960	34.21	40.14	82.69	40.95	44.04	37.38	52.24	36.27	39.73			
	HEMBA1006973	11.14	12.47	24.84	14.07	12.49	8.94	10.47	5.46	6.01			
	HEMBA1006974	9.69	21.72	26.59	5.58	10.54	8	10.23	6.86	3.65			
	HEMBA1006976	5.49	4.82	13.28	5.67	2.91	2.68	2.79	1.22	3.42			
	HEMBA1006989	5.64	5.97	15.87	14.35	9.67	15.25	5.09	3.23	6.48			
	HEMBA1006993	22.88	33.04	62.59	43.82	36.96	35.47	29.4	20.95	25.28			
50	HEMBA1006996	6.77	6.15	10.45	9.29	8.92	7.56	4.85	2.62	3.17	*		-
	HEMBA1007001	13.6	18.68	46.24	26.01	27.9	24.22	17.93	11.6	13.83			
	HEMBA1007002	38.2	51.66	86.51	157.46	90.61	115.16	37.83	43.86	26.69			
	HEMBA1007013	4.23	5.6	9.85	5.49	4.83	5.04	4.32	1.34	5.39			
	HEMBA1007016	13.73	18.8	46.37	32.25	24.75	25.55	26.93	13.32	18.08			
	HEMBA1007017	1.76	2.36	7.34	6.45	3.5	5.8	4.75	0.45	2.16			
55	HEMBA1007018	12.78	19.44	26.15	6.88	7.17	10.67	5.95	5.18	4.75	*		-
	HEMBA1007044	4.27	3.89	8.13	7.26	4.08	4.08	4.49	2.95	4.25			
	HEMBA1007045	3.76	6.62	12.6	6.66	6.82	7.16	7.91	2.23	5.58			



Table 380

	HEMBA1007051	8.21	9.64	21.16	10.38	7.94	9.61	8.59	4.82	5.46		
	HEMBA1007052	0.84	3.34	5.89	3.8	5.54	5	4.04	2.23	3.75		
5	HEMBA1007053	13.43	20.61	15.83	23.76	9.7	6.82	3.37	2.88	5.47	**	-
	HEMBA1007057	6.84	7.67	12.49	5.42	9.68	14.27	10.77	4.02	8.83		
	HEMBA1007062	5.25	11.04	5.4	4.94	7.78	6.88	7.11	2.74	5.57		
	HEMBA1007063	19.82	23.76	40.56	22.16	18.37	20.33	18.69	15.25	20.25		
	HEMBA1007066	7.17	6.3	7.54	7.55	3.16	6.35	4.34	2.31	5.66	*	-
10	HEMBA1007069	6.08	6.94	13.93	10.41	5.55	7.88	5.56	3.75	4.11		
	HEMBA1007073	5	7.14	13.19	9.06	6.96	8.85	10.68	5.02	4.92		
	HEMBA1007076	9.13	8.92	19.82	9.03	17.18	17.73	15.84	7.01	8.52		
	HEMBA1007078	47.57	62.26	92.7	36.29	60.73	51.72	32.07	18.35	34.97		
	HEMBA1007080	86	60.21	81.69	89.81	65.76	74.19	50.6	40.71	38.08	*	-
	HEMBA1007084	10.6	15.68	20.31	13.17	16.74	11.58	13.37	8.47	13.17		
15	HEMBA1007085	27.29	31.32	26.53	13.81	11.35	9.85	7.06	8.85	9.17	**	**
	HEMBA1007087	17.6	23.13	29.36	17.3	13.84	15.36	6.49	22.47	10.72		
	HEMBA1007089	21.17	21.1	33.63	20.7	38.69	28.03	18.24	32.57	32.51		
	HEMBA1007095	201.88	116.22	315.3	326.58	303	223.56	75.5	112.08	127.01		
	HEMBA1007101	27.84	40.49	45.85	23.93	27.74	34.28	41.09	23.85	46.77		
	HEMBA1007104	4.09	6	7.77	5.68	5.26	4.31	5.49	1.3	6.52		
20	HEMBA1007106	21.73	33.28	23.78	16.4	24.34	20.37	10.72	5.09	4.25	**	-
	HEMBA1007112	9.74	14.28	16.52	10.26	12.13	8.53	8.39	3.2	3.6	*	-
	HEMBA1007113	21.85	25.07	43.45	24.93	19.55	20.96	26.57	21.39	27.54		
	HEMBA1007121	143.44	168.43	201.05	310.6	189.7	223.39	139.17	100.56	162.13		
	HEMBA1007129	6.41	8.28	18.59	3.42	2.84	6.23	5.66	3.45	4.93		
25	HEMBA1007147	12.43	15.07	27.38	13.28	12.69	11.69	10.77	9.49	8.81		
	HEMBA1007149	15.43	22.2	36.85	20.24	33.61	28.67	16.97	12.22	16.92		
	HEMBA1007151	6.66	4.91	10.19	4.89	4.76	3.64	3.37	0.61	3.29		
	HEMBA1007172	5.54	5.79	15.25	6.45	6.57	4.48	5.2	2.26	4.93		
	HEMBA1007174	5.55	6.74	11.4	7.96	7.31	3.31	8.36	1.4	3.1		
	HEMBA1007176	10.89	13.76	22.08	12.85	11.37	10.5	5.77	8.47	15.97		
	HEMBA1007178	12.93	22.04	21.56	10.13	15.89	11.16	5.44	5.45	3.49	**	-
30	HEMBA1007185	12.08	13.89	28.24	5.12	12.57	13.87	7.15	7.65	10.67		
	HEMBA1007186	7.21	3.2	19.91	4.57	4.73	5.62	4.03	0.89	3.73		
	HEMBA1007194	17.48	18.75	30.8	17.47	18.26	18.1	18.81	10.34	19.89		
	HEMBA1007200	4.21	4.82	12.05	2.35	4.05	3.94	2.19	1.93	1.96		
	HEMBA1007203	17.41	23.17	30.14	16.76	21.31	8.75	11.68	7.36	6.25	*	-
	HEMBA1007206	25.5	42.75	37.89	30.71	35.28	24.97	38.96	21.71	36.83		
35	HEMBA1007224	24.39	40.17	34.49	15.91	19.51	9.53	6.52	8.53	10.32	*	**
	HEMBA1007226	89.72	73.23	106.85	134.34	88.67	116.09	67.3	41.82	79.65		
	HEMBA1007240	13.54	17.35	25.69	5.08	7.14	11.16	4.24	5.15	6.41	*	-
	HEMBA1007241	5.35	7.7	9.62	3.24	3.12	3.91	4.59	2.56	3.21	*	*
	HEMBA1007242	4.41	5.32	8.31	2.05	4.24	3.88	2.68	0.75	5.03		
	HEMBA1007243	111.71	101.13	126.82	187.45	120.72	165.9	80.87	65.01	83.79	*	-
40	HEMBA1007251	4.65	5.56	13.42	3.87	5.2	4.27	3.75	1.77	3.34		
	HEMBA1007256	7.71	17.43	18.8	11.41	15.37	11.45	13.72	5.68	6.36		
	HEMBA1007267	27.14	33.68	57.79	28.23	30.36	27.93	22.24	21.62	27.1		
	HEMBA1007273	5.82	10.89	12.53	5.12	4.08	4.32	3.9	1.99	5.52		
	HEMBA1007279	8.03	6.83	14.11	6.96	6.78	5.74	5.78	2.58	3.49		
	HEMBA1007281	4.41	6.17	11.59	1.95	1.64	1.99	3.42	2.15	2.75		
45	HEMBA1007283	10.13	14.5	18.59	11.27	10.46	9.5	8.86	8.35	11.65		
	HEMBA1007288	10	10.12	23.07	7.33	8.9	6.31	9.07	7.22	9.19		
	HEMBA1007291	3.94	6.53	14.21	2.35	5.74	4.15	6.79	3.29	5.42		
	HEMBA1007299	60.36	57.45	88.44	47.01	83.94	54.92	41.98	17.99	24.76	*	-
	HEMBA1007300	10.43	10.11	14.15	17.47	5.8	7.51	10.92	2.6	3.93		
	HEMBA1007301	10.28	11.15	10.5	7.08	5.07	5.8	3.91	4.02	3.67	**	**
50	HEMBA1007319	7.15	12.6	10.93	3.57	6.52	4.89	3.16	3.33	2.24	*	*
	HEMBA1007320	6.22	6.62	11.18	5.17	5.74	4.76	5.15	2.1	2.94		
	HEMBA1007322	281.14	504.93	265.82	479.23	433.13	233.63	384.76	246.29	107.4		
	HEMBA1007323	3.87	5.98	13.69	3.16	3.64	1.67	4.69	0.43	1.85		
	HEMBA1007326	33.32	37.02	90.88	53.8	48.19	37.22	52.37	23.73	38.43		
	HEMBA1007327	14.51	15.7	50.08	17.82	23.55	19.83	20.48	9.78	17.51		
55	HEMBA1007332	15.93	13.1	23.53	14.44	19.66	12.93	14.13	7.11	7.2		
	HEMBA1007341	8.96	9.53	11.63	7.92	6.35	6.27	7.48	4.06	5.93	*	*
	HEMBA1007342	5.2	5.9	6.99	1.75	3.52	2.76	4.48	1.49	2.47	*	*

Table 381

	HEMBA1007347	16.98	22.65	29.56	14.57	13.83	11.3	16.82	11.86	19.8			
5	HEMBA1007353	5.79	10.55	11.68	3.83	9.63	8.03	10.26	4.85	8.24			
	HEMBA1000005	12.22	17.75	30.52	11.82	12.78	11.43	13.73	6.39	17.44			
	HEMBA1000008	18.71	35.13	41.01	19.83	22.41	13.75	23.85	15.07	25.11			
	HEMBA1000018	26.09	49.37	73.92	38.01	40.34	30.35	46.13	23.51	34.37			
	HEMBA1000024	16.68	21.57	43.98	24.42	20.7	22.54	19.03	14.92	22.2			
	HEMBA1000025	4.76	6.51	12.97	5.38	4.72	5.89	4.38	2.53	3.35			
10	HEMBA1000030	20.29	17.68	33.24	12.16	16.77	10.61	16.77	10.43	14.37			
	HEMBA1000036	14.36	14.21	18.16	2.88	10.75	5.3	7.22	6.69	3.23	*	**	-
	HEMBA1000037	11.11	16.21	12.93	4.27	8.42	4.3	6.83	2.67	4.79	*	*	-
	HEMBA1000039	8.22	15.6	26.39	9.92	10.66	6.88	12.98	7.81	13.65			
	HEMBA1000044	11.18	16.44	31.14	11.2	12.12	8.02	10.52	6.21	8.17			
	HEMBA1000048	8.23	14.79	19.17	7.61	10.2	7.2	15.14	3.23	4.66			
15	HEMBA1000050	12.03	11.84	30.06	14.4	13.92	13.02	11.35	6.38	12.59			
	HEMBA1000054	10.07	11.4	26.35	13.58	11.4	7.91	11.76	6.55	12.26			
	HEMBA1000055	458.88	310.46	850.13	127.99	485.16	208.47	362.27	384.63	141.27			
	HEMBA1000059	37.26	47.72	97.02	40.48	50.48	36.83	47.77	33.17	34.67			
	HEMBA1000072	84.93	93.08	177.56	168.05	149.4	148.43	84.23	55.56	75.03			
	HEMBA1000081	14.03	23.77	42.88	15.97	19.18	19.43	14.35	5.64	10.31			
20	HEMBA1000083	11.03	18.35	42.57	17.47	14.86	14.26	18.14	9.46	16.73			
	HEMBA1000089	12.54	18.95	30.4	15.64	14.81	12.6	22.7	8.13	18.39			
	HEMBA1000094	10.67	10.41	27.93	13.66	21.42	16.12	14.95	8.63	10.48			
	HEMBA1000097	6.26	10.91	14.76	6.71	9.5	4.54	15.21	6.91	3.77			
	HEMBA1000099	14.89	12.94	32.83	17.41	17.02	13.25	13.99	10.91	12			
	HEMBA1000103	79.17	84.17	154.39	129.48	133.3	142.91	117.04	80.44	93.95			
25	HEMBA1000106	13.4	15.97	19.47	7.19	4.59	5.52	5.12	3.42	4.98	**	**	-
	HEMBA1000113	4.8	10.67	20.57	6.45	7.88	9.01	9.02	3.11	6.76			
	HEMBA1000119	3.97	10.01	14.45	4.41	4.33	3.8	9.37	5.02	5.7			
	HEMBA1000133	88.66	47.28	101.21	23.18	118.13	70.04	134.7	41.76	81.57			
	HEMBA1000134	13.38	15.77	31.72	20.8	11.19	14.5	6.59	5.64	9.53			
	HEMBA1000136	34.17	26.36	69.3	67.42	34.73	49.05	25.95	21.33	26.27			
30	HEMBA1000141	7.91	11.34	20.35	10.92	8.05	11.46	11.73	5.94	9.7			
	HEMBA1000144	8.4	6.34	18.36	7.4	9.42	9.69	10.21	5.05	11.22			
	HEMBA1000147	3.5	3.8	22	5.61	6.52	8.28	7.06	1.83	3.83			
	HEMBA1000152	1.94	5.3	5.59	10.75	5.38	4.1	5.98	1.86	3.56			
	HEMBA1000154	7.08	8.64	11.01	9.8	10.82	8.45	9.52	5.05	11.09			
	HEMBA1000155	7.22	13.83	13.07	9.95	12.99	12.51	9.62	5.43	10.29			
35	HEMBA1000173	36.12	47.88	77.86	40.67	28.34	43.42	25.94	23.15	34.58			
	HEMBA1000175	4.3	6.41	7.7	6	3.69	3.11	3.98	4.45	4.04			
	HEMBA1000176	23.34	24.4	50.1	18.86	26.55	28.15	17.6	14.1	16.3			
	HEMBA1000198	1.73	5.17	9.68	5.19	3.63	4.66	4.31	1.03	3.4			
	HEMBA1000208	2.42	2.22	6.16	4.71	3	3.25	2.71	1.91	2.68			
	HEMBA1000209	4.99	7.73	19.16	5.65	5.94	7.5	3.72	1.31	4.4			
40	HEMBA1000212	4.66	5.69	7.88	3.69	6.97	3.08	4.71	1.75	3.95			
	HEMBA1000215	16.57	20.63	27.19	17.82	25.31	15.88	26.39	12.95	25.36			
	HEMBA1000217	25.38	37.33	52.96	16.88	15.01	12.09	9.3	23.54	15.2	*		-
	HEMBA1000218	31.37	54.57	73.09	37.79	38.52	34.06	37.08	24.06	36.49			
	HEMBA1000226	12.28	16.29	20.13	10.11	7.98	11.16	5.4	9.82	9.11	*		-
	HEMBA1000230	5.26	3.6	7.07	0.71	2.52	2.36	2.7	2.25	2.54	*	*	-
45	HEMBA1000240	5.06	6.06	9.84	4.39	4.5	5.46	2.75	2.24	3.3	*		-
	HEMBA1000244	7.48	12.78	15.39	11.19	10.98	11.37	6.63	4.57	10.35			
	HEMBA1000250	1.27	3.14	7.4	1.44	3.59	2.75	1.47	0.52	2.71			
	HEMBA1000258	10.17	16.3	24.98	15.18	17.62	13.97	14.16	8.49	16.99			
	HEMBA1000264	26.46	35.45	52.88	26.93	18.98	21.08	16.44	18.13	29.32			
	HEMBA1000266	12	14.67	15.28	5.33	5.8	4.87	9.31	5.79	7.42	**	*	-
50	HEMBA1000272	8.27	9.13	14.25	3.35	4.95	7.95	4.41	2.77	4.49	*		-
	HEMBA1000274	6.98	5.53	13.54	4.71	5.52	4.64	3.24	3.87	5.65			
	HEMBA1000276	5.09	3.14	11.53	3.19	3.43	4.43	2.41	0.94	4.11			
	HEMBA1000284	6.8	5.53	21.28	3.19	4.36	4.46	4.47	2.08	4.87			
	HEMBA1000307	8.46	14.9	24.21	13.5	12.6	8.38	8.3	4.98	7.88			
	HEMBA1000309	5.61	8.47	14.17	8.25	9.84	9.39	9.88	4.06	6.44			
55	HEMBA1000312	6.97	8.62	14.26	14.76	8.04	11.17	5.36	4.07	7.05			
	HEMBA1000317	7.52	4.64	7.99	3.4	3.92	3.39	4.7	5.98	4.31	*		-
	HEMBA1000318	6.93	8.7	14.09	8.17	6.23	6.97	7.59	3.11	9.29			

Table 382

	HEM881000332	4.52	4.05	10.22	2.71	3.85	3.38	4.09	2.98	4.92				
	HEM881000335	4.77	4.71	13.27	5.2	6.34	6.3	5.06	1.38	4.17				
5	HEM881000336	4.61	9.32	11.37	1.79	3.32	1.88	2.23	1.53	1.7	*	*	-	-
	HEM881000337	29.33	35.43	67.58	48.11	46.55	55.37	21.92	22.71	26.93				
	HEM881000338	34.7	54.08	50.89	33.23	39.29	35.27	51.12	24.63	33.57				
	HEM881000339	10.36	11.59	21.89	13.7	11	9.9	8.4	6.43	14.47				
	HEM881000341	7.15	6.94	11.5	5.95	5.91	6.13	8.18	5.44	9.71				
10	HEM881000343	22.54	22.93	36.07	24.96	20.99	25.34	24.47	20.51	25.26				
	HEM881000354	24.93	29.93	37.49	16.95	17.28	19.25	24.74	17.57	19.26	*		-	
	HEM881000358	4.2	3.56	9.08	2.24	3.75	2.51	2.41	0	3.07				
	HEM881000369	7.77	9.59	8.26	0	3.16	0.74	4.97	3.09	8.59	**		-	
	HEM881000373	4.9	5.6	9.86	3.73	5.67	3.02	3.88	2	4.12				
	HEM881000374	33.91	39.77	79.58	37.61	43.98	33.27	46.4	29.37	24.06				
15	HEM881000376	23.61	37.46	51.78	28.25	29.92	24.65	24.75	22.13	31.75				
	HEM881000383	18.87	23.34	28.75	7.22	8.14	5.48	8.08	3.98	4.53	**	**	-	-
	HEM881000391	18.94	23.82	39.78	18.85	17.85	18.64	26.87	13.66	21.63				
	HEM881000399	7.91	9.01	13.97	2.99	3.3	3.33	3.37	1.8	1.69	*	*	-	-
	HEM881000402	5.66	7.15	13.91	3.49	5.23	2.79	6.8	2.16	2.32				
	HEM881000404	4.49	5.13	14.15	2.37	3.5	4.1	3.34	1.25	1.09				
20	HEM881000407	10.22	16.01	27.46	10.21	12.59	7.8	5.46	2.69	5.89				
	HEM881000420	8.96	13.82	23.72	10.31	11.56	10.07	12.86	5.36	9.15				
	HEM881000430	87.5	75.56	120.02	34.45	32.4	42.69	83.02	74.93	33	*		-	
	HEM881000434	34.1	37.7	48.77	30.73	22.51	21.34	32.9	22.77	33.21	*		-	
	HEM881000438	4.47	5.36	6.73	3.08	3.98	3.03	2.33	1.63	2.04	*	**	-	-
	HEM881000441	14.04	26.42	32.37	16.04	15.64	13.8	26.09	16.54	18.05				
25	HEM881000447	26.11	49.46	42.13	39.56	42.28	10.3	26.83	15.38	20.58				
	HEM881000449	4.61	5.17	16.11	3.66	5.27	3.1	5.36	1.18	6.41				
	HEM881000453	36.46	39.41	48.95	17.29	27.48	11.55	15.42	4.83	8.75	*	**	-	-
	HEM881000455	7.98	15.4	31.12	12.14	13.6	12.23	19.02	4.77	15.17				
	HEM881000472	8.9	8.65	20.38	10.03	8.41	7.69	7.24	3.85	5.6				
	HEM881000480	18.47	20.31	37.47	19.05	17.04	11.84	20.16	15.95	20.84				
30	HEM881000486	36.69	36.48	47.19	21.3	19.24	16.88	39.82	23.52	22.96	**		-	
	HEM881000487	6.37	6.26	12.27	7.11	4.47	4.08	6.03	4.45	5.18				
	HEM881000490	32.85	71.05	75.4	38.48	33.85	25.5	47.17	24.97	28.6				
	HEM881000491	10.98	13.88	21.94	11.39	11.14	7.83	9.44	3.7	10.75				
	HEM881000492	11.93	15.38	18.28	8.6	7.89	5.65	7.79	2.28	4.01	*	*	-	-
	HEM881000493	3.37	12.88	19.63	10.93	27.47	71.09	13.51	1.84	8.84				
35	HEM881000510	11.39	18.53	31.92	20.35	17	14.3	15.03	12.6	21.32				
	HEM881000516	5	6.48	9.48	3.37	2.52	5.44	4.17	3.02	4.74				
	HEM881000518	5.79	7.56	16.99	3.63	4.25	4.51	8.74	3.95	5.88				
	HEM881000523	16.51	22.61	33.14	14.54	14.09	13.74	17.51	11.52	13.77				
	HEM881000530	6.45	6.62	14.38	4.57	5.23	3.03	6.95	3.14	3				
	HEM881000542	11.01	10.05	25.81	5.58	5.42	6.88	5.64	1.26	2.47				
40	HEM881000550	7.5	9.67	18.88	5.5	6.7	4.85	3.66	1.58	2.78				
	HEM881000554	23.66	38.54	60.71	31.87	34.21	23.57	36.99	19.84	22.96				
	HEM881000556	5.71	9.66	13.39	4.65	5.23	10.47	3.94	4.86	6.74				
	HEM881000564	7.31	9.82	18.45	11.61	10.28	10.62	15.74	5.76	7.4				
	HEM881000567	20.61	20.17	47.53	8.75	7.89	6.38	13.88	8.67	4.74				
	HEM881000569	5.63	6.5	12.71	2.7	3.07	4.45	4.1	3.02	2.02				
45	HEM881000573	32.51	36.2	72.29	43.4	30.21	37.17	37	20.09	25.58				
	HEM881000575	14.84	26.39	42.18	17.14	17.78	15.29	22.14	11.44	16.53				
	HEM881000579	12.25	14.06	28.61	6.45	6.01	11.92	12.64	5.71	5.94				
	HEM881000585	4.75	6.58	10.45	5.85	6.89	6.63	6.35	0.91	4.03				
	HEM881000586	9.22	12.19	32.5	16.92	12.87	17.45	7.51	6.24	9.01				
	HEM881000589	11.66	16.54	23.61	18.44	15.28	16.1	11.67	7.91	7.82				
50	HEM881000591	12.71	17.74	34.25	24.96	19.88	19.6	12.6	9.24	10.66				
	HEM881000592	4.57	3.51	5.52	1.66	2.6	2.47	2.07	3.49	1.32	*		-	
	HEM881000593	91.28	145.08	255.41	284.78	269.98	262.29	122.51	62.28	150.94				
	HEM881000595	28.02	34.64	53.56	11.28	18.32	41.15	22.88	29.26	17.38				
	HEM881000598	22.01	31.15	65.04	24.88	33.54	29.35	68.32	20.78	23.46				
	HEM881000611	2.41	5.2	8.28	7.8	5.78	3.85	5.15	1.83	3.38				
55	HEM881000617	53.65	47.37	106.59	110.75	55.04	84.65	42.52	37.92	47.84				
	HEM881000623	31.42	31.62	79.25	50.87	28.93	40.28	29.97	27.06	51.77				
	HEM881000630	5.75	17.04	13.07	8.82	8.82	8.76	7.96	4.83	11.56				

Table 383

	HEM881000631	17.85	20.22	28.17	18.29	17.71	18	15.1	13.03	22.53			
	HEM881000632	9.09	8	17.51	9.07	9.79	9.7	5.89	4.13	8.31			
5	HEM881000636	2.41	3.55	6.37	2.23	5.22	2.73	5.28	1.01	4.17			
	HEM881000637	10.09	17.58	15.59	10.48	18.82	18.4	10.07	3.67	7.99			
	HEM881000638	2.99	4.17	4.52	3.32	2.17	3.48	2.49	1.75	2.68	*		
	HEM881000642	39.5	47.36	81.46	47.61	39.34	45.01	39.82	28.49	56.57			
	HEM881000643	19.66	15.32	32.08	23.95	12.4	14.81	11.1	10.59	13.67			
10	HEM881000649	12.99	15.1	28.14	16	12.05	14.32	13.77	8.35	17			
	HEM881000652	14.35	8.01	17.67	7.91	13.41	10.82	9.88	9.25	11.18			
	HEM881000655	4.61	7.58	7.57	5.6	5.2	3.31	4.16	0.72	5.12			
	HEM881000665	4.16	6.24	9.15	3.47	7.38	6.78	5.21	1.62	5.11			
	HEM881000668	16.93	27.34	0.25	1.82	1.14	0.36	23.87	15.76	19.86			
	HEM881000671	38.43	46.48	92.78	44.14	31.73	40.3	25.53	28.64	41.28			
15	HEM881000673	32.99	36.97	43.71	17.4	18	19.87	6.02	26.42	8.4	**	*	-
	HEM881000679	47.01	69.39	88.27	46.41	43.74	44.85	52.81	42.78	53.45			
	HEM881000684	6.8	10.16	24.24	9.32	9.77	12.54	6.96	8.48	13.11			
	HEM881000692	16.03	14.55	25.59	15.28	15.92	17.55	16.09	8.5	14.57			
	HEM881000693	1.76	2.64	8.52	1.53	4.27	2.95	4.06	0.19	6.13			
	HEM881000705	14.59	17.08	31.29	17.89	15.24	18.52	13.25	7.08	17.6			
20	HEM881000706	11.29	12.22	20.56	12.35	17.3	12.09	6.4	4.7	7.15	*		-
	HEM881000709	45.75	62.83	118.05	70.74	40.37	58.09	48.11	45.53	67.69			
	HEM881000714	31.43	34.95	47.38	12.83	21.37	16.81	5.14	8.31	8.35	*	**	-
	HEM881000725	5.12	8.87	10.38	4.23	3.1	4.36	4.23	1.66	4.96			
	HEM881000726	0.86	1.95	5.91	0.06	0.38	0.65	0.77	3.05	1.2			
	HEM881000729	6.42	9.45	14.46	7.38	5.18	5.16	5.32	4.5	6.56			
25	HEM881000738	18.18	14.39	28.4	16.66	7.78	8.45	31.84	5.87	7.73			
	HEM881000749	19.05	25.67	36.38	23.07	19.8	20.09	17.18	15.06	19.35			
	HEM881000763	2.4	3.95	6.27	1.43	7.01	5.93	4.26	0.57	3.97			
	HEM881000770	32.56	40.83	87.59	46.89	28.6	43.89	33.53	25.96	52.34			
	HEM881000774	35.04	53.35	80.31	43.91	38.96	45.26	39.09	37.25	56.98			
	HEM881000777	45.62	74.38	70.43	17.25	25.76	25.38	18.75	21.39	27.43	*	*	-
30	HEM881000781	6.33	5.26	11.47	6.25	5.6	4	3.41	2.88	6.03			
	HEM881000788	18.37	23.49	32.23	14.46	15.9	16.37	22.44	12.27	19.59			
	HEM881000789	23.79	24.39	34.32	14.31	19.85	15.3	18.54	10.27	14.08	*	*	-
	HEM881000790	5.59	8.56	17.48	2.6	6	2.29	4.26	1.79	5.06			
	HEM881000794	18.79	29.68	40.8	14.17	25.07	14.74	20.31	17.36	24.13			
	HEM881000807	12.94	8.25	2.03	1.02	2.13	2.36	2.69	4.28	6.87			
35	HEM881000809	78.77	111.21	120.34	77.13	62.86	41.38	80.78	69.07	111.98			
	HEM881000810	10.52	9.56	13.14	4.85	2.89	5.55	9.37	2.32	10.71	**		-
	HEM881000821	11.49	9.52	21.32	7.91	10.41	6.87	11.4	5.99	7.83			
	HEM881000822	14.47	17.81	31.19	12.64	15.48	12.05	15.29	6.81	15.5			
	HEM881000826	7.31	8.22	12.01	4.01	6.22	5.16	2.28	1.16	3.63	*		-
	HEM881000827	3.32	10.97	13.01	2.13	2.92	3.29	2.14	1.1	3.35			
40	HEM881000831	2664.2	3968.9	2993.4	2288.3	2955.9	3122.5	3699.5	1769.3	603.46			
	HEM881000835	65.9	87.92	134.3	99.52	82.05	71.78	46.56	49.76	78.94			
	HEM881000840	22.85	22.57	43.26	24.08	23.34	18.79	20.99	18.48	32.32			
	HEM881000848	11.78	12.27	18.41	9.27	11.15	6.47	11.75	6.28	10.74			
	HEM881000852	6.96	7.13	13.91	5.13	5.29	6.06	3.72	3.05	2			
	HEM881000857	14.9	19.2	33.57	16.67	15.76	14.92	14.34	9.21	17.14			
45	HEM881000858	18.62	21.62	40.52	17.01	24.14	29.4	19.12	14.81	25.58			
	HEM881000867	3.35	5.16	11.87	1.01	3.43	0.49	5.8	0.59	7.29			
	HEM881000870	5.48	10.65	17.84	3.33	10.48	4.74	3.16	0.41	3.45			
	HEM881000876	9.67	10.87	29.49	19.7	15.97	14.54	9.25	6.54	15.24			
	HEM881000881	16.87	17.18	33.12	17.09	13.5	10.07	12.12	11.55	18.55			
	HEM881000883	6.22	6.79	8.96	2.61	2.5	1.97	4.54	1.83	3.25	**	*	-
50	HEM881000887	5.96	5.57	6.2	3.69	2.17	1.88	2.97	1.27	2.62	**	**	-
	HEM881000888	3.12	5.25	10.45	4.39	3.56	2.35	3.24	2.38	1.97			
	HEM881000890	10.06	35.98	23.82	9.78	19.94	41.91	13.4	7.59	9.49			
	HEM881000893	34.65	25.07	51.31	20.43	19.67	19.95	21.33	13.24	12.88			
	HEM881000900	14.11	15.32	20.53	11.04	14.54	9.38	11.56	4.15	3.3	*		-
	HEM881000905	8.7	11.8	4.84	3.81	3.66	3.74	10.34	4.58	8.59			
55	HEM881000908	10.34	11.07	11.16	10.97	10.92	24.1	19.82	7.35	8.29			
	HEM881000910	14.49	13.52	29.52	12.54	13.67	12.24	17.07	12.01	16.77			
	HEM881000913	52.28	41.72	87.34	40.16	51.04	32.05	56.11	40.33	43.91			

Table 384

	HEM881000915	26.06	60.99	57.47	25.29	36.05	22.49	27.81	17.27	27.94			
5	HEM881000917	5.69	5.32	12.64	3.03	4.44	3.24	2.96	0.58	2.57			
	HEM881000927	17.9	20.69	49.41	20.99	18.29	12.76	18.76	15.57	19.4			
	HEM881000932	14.04	31.9	58.79	23.84	30.24	22.56	24.51	13.79	19.35			
	HEM881000933	73.2	82.97	106.78	17.69	17.17	51.59	30.19	46.68	77.12	*	-	
	HEM881000936	28.64	37.39	39.34	11.49	17.42	18.08	9.46	19.76	21.12	**	*	-
	HEM881000939	13.01	16.47	24.62	8.79	10.18	11.8	13.33	5.75	13.18			
10	HEM881000941	55.55	67.95	96.78	34.29	51.94	34.02	64.38	50.22	47.74			
	HEM881000947	13.1	15.93	33.36	11.69	15.06	7.82	14.81	8.66	11.7			
	HEM881000954	9.7	14.84	29.47	10.7	10.34	11.24	13.58	8.18	14.09			
	HEM881000959	5.31	7.05	16.81	1.63	2.59	1.53	2.83	0	2.89			
	HEM881000973	7.09	9.47	31.83	11.47	11.07	10.69	11.63	4.69	9.55			
	HEM881000975	3.47	3.38	0.39	0.25	0.11	0.78	2.64	0.48	3.5			
15	HEM881000981	13.64	11.74	28.6	8.77	7.91	9.41	10.88	6.85	13.87			
	HEM881000985	21.62	19.08	51.54	22.07	25.82	18.12	29.3	14.45	17.75			
	HEM881000991	46.57	60.97	104.38	49.12	52.31	37.89	58.02	46.82	42.32			
	HEM881000996	7.55	10.13	19.44	15.43	7.58	7.76	25.49	7.93	12.48			
	HEM881001000	8.66	10.27	29.46	13.94	12.61	10.4	13.32	7.07	9.02			
	HEM881001004	4.52	20.53	22.05	7.15	7.85	4.71	7.51	4.91	9.37			
20	HEM881001008	27.45	57.49	106.29	36.82	29.09	41.72	54.86	25.88	43.51			
	HEM881001011	13.92	18.59	22.13	8.85	6.12	13.6	9.78	8.17	13.65			
	HEM881001014	4.93	5.88	7.48	5.94	4.03	6.17	3.66	1.76	2.96	*	-	
	HEM881001020	38.49	45.64	94.13	52.12	43.15	44.7	42.48	28.95	25.72			
	HEM881001024	14.35	17.88	33.12	21.84	15.86	15.33	12.31	9.54	11.76			
	HEM881001026	36.33	37.82	64.87	35.84	31.03	31.81	34.99	27.91	28.23			
25	HEM881001037	29.37	38.91	99.73	42.44	38.61	41.96	49.51	23.14	48.42			
	HEM881001042	40.43	19.68	79.17	12.87	30.43	38.57	43.54	27.06	24.73			
	HEM881001046	1.02	3.17	4.37	2.13	2.63	1.33	3.19	0	2.81			
	HEM881001047	3.32	3.99	7.05	6.87	5.14	9.57	4.92	2.39	5.02			
	HEM881001048	14.93	18.87	36.47	38.03	15.11	21.97	9.91	8.51	13.37			
	HEM881001051	16.67	10.51	26.31	24.66	18.42	23.37	16.85	8.02	15.72			
30	HEM881001056	5.76	6.07	15.19	9.62	10.04	7.15	7.61	2.99	9.72			
	HEM881001058	13.02	13.37	20.82	14.04	12.97	13.5	13.64	8.33	17.02			
	HEM881001060	6.48	6.79	11.56	3.09	7.6	8.52	5.42	2.73	5.08			
	HEM881001063	7.02	9.34	7.27	6.14	6.79	5.01	6.52	5.39	11.16			
	HEM881001068	12.88	13.51	18.25	11.13	9.67	11.92	6.97	9.12	12.67			
	HEM881001082	19.71	21.28	25.07	26.2	26.41	15.74	14.59	12.53	27.85			
35	HEM881001095	9.14	8.65	18.5	8.62	9.69	8.93	5.69	6.23	9.72			
	HEM881001096	44.08	45.29	88.46	46.23	37.21	42.49	31	20.55	25.13			
	HEM881001101	14.24	13.37	19.97	9.53	14.04	14.7	13.73	9.26	15.99			
	HEM881001102	5.29	6.01	11.42	4.54	5.69	5.17	5.82	3.61	6.55			
	HEM881001104	38.08	39.86	49.87	41.44	36.7	31.13	23.82	16.12	29.93	*	-	
	HEM881001105	44.24	54.5	42.57	26.76	34.74	25.96	40.78	32.97	47.69	*	-	
40	HEM881001112	7.32	12.27	12.46	6.67	5.72	6.06	2.52	6.54	5.01	*	-	
	HEM881001113	12.36	16.73	27.57	10.87	11.17	11.23	11.03	6.35	13.81			
	HEM881001114	10.5	25.04	16.53	8.31	9.62	7.81	7.26	6.53	13.76			
	HEM881001115	5.38	5.54	12.69	5.57	5.33	6.84	5.79	8.01	10.93			
	HEM881001117	24	32.48	48.34	30.8	26.94	25.33	34	33.8	46.28			
	HEM881001119	6.59	8.79	10.75	5.08	5.94	5.54	5.24	3.59	5.78	*	-	
45	HEM881001126	22.85	31.95	38.8	19.87	19.28	19.37	24.09	9.52	26.55			
	HEM881001133	2.49	4.42	8.71	2.43	5.35	3.57	4.22	0.99	2.59			
	HEM881001137	7.73	11.05	0	0.73	0.56	0.68	7.84	6.26	16.01			
	HEM881001142	3.94	3.85	6.48	2.73	4.14	2.88	2.5	3.32	8.04			
	HEM881001145	7.24	10.68	17.23	5.39	7.36	5.26	4.34	3.98	7.6			
	HEM881001151	3.26	6.63	6.67	3.5	3.71	2.34	0.95	2.94	4.05			
50	HEM881001153	3.1	3.77	9.68	1.47	2.32	1.7	2.21	0	1.53			
	HEM881001158	5.14	4.68	9.64	3.27	3.84	3.55	2.97	1.38	2.99			
	HEM881001169	31.33	46.44	55.42	27.9	34.88	25.03	41.78	26.83	37.34			
	HEM881001170	8.62	15.69	19.05	7.59	11.25	8.63	12.14	5.58	9.38			
	HEM881001175	2.65	3.14	5.1	4.52	2.61	4.91	2.72	1.86	6.12			
	HEM881001177	5.44	6.28	5.09	1.64	3.43	6.94	2.77	2.32	6.91			
55	HEM881001182	18.97	18.18	22.47	9.28	11.35	10.35	7.83	8.39	8.5	**	**	-
	HEM881001192	9.02	9.64	12.65	5.82	4.73	5.18	6.79	2.78	10.91	*	-	
	HEM881001199	4.71	4.4	13.79	2.26	2.76	5.59	3.91	3.02	2.96			

Table 385

	HEM881001200	13.2	15.34	26.9	9.43	12.58	11.64	13.55	8.01	17.32			
5	HEM881001208	18.63	26.31	21.34	16.48	23.59	8.33	19.57	7.02	6.33			
	HEM881001209	6.61	9.43	16.76	4.47	13.17	7.28	9.02	4.73	7.13			
	HEM881001210	2.22	5.57	9.4	5.43	2.97	2.71	2.73	1.63	4.83			
	HEM881001215	9.7	12.03	15.37	9.6	10.02	9.52	8.36	4.91	10.29			
	HEM881001217	10.51	10.25	17.62	6.77	6.49	7.62	10.25	4.74	16.86			
	HEM881001218	6	5.57	10.2	5.12	3.8	3.11	4.86	3.23	6.96			
10	HEM881001221	26.87	26.88	47.38	27.34	25.86	18.24	28	17.58	20.46			
	HEM881001224	16.71	16.42	17.84	3.84	6.91	9.28	7.94	2.93	4.93	**	**	-
	HEM881001230	17.23	21.95	42.64	15.78	20.28	10.72	28.16	18.31	25.4			
	HEM881001234	6.94	12.6	13.24	4.58	8.31	8.14	5.53	1.54	8.42			
	HEM881001235	4.87	3.91	1.57	0	1.12	0.17	1.32	0.88	4.29	*		-
	HEM881001237	5.75	2.45	7.86	3.45	3.48	1.87	2.9	1.6	4.06			
15	HEM881001242	16.88	13.35	16.55	9.1	8.16	9.95	11.54	6.31	10.57	**	*	-
	HEM881001244	35.65	49.79	60.5	32.41	25.43	27.28	45.76	28.88	37.22			
	HEM881001249	22.08	31.03	56.18	21.17	26.84	20.21	27.38	14.91	24.06			
	HEM881001253	28.9	34.49	70.42	28.32	28.95	21.57	41.19	24.41	34.07			
	HEM881001254	7.43	6.21	17.96	4.5	6.62	3.53	4.22	0.83	3.95			
	HEM881001266	69.19	45.43	92.09	93.11	71.97	69.72	54.64	34.46	57			
20	HEM881001267	104.19	98.07	152.36	13.92	33.06	57.1	34.39	45.85	70.55	*	*	-
	HEM881001271	34.55	33.29	51.36	34.34	20.46	23.71	30.23	24.87	29.48			
	HEM881001282	9.97	10.71	15.91	7.88	6.97	9.33	8.95	7.26	10.69			
	HEM881001287	3.47	3.55	8.03	3.1	1.84	1.48	2.02	1.47	1.7			
	HEM881001288	15.95	79.12	35.23	25.95	31.84	28.36	30.82	15.48	12.44			
	HEM881001289	22.37	27.51	58.3	21.33	26.2	17.4	27.36	15.96	26			
25	HEM881001290	4.47	6.46	15.08	5.02	4.85	3	3.41	2.52	3.43			
	HEM881001294	300.12	442.69	478.77	294.44	431.41	291.22	536.94	211.14	291.4			
	HEM881001299	11.76	27.27	23.84	14.94	18.67	41.4	14.69	12.85	20.6			
	HEM881001302	14.9	20.75	33.76	16.74	10.48	13.15	15.46	13.18	16.41			
	HEM881001304	20.54	137.19	27.35	22.15	29.27	12.7	29.77	14.5	13.73			
	HEM881001314	6.45	11.88	16.63	9.21	7.91	6.84	9.36	5.15	7.34			
30	HEM881001315	4.17	4.2	11.99	3.59	3.25	2.94	5.12	2.66	3.24			
	HEM881001317	58.08	165.69	115.47	26.35	66.22	33.54	41.88	11.39	13.42	*		-
	HEM881001326	7.12	11.9	25.13	9.45	10.76	5.58	7.57	2.53	8.72			
	HEM881001331	60.43	105.03	131	66.61	74.76	59.35	124.09	50.05	41.99			
	HEM881001335	0.53	0.14	1.28	1.92	0.74	0.41	1.38	0	1.24			
	HEM881001337	19.31	21.8	38.53	21.67	17.28	16.88	20.3	14.12	26.23			
35	HEM881001339	6.1	5.5	14.98	6.52	5.57	3.43	4.24	2.59	4.91			
	HEM881001344	11.08	7.69	21.58	3.98	10.13	4.45	6.01	7.37	4.42			
	HEM881001346	14.51	8.09	19.68	7.72	9.53	5.04	11.31	3.15	5.25			
	HEM881001348	2.18	3.12	12.35	0.43	2.84	1.52	3.82	0.54	2.87			
	HEM881001350	52.05	108.41	129.66	78.51	93.58	81.19	64.58	43.45	65.59			
40	HEM881001356	7.52	9.31	26.43	13.44	18.12	16.4	11.29	5.29	11.49			
	HEM881001364	8.27	9.27	21.55	13.04	8.88	12.02	9.82	4.71	9.74			
	HEM881001366	11.82	16.33	29.77	17.62	9.11	9.15	17.69	10.49	12.45			
	HEM881001367	34.9	33.46	79.86	33.05	29.6	26.79	45.62	23.04	29.37			
	HEM881001369	13.59	34.47	15.16	9.61	17.82	9.58	10.33	11.36	4.3			
	HEM881001380	5.78	6.69	14.57	4.06	3.91	3.5	3.91	2.87	4.28			
	HEM881001381	7.8	18.4	21.36	7.96	16.58	12.19	13.62	2.72	8.14			
45	HEM881001384	64.99	90.97	10.61	0.27	3.72	0.15	67.41	60.83	3.42			
	HEM881001387	12.67	18.5	30.56	17.22	19.87	15.36	19.61	9.85	12.99			
	HEM881001394	1.26	2.69	4.65	6.43	2.24	3.63	0.47	1.11	0.58			
	HEM881001407	7.9	11.42	30.12	19.8	14.97	11.43	10.87	6.27	10.35			
	HEM881001410	2.04	3.94	3.61	2.8	2.74	2.85	1.42	0.21	2.14			
	HEM881001413	4.48	4.13	8.85	5.53	3.83	5.6	1.34	2.67	1.9			
50	HEM881001419	11.47	23.84	24.98	19.26	14.85	15.61	11.95	7.31	16.96			
	HEM881001421	5.76	4.41	16.42	7.89	11.28	6.94	5.16	2.14	5.02			
	HEM881001424	2.91	4.4	4.11	0.76	0	0.56	5.88	1.84	0.07	**		-
	HEM881001426	14.06	23.97	51.32	27.45	25.66	29	18.89	8.5	8.91			
	HEM881001429	6.88	11.32	20.01	14.76	14.71	20	10.35	6.2	12.32			
	HEM881001436	18.71	17.94	33.05	24.24	11.69	16.55	21.47	12.89	21.69			
55	HEM881001443	19.58	21.95	43.4	20.44	16.81	19.91	22.72	13.56	24.01			
	HEM881001449	35.58	35.95	71.7	35.81	35.7	39.37	42.62	30.92	51.15			
	HEM881001454	4.44	10.09	10.48	10.32	5.73	8.72	4.72	2.95	5.93			

Table 386

	HEM881001458	9.69	12.19	21.36	34.84	17.29	10.08	13.2	9.97	12.41			
	HEM881001461	19.67	23.1	39.56	20.5	28.42	24.75	17.54	14.4	25.15			
5	HEM881001463	19.56	21.33	35.61	31.93	33.77	43.28	30.72	20.68	36.42			
	HEM881001464	28.01	27.99	31	14.62	14.82	15.04	16.45	13.58	23.87	++	*	-
	HEM881001466	15.16	15.92	27.83	19.85	13.38	15.96	13.7	10.31	15.02			
	HEM881001482	17.23	20.81	35.32	19.01	19	19.25	19.83	14.79	21.88			
	HEM881001500	41.82	45.54	68.26	37.83	39.48	37.77	46.2	37.01	39.45			
10	HEM881001505	20.94	22.59	32.35	26.78	22.08	24.15	26.64	17.19	32.59			
	HEM881001521	8.53	7.62	10.6	8.16	6.3	6.64	6.41	3.73	7.14			
	HEM881001527	2.99	3.88	4.38	4.6	7.15	3.37	3	1.09	4.09			
	HEM881001530	3.48	3.01	4.27	1.8	4.75	3.13	7.05	4.01	3.15			
	HEM881001531	36.17	50.68	53.86	24.43	15.05	19.88	14.37	19.2	25.31	*	*	-
	HEM881001532	17.53	24.2	32.45	18.39	15.75	13.6	15.22	13.76	17.31			
15	HEM881001535	12.38	16.91	23.89	12.47	13.36	10.82	9.04	12.27	13.78			
	HEM881001536	66.38	84.8	143.72	91.2	78.03	69.03	101.64	71.92	118.47			
	HEM881001537	11.79	11.39	16.93	9.29	11.02	10.91	6.73	5.87	10.85			
	HEM881001542	14.96	22.23	29.71	13.95	16.64	16.35	12.71	5.92	15.48			
	HEM881001543	23.66	28.65	30.69	20.28	24.21	31.58	17.34	19.58	58.07			
	HEM881001547	23.94	50.04	39.45	14.74	15.27	12.72	12.08	2.84	4.52	*	*	-
20	HEM881001548	3.11	4.4	5.6	1.9	1.94	2.29	3.65	4.19	3.74	*	*	-
	HEM881001551	3.8	7.07	10.09	4.64	4.24	4.26	3.14	1.65	6.16			
	HEM881001555	8.19	9.59	15.51	4.72	6.09	5.64	3.45	5.22	5.59			
	HEM881001562	17.05	18.48	38.18	19.29	13.39	17.57	16.22	12.15	22.52			
	HEM881001564	38.37	50	64.37	49.41	38.27	48.76	40.56	25.46	46.57			
	HEM881001565	18.11	21.08	35.2	23.9	18.29	10.69	18.09	9.6	15.5			
25	HEM881001569	18.83	22.86	28.98	20.6	18.61	17.83	18.18	11.82	14.18			
	HEM881001573	3.68	5.99	8.15	7.26	5.87	2.52	10.81	4.11	5.2			
	HEM881001585	31.55	42.11	57.35	32.5	28.22	32.05	31.45	26.22	33.57			
	HEM881001586	19.62	27.08	60.2	25.12	17.34	21.21	21.42	13.56	26.31			
	HEM881001588	3.6	1.4	8.8	2.53	0.56	1.81	2.28	0.36	3.78			
	HEM881001595	10.36	11.37	25.05	8.69	10.88	9.92	9.72	7.65	13.65			
30	HEM881001596	50.23	70.48	94.67	85.43	78.99	83.08	60.67	47.9	57.78			
	HEM881001599	12.08	19.55	22.95	3.76	11.11	7.77	4.14	3.06	5.8	*	*	-
	HEM881001603	15.69	23.5	36.56	18.96	19.27	14.23	19.02	14.12	17.69			
	HEM881001606	8.92	10.53	14.14	3.61	11.6	8.26	6.12	2.83	3.66	*	*	-
	HEM881001612	12.97	18.3	27.94	17.56	18.03	14.45	13.69	13.84	21.14			
	HEM881001618	47.24	51.05	53.93	31.05	43.7	40.99	38.7	45.72	63.89	*	*	-
35	HEM881001619	21.53	28.8	35.45	21.69	15.6	18.53	19.99	9.27	17.16			
	HEM881001623	32.27	35.63	43.91	23.19	18.98	32.29	44.61	25.32	56.22			
	HEM881001625	8.57	7.58	12.04	5.34	5.5	6.91	4.26	3.63	6.59	*	*	-
	HEM881001630	10.5	14.13	23.29	7.12	9.43	7.75	11.72	5.74	8.87			
	HEM881001635	8.75	10.43	14.63	5.84	10.39	7.88	13.65	6.82	10.88			
	HEM881001637	32.58	33.36	51.7	33.85	36.88	33.36	45.82	19.62	25.12			
40	HEM881001641	50.01	60.79	92.28	48.36	49.98	43.85	47.93	38.87	56.74			
	HEM881001653	12.57	22.18	30.48	17.59	15.29	13.82	24.06	13.06	30.12			
	HEM881001665	3.93	2.53	9.42	3.83	1.95	2.69	2.78	1.9	1			
	HEM881001666	19.92	21.89	36.37	13.51	17.12	14.78	11.97	10.86	17.21			
	HEM881001667	16.89	20.47	51.29	17.31	18.04	14.47	10.43	9.14	14.45			
	HEM881001668	4.06	3.82	13.97	2.65	3.74	1.89	2.27	0.07	2.33			
45	HEM881001669	4.2	4.89	17.86	5.72	6.1	3.19	6.26	1.74	4.46			
	HEM881001670	46.37	46.73	48.84	13.56	78.84	42.13	34.32	15.02	19.72	*	*	-
	HEM881001673	67.96	61.75	141.78	71.26	44.3	44.21	62.82	56.55	66.02			
	HEM881001675	17.04	14.33	30.97	18.1	10.45	10.58	21.47	8.1	12.88			
	HEM881001679	6.24	17.91	21.96	5.19	4.96	3.87	10.86	6.26	8.43			
	HEM881001684	10.61	21.58	17.28	4.97	9.8	7.91	15.07	5.39	2.51			
50	HEM881001685	5.57	8.99	14.97	3.84	6.75	3.87	5.52	1.85	2.86			
	HEM881001695	5.09	9.94	17.45	5.82	8.3	5.19	6.66	2.16	2.97			
	HEM881001703	4.68	6.84	16.43	5.87	6.69	4.05	8.72	2.46	4.64			
	HEM881001704	5.61	7.88	21.01	10.94	17.96	9.05	14.4	6.3	9.45			
	HEM881001706	7.42	2.91	5.37	4.07	5.66	4.18	6.33	3.36	3.19			
	HEM881001707	3.87	5.86	5.44	3.17	4.08	5.01	5.27	1.48	7.88			
55	HEM881001717	14.88	12.76	30.35	13.57	11.78	8.58	13.5	11.39	12.48			
	HEM881001731	39.25	68.03	95.93	39.11	36.32	32.38	46.55	35.06	44.86			
	HEM881001734	5.17	6.48	12.05	1.52	7.19	2.49	5.94	1.69	6.44			

Table 387

	HEM881001735	41.8	74.33	131.1	48.7	40.13	60.42	53.81	28.45	83.52
	HEM881001736	7.77	13.39	28.59	8.57	9.16	5.35	8.09	5.45	9.42
5	HEM881001747	2.69	8.82	13.53	4.41	6.88	3.98	4.96	1.05	3.48
	HEM881001749	10.28	24.28	26.11	5.15	8.2	10.2	5.99	4.27	10.01
	HEM881001753	10.3	11.05	20.9	9.25	9.8	9.74	6.82	5.36	10.12
	HEM881001756	6.53	8.08	12.86	3.9	3.99	4.72	5	3.97	3.65
	HEM881001757	7.8	24.09	26.61	6.4	12.83	5.96	11.18	14.36	9.41
10	HEM881001760	14.27	19.82	42.06	14.81	14.45	11.21	17.24	9.18	15.44
	HEM881001762	0.8	3.04	8.27	0.57	4.82	0.71	2.56	0.81	3.52
	HEM881001780	13.76	23.09	49.83	16.38	14.53	12.62	15.44	6.8	13.71
	HEM881001785	6.49	12.36	24.07	15.82	12.17	15.29	9.31	2.84	7.32
	HEM881001788	25.43	19.69	45.01	19	16.71	23.01	19.54	20.38	26.43
	HEM881001793	5.14	15.25	7.48	1.07	13.29	8	16.96	8.27	6.44
15	HEM881001797	14.78	27.69	37.34	12.45	18.06	22.63	22.37	14.75	11.18
	HEM881001802	13.95	6.42	12.11	6	9.1	3.62	4.89	7.62	4.73
	HEM881001812	19.94	26.82	51.97	30.77	23.99	24.59	25.74	15.27	19.71
	HEM881001815	11.81	15.53	37.64	17.99	17.45	14.83	20.39	13.54	19.43
	HEM881001816	17.77	23.19	75.37	26.22	24.8	18.06	30.17	15.34	21.15
	HEM881001831	8.13	8.07	23.31	9.34	10.75	10.45	10.25	3.73	10.62
20	HEM881001834	14.4	18	35.74	22.13	11.64	13.05	15.55	10.35	12.6
	HEM881001836	30.28	39.5	43.48	42.55	36.92	34.82	31.2	18.99	16.41
	HEM881001839	14.36	16.68	38.4	17.83	16.75	14.74	12.83	10.7	10.84
	HEM881001841	25.77	32.45	51.17	33.9	26.13	25.07	27.91	22.04	19.78
	HEM881001844	15.48	34.84	44.55	31	24.08	23.04	21.12	16.3	25.7
	HEM881001847	17.89	27.89	60.83	26.2	23.47	23.52	21.19	9.97	20.24
25	HEM881001848	4.85	5.43	11.29	3.58	4.51	3.65	6.07	3.08	5.61
	HEM881001850	38.14	52.12	78.88	56.18	68.55	53.58	61.43	34.94	43.46
	HEM881001859	30.81	27.05	59.36	68.19	35.46	57.28	19.8	14.26	20.24
	HEM881001863	3.46	3.98	8.32	5.64	4.36	4.8	7.82	2.45	4.74
	HEM881001867	14.5	16.62	28.09	12.79	10.98	12.92	14.13	8.77	15.8
	HEM881001868	5.84	8.18	12.72	7.12	6.24	5.61	8.09	8.94	8.48
30	HEM881001869	54.86	64.59	94.37	86.31	67.89	82.85	80.48	51.3	89.82
	HEM881001872	6.07	11.98	13.6	18.68	9.46	7.21	18.78	6.55	10.02
	HEM881001874	3	3.3	6.61	4.59	12.05	11.19	3.13	1.36	5.74
	HEM881001875	12.99	18.2	23.61	26.52	29.44	24.9	34.89	17.55	28.83
	HEM881001880	18.04	17.79	33.89	31.27	17.63	20.15	14.84	10.37	14.08
	HEM881001899	34.29	45.59	63.32	39.63	32.89	31.82	35.58	26.2	35.72
35	HEM881001903	8.16	10.41	29.09	8.47	10.89	12.17	9.48	4.66	7.91
	HEM881001905	28.16	29.19	50.5	33.46	32.78	32.37	33.69	21.9	33.71
	HEM881001906	4.65	5.05	9.2	6.27	6.88	4.65	7.25	6.26	9.65
	HEM881001908	2.42	5.7	6.4	5.21	4.63	6.7	4.19	0.96	5.33
	HEM881001910	5.2	10.62	10.84	8.51	10.51	9.98	6.79	2.76	7.39
	HEM881001911	29.98	51.31	56.74	43.98	49.18	34.13	49.74	26.26	62.6
40	HEM881001915	21.14	31.44	37.82	20.71	15.99	14.9	18.9	21.96	29.35
	HEM881001921	7.15	10.68	16.34	7.38	7.15	5.66	5.97	5.19	7.01
	HEM881001922	17.41	22.59	26.93	13.84	10.93	18.21	23.02	11.95	17.79
	HEM881001925	13.97	12.3	26.77	11.6	11.78	10.4	15.51	12.85	15.94
	HEM881001930	40.03	59.19	73.92	44.03	41.91	43.37	40.7	31.14	54.53
	HEM881001944	1.94	5.58	8.4	6.66	4.5	5.16	2.67	2.16	4.4
45	HEM881001945	11.9	14.15	28.25	12.61	15.86	30.85	15.45	10.36	15.75
	HEM881001947	12.74	2.15	16.64	14.03	14.01	12.25	15.71	4.99	12.24
	HEM881001950	17.57	25.59	40.32	25.51	11.85	16.5	13.53	12.65	19.84
	HEM881001952	26.14	33.12	47.22	23.32	21.94	24.22	34.78	37.99	49.1
	HEM881001953	17.2	26.64	33.2	20.18	17.54	17.43	18.02	10.46	24.03
	HEM881001957	5.93	5.66	12.29	2.67	5.82	5.6	4.01	5.73	6.62
50	HEM881001959	4.28	3.66	11.59	1.82	2.82	5.97	1.57	2.64	3.72
	HEM881001962	11.92	43.87	27.13	12.9	32.94	14.36	12.1	15.99	21
	HEM881001967	34.68	44.03	60.34	44.77	38.71	38.73	44.26	27.2	37.33
	HEM881001973	28.25	35.18	38.62	28.67	29.33	21.67	37.28	18.87	23.03
	HEM881001978	70.1	95.85	135.62	108.46	60.16	80.87	54.72	61.03	86.88
	HEM881001983	4.69	4.06	8.04	3.84	5.22	5.54	5.15	3.31	5.57
55	HEM881001987	10.55	12.27	28.1	12.58	12.32	11.95	11.85	6.54	23.57
	HEM881001988	9.33	7.22	23.4	8.24	11.34	8.88	13.31	6.58	9.69
	HEM881001990	26.2	19.68	27.76	43.3	26.68	36.79	27.71	13.13	24.3



Table 388

	HEM881001996	27.04	42.61	48.67	17.55	24.82	18.56	28.17	23.4	25.36	*	-
	HEM881001997	14.71	23.01	29.3	15.9	17.15	12.6	18.98	11.27	17.5		
5	HEM881001999	15.2	22.46	20.51	13.68	17.9	14.36	19.76	8.32	11.63		
	HEM881002002	6.41	8.68	14.02	3.86	4.69	7.48	2.32	2.31	9.35		
	HEM881002005	13.93	14.9	24.54	14.07	12.64	13.23	24.2	15.6	24.4		
	HEM881002009	13.81	20.37	28.5	12.9	13.24	9.2	14.63	11.53	16.62		
	HEM881002013	35.52	43.43	61.55	22.34	25.62	25.39	38.97	23.31	36.2	*	-
10	HEM881002015	17.64	16.37	26.67	10.62	13.94	14.86	13.44	9	13.73		
	HEM881002024	5.8	10.6	13.79	2.3	5.04	3.13	2.77	1.85	3.6	*	-
	HEM881002035	52.65	85.52	32.75	21.71	70.63	38.58	40.44	20.7	17.84		
	HEM881002039	4.95	5.73	12.99	4.99	10.04	5.87	7.91	2.61	3.57		
	HEM881002041	26.99	42.34	59.33	33.42	31.41	30.59	35.5	25.94	36.66		
	HEM881002042	7.32	8.11	15.44	8.43	5.37	4.7	6.95	4.45	6.64		
15	HEM881002043	15.38	16.33	33.37	9.15	15.16	12.75	12.63	10.91	12.91		
	HEM881002044	6.28	7.19	15.99	4.63	6.03	3.49	8.95	3.61	5.78		
	HEM881002045	13.55	14.05	38.81	21.11	17.68	16.3	14.27	7.83	17.46		
	HEM881002049	20.72	21.4	45.82	13.96	20.22	15.6	21.11	13.82	17		
	HEM881002050	12.83	16.25	37.04	11.52	18.46	11.6	18.41	9.54	14.5		
	HEM881002051	28.94	18.92	52.44	23.53	26.05	15.13	33.91	14.41	28.65		
20	HEM881002068	64.56	61.13	134.22	53.82	39.3	49.08	48.07	48.15	30.52		
	HEM881002069	20.88	27.08	36.85	26.67	17.79	18.95	23.6	16.68	23.73		
	HEM881002075	15.68	17.27	22.02	11.81	12.44	12.63	5.87	5.58	11.32	*	-
	HEM881002079	27.46	41.14	33.47	23.15	21.35	9.24	13.25	11.63	12.65	**	-
	HEM881002080	27.32	43.03	71.5	48.33	38.81	19.92	37.68	22.99	28.59		
	HEM881002082	11.54	12.93	24.86	5.24	21.72	15.36	15.59	4.71	14.1		
25	HEM881002084	17.19	20.49	48.44	15.57	24.56	30.61	24.16	14.34	22.35		
	HEM881002088	4.86	8.19	14.88	4.12	8	4.95	6.55	2.38	8.06		
	HEM881002092	144.34	116.11	135.03	45.77	56.49	60.46	15.5	25.51	16.94	**	**
	HEM881002094	15.12	19.26	35.12	17.76	15.07	8.88	14.96	9.23	22.31		
	HEM881002103	5.46	7.53	11.18	8.4	4.51	4.6	8.52	3.47	4.97		
	HEM881002109	59.58	83.46	107.06	62.19	50.92	51.12	65.01	50.9	42		
30	HEM881002115	5.46	60.72	14.77	39.13	16.84	5.85	5.92	6.74	5.3		
	HEM881002120	6.4	5.75	12.8	2.74	5.51	2.64	3.13	1.57	3.49		
	HEM881002121	19.45	25.43	55.52	28.56	24.08	19.83	25.58	15.89	20.17		
	HEM881002134	10.91	24.24	43.39	24.03	23.79	24.09	19.26	8.44	14.1		
	HEM881002136	18.33	18.78	45.57	23.81	13.25	20.44	11.9	15.85	24.31		
	HEM881002138	50.09	51.59	110.11	35.51	42.15	39.79	27.69	28.58	25.22		
35	HEM881002139	8.36	15.47	10.43	4.01	4.89	4.74	7.89	6.83	4.81	*	-
	HEM881002141	9.19	16.96	13.1	1.9	10.98	7	5.65	7.53	4.35		
	HEM881002142	6.36	8.37	8.62	2.74	2.82	2.25	4.04	2.02	5.71	**	*
	HEM881002145	10.49	16.24	32.26	9.14	12.19	10.34	12.54	5.18	7.82		
	HEM881002152	24.88	22.9	59.51	8.84	21.58	20.2	34.39	10.44	7.92		
	HEM881002162	46.61	80.75	107.44	66.24	81.5	44.12	82.89	47.69	70.76		
40	HEM881002173	3.55	25.4	7.84	5.45	25.86	14.76	4.91	5.53	5.99		
	HEM881002189	5.91	5.36	11.91	4.49	4.74	3.73	7.69	4.5	2.15		
	HEM881002190	8.05	5.19	7.81	3.82	3.51	3.24	3.4	1.73	2.03	*	*
	HEM881002193	13.5	31.42	40.95	12.51	15.71	29.81	30.17	23.34	31.46		
	HEM881002217	11.76	15.56	34.59	12.72	11.26	16.37	17.63	11.07	12.8		
	HEM881002218	25.74	52.63	73.43	32.82	28.59	24.52	35.6	20.64	25.88		
45	HEM881002228	108.24	84.59	214.25	80.62	78.36	108.65	166.71	123.42	65.1		
	HEM881002232	10.76	24.39	31.98	19.41	21.33	17.37	22.17	6.39	14.13		
	HEM881002245	29.32	39.47	46.03	33.69	25.42	30.62	28.25	20.36	26.6		
	HEM881002247	23.04	30.4	36.26	21.55	23.11	19.18	30.01	21.82	18.27		
	HEM881002249	8.45	5.4	12.8	9.1	8.18	7.58	2.92	2.96	4.18		
	HEM881002254	13.55	8.54	22.22	9.35	11.14	10.19	5.38	9.93	4.18		
50	HEM881002255	24	39.55	56.2	39.15	37.05	37.31	39.64	23.55	35.88		
	HEM881002266	19.55	37.2	69.12	27.4	30.03	37.09	27.79	17.42	23.42		
	HEM881002271	8.4	14.75	33.73	16.63	15.77	17.75	17.9	8.81	11.82		
	HEM881002280	0	1.32	3.2	1.59	2.57	0.19	2.26	0	1.09		
	HEM881002296	13.25	17.07	48.86	29.84	17.46	25.16	17	14.47	20.56		
	HEM881002309	7.2	17.96	22.84	22.43	7.83	12.63	8.34	8.09	9.04		
55	HEM881002302	8.19	9.95	13.55	11.87	6.29	9.78	7.21	2.24	3.19	*	-
	HEM881002306	4.46	4.94	10.04	8.42	4.47	9.84	5.18	3.92	6.24		
	HEM881002316	9.41	18.69	11	13.6	12.17	15.43	7.32	2.42	6.96		

Table 389

	HEM881002326	6.79	10.97	11.32	21.02	12.83	6.76	6.12	3.86	6.53		
5	HEM881002327	29.86	39.37	46.64	28.75	34.27	35.49	23.76	23.05	28.43		
	HEM881002329	12.21	17.09	28.97	18.73	8.27	19.71	9.42	11.59	11.1		
	HEM881002340	3.57	5.21	5.98	7.77	3.22	9.25	5.09	2.16	1.79		
	HEM881002342	6.21	7.8	10.28	6	3.29	3.42	3.33	3.85	5.15	*	-
	HEM881002358	32.09	38.53	65.28	39.45	32.86	34.65	33.44	21.57	27.85		
	HEM881002359	3.96	3.69	6.45	3.93	4.64	4.39	3.95	0.63	2.74		
10	HEM881002364	3.43	4.07	8.33	6.97	4.3	5.26	4.27	1.48	3.01		
	HEM881002366	7.13	10.16	14.56	9.95	9.83	9.89	9.48	6.8	10.03		
	HEM881002371	17.53	29.76	21.32	21.87	21.71	16.54	9.41	9.09	4.87	*	-
	HEM881002381	7.92	12.33	16.15	8.95	3.96	8.62	4.76	5.05	4.4	*	-
	HEM881002383	135.68	179.56	228.28	286.57	191.47	226.83	107.86	116.89	120.62		
	HEM881002387	23.79	23.11	43.55	20.25	12.08	15.04	3.85	6.21	4.42	*	-
15	HEM881002409	13.31	12.51	22.34	8.77	11.21	10.89	4.44	4.37	4.87	*	-
	HEM881002413	3.49	3.12	9.08	4.81	2.78	4	1.3	1.86	1.66		
	HEM881002415	2.64	3.61	7.39	2.66	2.05	3.42	0.86	1.28	2.41		
	HEM881002424	6.07	9.92	9.97	6.37	9	12.89	6.72	4.73	6.15		
	HEM881002425	4.48	7.81	11.5	5.69	9.56	5.52	4.13	1.79	5.11		
	HEM881002427	29.25	30.49	60.22	43.33	23.55	33.03	24.65	22.4	31.01		
20	HEM881002442	6.2	17.54	17.42	9.79	7.28	9.01	4.36	12.11	11.81		
	HEM881002447	110.71	207.61	155.4	83.72	84.2	96.3	26.65	37.71	31.85	*	-
	HEM881002453	5.36	5.98	9.95	2.72	2.55	3.56	2.41	1.81	3.86	*	-
	HEM881002457	16.89	16.27	19.17	6.78	17.09	11.88	7.07	5.54	6.6	**	-
	HEM881002458	23.11	31.15	52.26	31.43	27.93	29.52	25.75	14.57	26.97		
	HEM881002463	24.77	42.25	57.37	32.51	37.48	24.85	28.18	20.41	30.3		
25	HEM881002465	3.27	5.17	9.01	3.69	4.27	4.31	3.51	0.9	2.26		
	HEM881002477	4.25	7.51	5.14	7.06	3.76	4.24	1.98	3.33	2.58	*	-
	HEM881002479	20.58	32.93	33.42	17.09	21.13	16.76	11.95	15.32	21.36		
	HEM881002489	48.69	62.6	67.58	34.04	44.48	57.32	35.3	36.02	39.44	*	-
	HEM881002492	11.53	17.66	26.19	13.16	10.94	12.55	11.2	5.85	15.28		
	HEM881002495	5.18	3.21	9.5	2.92	4.34	3.1	3.82	2.25	3.88		
30	HEM881002502	34.71	31.95	38.03	46.31	31.48	35.99	26.54	23.82	25.15	**	-
	HEM881002509	11.07	15.55	26.84	12.73	16.51	11.29	10.77	7	12.74		
	HEM881002510	28.51	45.37	36.84	31.94	38.1	20.25	23.53	21.31	17.08	*	-
	HEM881002520	14.34	15.62	18.28	10.3	7.17	4.37	1.27	2.73	3.96	*	-
	HEM881002522	27.23	55.84	54.45	41.8	39.8	28.31	15.32	22.78	36.38	**	-
	HEM881002527	2.56	2.91	5.88	1.86	2.03	3.34	1.71	1.04	2.87		
35	HEM881002530	5.16	6.33	11.67	5.25	3.42	5.09	4.28	2.92	7.5		
	HEM881002531	26.73	31.41	45.92	22.42	21.99	29.07	24.79	13.7	18.84		
	HEM881002534	27.18	46.28	57.65	25.13	29.76	23.09	34.17	26.17	36.08		
	HEM881002536	13.04	20.55	23.13	9.22	13.07	13	15.33	12.24	18.4		
	HEM881002544	23	32.2	43.29	21.03	30.23	27.52	19.17	15.09	14.85		
	HEM881002545	3.59	4.33	9.7	5.81	3	3.56	1.12	0.96	13.79		
40	HEM881002550	7.33	13.21	13.27	3.83	6.5	4.73	2.81	3.61	2.61	*	-
	HEM881002556	19.36	24.38	22.91	7.86	11.05	11.87	7.3	3.24	5.41	**	-
	HEM881002571	7.32	4.72	8.5	4.01	3.71	2.33	1.87	1.16	2.04	*	-
	HEM881002579	3.21	4.8	10.5	2.3	2.84	2.3	2.51	1.04	2.73		
	HEM881002582	9.95	12.82	19.84	6.39	8.66	6.74	3.36	2.01	3.49	*	-
	HEM881002584	4.7	5.64	13.38	4.24	5.58	5.79	3.53	1.46	2.34		
45	HEM881002587	8.59	15.17	29.93	11.81	13.87	11.06	10.85	4.49	11.04		
	HEM881002590	27.91	31.34	78.12	45.05	22.1	24.36	21.48	22.81	39.4		
	HEM881002596	9.4	9.36	12.16	12.87	8.92	9.94	3.39	4.59	5.2	**	-
	HEM881002600	7.35	8.89	8.63	4.2	3.37	4.13	3.83	2.53	0.85	**	-
	HEM881002601	13.59	25.38	25.69	13.58	12.98	10.65	15.53	14.47	12.11		
	HEM881002603	4.01	4.35	8.49	3.09	3.23	2.33	3.4	1.13	1.07		
50	HEM881002607	5.59	8.75	13.05	6.25	8.3	3.46	5.04	2.83	4.29		
	HEM881002610	6.17	9.3	18.74	7.02	8.85	5.16	5.21	2.01	3.82		
	HEM881002613	5.1	6.85	16.57	4.47	6.62	3.43	4.07	1.86	3.63		
	HEM881002614	108.18	118.26	257.79	160.19	127.61	115.27	80.95	70.77	100.61		
	HEM881002615	3.76	4.74	6.46	3.53	4.89	3.11	2.31	1.58	0.85	*	-
	HEM881002617	15.34	16.43	20.69	14.06	10.46	7.36	16.03	9.38	12.23		
55	HEM881002623	43.46	62.43	70.11	89.32	59.95	64.13	46.57	40.8	51.16		
	HEM881002624	20.45	39.7	56.1	29.45	24.85	24.11	26.5	22.1	22.65		
	HEM881002631	12.8	24.72	22.26	5.67	13.71	7.87	12.49	14.8	9.64		

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	HEM881002635	3.81	5	11.37	1.21	3.62	1.08	2	1.05	2.82			
	HEM881002644	6.38	7.38	19.6	6.87	6.62	5.91	7.04	3.57	7.83			
5	HEM881002654	44.15	47.27	98.13	55.06	50.78	51.15	27.74	20.25	41.98			
	HEM881002661	16.29	22.35	33.51	18.43	18.3	14.62	15.42	10.61	19.12			
	HEM881002663	12.29	20.14	24.54	5.77	16.48	12.72	3.66	7.87	3.2	*		-
	HEM881002664	26.04	27.32	31.97	12.71	14.38	12.28	15.87	10.5	16	**	**	-
	HEM881002677	2.85	4.67	7.35	1.19	3.8	1.22	2.58	0.54	2.04			
10	HEM881002683	408.12	530.85	581.04	161.92	536.41	322.12	493.61	190.86	318.34			
	HEM881002684	5.89	14.15	21.74	5.64	5.67	5.5	2.78	0.53	2.33			
	HEM881002686	2.08	2.21	13.73	0.94	2.87	1.96	2.53	0.03	2.4			
	HEM881002692	6.27	8.28	18.48	7.56	4.81	4.6	4.23	1.22	6.95			
	HEM881002693	37.13	59.89	50.13	8.18	9.08	32.77	12.89	24.23	25.51	*	*	-
	HEM881002697	12.19	19.73	29.39	11.74	11.32	12.96	13.01	7.86	10.37			
15	HEM881002699	12.29	7.97	29.87	3.99	12.05	3.69	6.19	2.34	1.91			
	HEM881002702	4.21	4.82	9.81	4.02	2.81	2.59	2.32	3.46	2.32			
	HEM881002705	42.01	58.09	92.41	42.52	47.93	35.39	82.62	52.43	59.52			
	HEM881002712	82.07	113.22	149.92	77.66	93.78	72.72	96.78	72.75	86.71			
	IMR321000028	2.68	4.75	13.62	4.72	4.88	2.62	2.74	1.07	1.92			
	IMR321000031	7.53	10.04	0	0.26	16.99	0.79	7.55	3.43	9.54			
20	IMR321000034	9.42	10.78	32.44	15.73	16.03	17.46	6.96	5.24	7.94			
	IMR321000039	1.72	2	2.81	3.07	3.78	1.79	0.76	0	1.77			
	IMR321000044	5.65	7.08	18.45	11.11	7.14	7.03	4.83	2.08	3.62			
	IMR321000063	10.51	11.67	19.12	13.18	11.6	12.05	6.47	7.76	7.56			
	IMR321000085	3.33	5.05	8.66	2.61	3.29	3.45	1.96	0.92	3.07			
	IMR321000089	3.15	5.89	14.29	4.37	6.53	5.77	3.28	1.07	2.45			
25	IMR321000091	59.8	78.47	131.41	171.62	125.26	143.68	43.76	27.21	45.98			
	LIVER1000004	4.13	4.93	5.75	3.08	2.76	4.02	2.18	1.07	1.36	**		-
	LIVER1000008	10.35	13.6	22.11	11.7	10.53	14.7	11.26	5.83	10.54			
	LIVER1000011	59.6	50.92	129.92	124.27	66.83	94.45	48.23	37.68	48.06			
	LIVER1000022	2.42	3.87	7.13	5.18	2.89	5.96	3.99	0.85	2.2			
	LIVER1000025	11.19	21.41	14.85	14.92	17.52	18.14	8.19	3.93	7.48	*		-
30	LIVER1000030	5.79	4.25	9.83	9.98	5.67	5.82	4.77	2.89	3.63			
	LIVER1000045	4.77	5.86	5.47	6.22	7.71	6.61	4.81	3.96	4.97			
	LIVER1000046	23.39	30.93	40.35	28.67	14.67	17.18	8.63	19.03	18.73			
	LIVER1000072	9.51	20.72	24.34	17.51	14.57	15.78	8.13	9.06	13.17			
	LIVER1000077	7.51	7.91	13.85	13.48	8.07	9.05	5.23	4.4	6.07			
	LIVER1000080	5.07	5.78	10.96	6.47	4.34	6.39	3.86	2.15	4.56			
35	LIVER1000086	11.03	13.61	23.46	8.67	23.05	12.3	11.46	8.1	16.78			
	LIVER1000092	10.59	15.75	23.53	19.18	22.61	13.71	8.85	6.69	7.35			
	LIVER1000095	51.53	68.53	98.85	69.98	49.46	69.44	74.79	43.47	64.56			
	LIVER1000097	8.95	15.6	14.45	10.75	13.82	9.14	5.8	2.85	3.46	*		-
	LIVER1000098	41.49	40.97	103.47	50.66	24.2	43.26	26.16	32.27	27.07			
	LIVER1000100	3.55	4.13	7.44	3.5	3.68	3.78	2.58	3.54	3.3			
40	LIVER1000101	44.76	62.72	56.32	36.92	31.17	34.9	40.25	36.83	38.75	*	*	-
	LIVER1000106	3.93	4.77	8.45	2.61	3.61	4.62	2.14	3.23	3.22			
	LIVER1000108	6.19	8.29	14.94	4.01	4	6.54	5.47	6.84	5.37			
	LIVER1000115	1.31	3.43	5.31	1.07	1.91	1.17	0.78	1.21	1.27			
	LIVER1000120	5.87	8	12.35	7.59	6.45	6.85	5.23	2.59	6.22			
45	LIVER1000138	5.5	7.3	19.82	7.01	10.38	6.37	5.23	4.12	9.23			
	LIVER1000146	4.13	5.06	8.45	8.15	4.26	4.91	1.55	2.41	3.37			
	LIVER1000148	10.81	16.45	14.93	9.88	11.05	13.74	6.11	8.29	5.5	*		-
	LIVER1000157	4.51	3.83	6.67	3.38	5.06	4.69	1.48	2.24	4.29			
	LIVER1000161	85.1	101.44	127.49	155.4	95.91	123.47	63.19	53.6	81.33			
	LIVER1000167	9.34	7.8	16.08	6.28	7.39	6.18	4.07	3.11	4.06	*		-
	LIVER1000174	14.38	23.84	29.19	10.08	10.54	10.6	4.27	1.62	4.26	*	*	-
50	LIVER1000185	15.55	11.69	24.81	3.86	12.76	7.24	6.4	3.76	4.58	*		-
	LIVER1000187	40.28	72.32	62.92	52.19	53.14	45.8	30.48	15.14	10.77	*		-
	LIVER1000190	13.01	13.24	16.57	5.85	5.19	5.07	2.85	4.77	5.27	**	**	-
	LIVER1000192	3.52	6.68	4.51	4.92	4.75	3.34	0.75	1.7	3.55			
	MAMMA1000009	5.18	9.12	9.31	4.2	4.16	3.51	1.94	1.4	2.13	*	*	-
	MAMMA1000015	5.78	4.65	11.74	5.4	3.83	5.36	2.48	1.65	3.15			
55	MAMMA1000019	8.71	5.86	17.78	9.05	5.32	5.22	3.67	4.83	8.34			
	MAMMA1000020	101.37	73.62	112.56	134.32	82.42	106.51	82.61	44.53	81.2			
	MAMMA1000024	19.83	36.9	36.17	7.46	24.94	15.61	12.77	15.51	6.89	*		-

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	MAMMA1000025	3.49	6.73	9.73	4.76	8.15	5.09	3.99	1.9	3.02			
5	MAMMA1000043	8.59	8.02	15.22	6.68	3.56	4.76	2.11	1.9	6.1			
	MAMMA1000045	9.03	8.98	17.21	11.43	6.71	9.34	5.16	4.47	6.29			
	MAMMA1000046	41.47	53.57	56.97	30.34	27.99	31.56	37.45	30.61	48.64	*	*	-
	MAMMA1000055	10.6	18.89	12.32	4.6	6.26	5.89	3.62	4.44	2.53	*	*	-
	MAMMA1000057	3.76	2.41	12.19	2.23	1.8	1.43	1.21	1.53	2.81			
	MAMMA1000060	10.21	8.2	18.54	5.99	7.11	5.88	5.98	4.17	6.29			
10	MAMMA1000069	143.75	270.15	259.45	49.26	67.48	38.63	33.36	39.16	49.31	*	*	-
	MAMMA1000084	3.34	5.16	10.93	3.47	4.79	2.05	3	0.67	2.88			
	MAMMA1000085	3.86	4.9	7.86	4.65	4.18	4.46	2.36	1.98	8.94			
	MAMMA1000092	1.88	4.62	8.98	3.96	2.75	3.09	2.27	0.07	1.18			
	MAMMA1000096	3.52	3.48	7.14	2.58	2.53	2.5	0.67	1.83	1.35			
	MAMMA1000097	4.98	3.73	8.88	2.04	2.02	1.49	1.93	0.71	1.64	*		-
15	MAMMA1000102	16.31	20.65	29.78	15.97	14.1	11.62	28.48	21.84	17.26			
	MAMMA1000103	24.25	30.87	39.49	18.45	29.7	17.72	21.24	13.56	7.51	*		-
	MAMMA1000106	8.95	10.76	22.4	12.82	11.13	10.63	6.32	4.47	6.45			
	MAMMA1000117	2.83	6.06	12.12	2.65	4.11	2.11	5.97	1.27	1.18			
	MAMMA1000118	8.06	8.77	19.58	14.56	12.82	9.23	5.17	8.7	14.06			
	MAMMA1000129	4	2.76	5.79	3.46	3.6	1.79	1.7	2.01	2.69			
20	MAMMA1000133	5.05	7.04	6.39	3.71	2.31	3.3	8.78	9.22	3.38	*		-
	MAMMA1000134	7.25	6.71	12.23	3.97	5.46	2.89	5.9	4.64	5.77			
	MAMMA1000139	8.81	13.92	27.94	9.57	7.21	7.44	10.8	7.32	10.69			
	MAMMA1000141	10.59	12.38	22.86	16.46	15.91	12.46	8.35	6.81	8.98			
	MAMMA1000143	47.46	88.55	73.36	60.42	67.69	52.39	70.22	26.61	57.3			
	MAMMA1000150	7.57	5.6	14.19	2.79	8.22	2.73	5.6	1.58	3.48			
25	MAMMA1000155	11.41	12.76	22.27	10.11	6.62	6.85	2.76	1.55	4.85	*		-
	MAMMA1000163	15.02	19.25	32.92	19.25	12.39	13.68	10.19	9.3	14.14			
	MAMMA1000171	7.6	10.37	13.24	2.98	2.32	1.89	2.54	1.28	1.33	**	**	-
	MAMMA1000173	6.75	5.29	9.57	2.32	2.23	1.04	2.07	1.37	0.99	*	*	-
	MAMMA1000175	3.46	6.59	11.02	3.52	2.3	2.43	3.53	1.51	2.66			
	MAMMA1000183	25.33	42.54	44.08	23.65	35.89	24.05	16.46	12.47	14.16	*		-
30	MAMMA1000191	5.92	8.95	18.7	5.23	6.43	6.14	3.97	2.29	6.56			
	MAMMA1000192	11.99	14.56	36.16	26.22	18.77	12.98	9.82	7.53	11.64			
	MAMMA1000193	3.19	3.37	6.86	4.95	4.82	4.54	1.06	1.39	2.14			
	MAMMA1000198	47.48	56.45	65.4	32.82	40.48	48.35	28.71	22.96	42.97	*		-
	MAMMA1000204	11.23	12.69	25.02	6.96	11.44	9.78	5.53	7.76	6.1			
	MAMMA1000207	12.4	7.47	19.55	6.26	5.09	4.84	6.03	8.39	7.97			
35	MAMMA1000214	8.42	8.75	15.08	9.58	9.32	7.56	7.33	4.95	7.33			
	MAMMA1000220	22.52	15.12	36.99	5.02	6.29	6.82	6.38	3.87	3.09	*	*	-
	MAMMA1000221	10.4	16.64	24.93	5.03	11.07	6.49	6.69	3.21	1.94	*		-
	MAMMA1000226	13.64	11.97	28.4	5.25	12.91	9.41	26	12.92	3.5			
	MAMMA1000227	14.38	17.15	40.21	23.86	16.67	19.14	13.63	7.29	12.46			
	MAMMA1000230	3.53	5.09	7.34	3.64	2.92	4.31	1.76	1.24	2.65	*		-
40	MAMMA1000241	2.76	3.88	6.29	2.63	1.66	1.65	1.27	0.15	1.78	*		-
	MAMMA1000245	6.45	7.89	22.51	9.95	8.51	9.68	6.76	3.1	4.13			
	MAMMA1000248	21.38	25.61	55.84	30.22	20.66	19.73	24.19	11.24	13.89			
	MAMMA1000251	5.31	4.84	10.73	2.94	4.44	3.42	3.67	1.53	2.11			
	MAMMA1000254	2.32	3.23	8.55	2.43	2.71	1.01	0.9	0.97	0.54			
	MAMMA1000257	2.97	3.77	9.11	1.37	3.58	0.82	2.27	0.96	1.23			
45	MAMMA1000262	45.74	36.4	0	0.39	0	0	34.58	23.42	46.99			
	MAMMA1000264	9.34	12.72	36.1	26.8	15.94	23	7.31	7.08	9.25			
	MAMMA1000266	0.66	1	3.04	2.63	2.61	0.59	0.15	0	1			
	MAMMA1000270	13.12	14.9	18.21	14.67	11.46	11.77	8.4	9.61	6.99	*		-
	MAMMA1000271	3.88	3.72	7.35	4.08	3.89	3.79	1.47	2.83	1.69			
	MAMMA1000277	41.4	51.52	103.66	30.74	33.8	53.69	17.12	13.52	16.27			
50	MAMMA1000278	11.35	16.91	37.8	22.57	16.53	16.11	10.35	6.71	12.84			
	MAMMA1000279	3.26	3.91	6.49	3.15	3.6	2.86	2.52	0.56	1.77			
	MAMMA1000283	29.38	33.95	49.97	69.77	34.21	54.3	27.86	21.79	21.83			
	MAMMA1000284	5.55	5.62	6.77	4.76	4.06	5.69	4.18	2.05	4.21	*		-
	MAMMA1000287	18.44	27.31	36.41	15.51	4.83	9.89	4.34	3.99	2.59	*	*	-
	MAMMA1000294	14.59	17.3	29.88	19.53	15.7	20.07	17.98	12.1	15.45			
55	MAMMA1000298	4.06	4.13	7.44	4.06	5.42	8.4	4.25	2.39	4.19			
	MAMMA1000302	3.99	3.48	11.09	6.9	6.86	5.91	4.93	2.1	3.71			
	MAMMA1000303	1.77	4.16	5.21	2.14	3.15	3.07	3.83	0.5	1.85			

Table 392

	MAMMA1000305	32.01	34.24	58.88	37.52	42.02	39.78	30.9	18.25	28.49			
	MAMMA1000307	7.32	11.17	15.9	9.52	5.29	9	4.83	4.75	5.32			
5	MAMMA1000309	13.21	12.45	16.61	13.37	8.5	8.68	5.45	4.69	8.26	**	-	
	MAMMA1000312	3.8	4.66	7.38	5.51	4.44	4.58	3.65	2.16	2.53			
	MAMMA1000313	5.23	3.78	8.22	6.32	8.18	4.37	4.06	1.99	2.36			
	MAMMA1000331	3.57	2.97	7.78	3.29	3.56	6.01	3.84	1.96	2.66			
	MAMMA1000335	1.93	3.97	7.5	5.14	3.16	3.87	4.24	1.18	2.51			
10	MAMMA1000339	4.85	7.71	8.76	4.7	9.96	8.63	2.97	1.94	3.31	*	-	
	MAMMA1000340	13.8	21.06	20.08	19.65	20.75	20	20.39	11.88	8.29			
	MAMMA1000348	6.6	5.86	10.24	5.86	4.39	5.28	1.91	2.51	3.44	*	-	
	MAMMA1000356	48.67	74.66	87.35	53.83	37.37	46.85	35.71	39.77	39.98			
	MAMMA1000358	9.54	13.7	18.74	8.76	9.05	7.26	6.27	7.75	6.04			
	MAMMA1000360	4.42	6.35	14.28	5.25	6.74	5.72	3.05	4.95	4.76			
15	MAMMA1000361	62.5	108.93	116.66	101.62	117.16	105.86	87.17	73.39	114.81			
	MAMMA1000363	4.98	6.13	8.18	4.8	3.56	6.25	3.82	2.21	3.44	*	-	
	MAMMA1000370	5.17	12.45	10.14	5.35	7.18	7.58	3.49	1.29	2.83	*	-	
	MAMMA1000371	2.39	4.39	9.15	3.68	6.58	4.68	2.76	1.36	2.71			
	MAMMA1000372	17.51	21.43	34.07	12.37	14.77	13.39	11.25	17.12	32.9			
	MAMMA1000385	2.59	3.13	9.36	4.39	3.21	2.85	3.43	3.75	2.78			
20	MAMMA1000388	15.23	16.36	27.37	8.49	18.09	20.18	11.94	20.32	17.28			
	MAMMA1000395	2.71	-2.65	9.67	2.23	1.16	2.27	1.54	2.51	1.57			
	MAMMA1000402	17.65	14.83	40.38	21.39	34.95	27.07	11.67	5.88	6.61			
	MAMMA1000403	4.76	5.81	8.95	2.66	5.93	4.73	3.53	2.03	3.28			
	MAMMA1000410	8.38	10.39	14.35	8.64	10.52	7.1	6.79	5.15	5.87	*	-	
	MAMMA1000413	13.08	31.41	34.59	25.16	26.53	19.73	20.54	9.59	10.58			
25	MAMMA1000414	26.2	35.15	53.64	41.13	33.28	34.97	22.92	16.5	31.45			
	MAMMA1000416	93.85	138.41	125.21	46.14	53.85	91.17	35.64	64.76	53.2	*	*	-
	MAMMA1000421	12.39	14.43	18.48	7.65	12.15	12.39	5.74	4.49	4.48	**	-	
	MAMMA1000422	142.54	131.07	148.31	147.75	137.43	173.26	122.42	112.28	99.77	*	-	
	MAMMA1000423	5.22	2.76	10.5	5.24	3.96	3.14	2.65	0.29	3.52			
	MAMMA1000424	16.73	20.92	35.59	20.88	21.28	23.97	15.73	11.76	16.32			
30	MAMMA1000429	9.36	15.84	18.54	7.22	10.71	6.57	4.21	3.75	2.1	*	-	
	MAMMA1000431	1.71	4.16	6.38	1.45	4.13	3.04	2.28	2.32	2.5			
	MAMMA1000432	63.4	133.96	122.67	9.74	51.75	20.93	35.92	64.94	54.93	*	-	
	MAMMA1000437	7.75	15.03	14.39	12.33	7.79	9.82	5.47	8.03	11.07			
	MAMMA1000444	7.3	9.64	12.3	7.17	6.74	4.04	4.84	3.63	6.39	*	-	
	MAMMA1000446	72.49	65.48	72.84	97.18	57.65	80.67	67.4	46.57	58.28			
35	MAMMA1000449	18.1	22.35	31.63	13.49	17.76	14	17.72	12.22	18.97			
	MAMMA1000457	18.4	25.87	17.2	2.76	17.71	11.5	15.1	3.75	16.53			
	MAMMA1000458	7.78	16.72	16.75	9.69	10.94	4.65	4.37	2.84	7.72			
	MAMMA1000468	16.03	28.35	43.07	20.2	27.28	30.25	21.32	9.68	14.64			
	MAMMA1000472	6.66	14.63	17.94	8.59	8.34	7.38	4.92	4.41	8.54			
	MAMMA1000473	18.92	28.23	28.07	15.83	15.65	17.15	17.93	13.07	20.76	*	-	
40	MAMMA1000477	3.29	5.76	7.67	2.77	2.69	3.84	2.99	1.75	1.93			
	MAMMA1000478	3.8	4.66	7.21	2.84	2.45	2.89	2.43	1.21	0.87	*	-	
	MAMMA1000483	141.82	256.33	267.79	98.09	257.9	180.98	169.43	158.7	175.76			
	MAMMA1000490	11.74	16.92	30.01	11.37	13.37	11.4	15.98	7.97	17.05			
	MAMMA1000496	29.48	25.33	53.38	30.03	31.05	22.35	19.18	13.04	15.93			
	MAMMA1000500	4.21	8.78	19.16	2.1	8.22	5.73	7.01	0.97	6.78			
45	MAMMA1000501	3.3	3.92	7.8	5.4	3.37	3.89	2.1	0.03	4.12			
	MAMMA1000503	8.55	8.62	11.61	8.76	3.91	6.21	3.65	2.45	1.88	**	-	
	MAMMA1000506	19.56	37.71	40.79	41.28	34.62	14.86	17.29	25.75	7.33			
	MAMMA1000510	6.43	9.68	12.68	8.8	8.42	5.47	7.38	4.77	5.1			
	MAMMA1000515	16.44	20.18	30.29	25.14	20.54	20.81	15.29	9.87	15.02			
	MAMMA1000516	5.05	38.96	14.92	3.26	5.69	7.88	10.33	1.91	1.96			
50	MAMMA1000522	27.99	43.17	68.38	38.83	18.51	22.66	24.89	20.61	23			
	MAMMA1000524	5.97	11.73	10.41	4.38	10.1	5.92	5.73	2.46	2.76	*	-	
	MAMMA1000528	3.99	4.53	7.16	4.83	4.31	6.82	4.96	1.75	1.88			
	MAMMA1000534	20.75	20.93	19.83	14.18	15.4	10.89	14.95	12.85	11.39	**	**	-
	MAMMA1000541	7.6	8.83	11.36	1.44	4.17	2.11	2.2	1.84	1.98	**	**	-
	MAMMA1000550	2.63	1.99	8.54	2.03	3.94	1.32	3.32	0.71	2.83			
55	MAMMA1000556	761.19	1381.9	1153	543.64	1435.2	1032.9	1229.3	435.34	855.29			
	MAMMA1000559	6.09	5.3	11.69	2.67	3.19	2.37	2.27	0.81	3.09			
	MAMMA1000565	3.15	5.75	13.35	1.46	4.28	0.82	2.18	0.1	1.13			

Table 393

	MAMMA1000567	2.83	9.61	12.53	4.59	4.66	3.08	3.91	1.78	2.49			
	MAMMA1000576	14.4	23.94	41.43	6.77	7.53	16.66	14.73	20.93	24.41			
5	MAMMA1000582	342.62	404.06	589.09	206.24	397.1	307.2	196.5	234.99	295.12			
	MAMMA1000583	3.44	4.94	9.73	2.95	5.37	2.97	1.64	1.64	2.31			
	MAMMA1000585	10.36	9.76	14.3	7.6	6.3	4.54	9.1	4.55	7.57	*	-	
	MAMMA1000587	9.1	16.85	23.22	12.86	13.24	10.32	9.64	5.62	11			
	MAMMA1000591	24.67	34.19	52.67	17.16	22.85	23.65	15.05	11.26	16.03			
10	MAMMA1000594	25.66	32.59	51.71	40.6	49.12	36.4	18.51	9.64	20.88			
	MAMMA1000597	10.5	17.98	38.06	21.57	17.46	15.09	12.1	5.53	10.65			
	MAMMA1000605	8.03	8.9	14.02	3.22	4.68	8.25	3.07	3.06	5.3	*	-	
	MAMMA1000612	3.76	3.67	7.3	1.87	2.17	1.53	2.62	0.72	2.53			
	MAMMA1000614	8.91	9.36	17.48	7.74	5.34	6.31	7.11	2.55	5.61			
	MAMMA1000616	10.09	7	22.98	5.69	13.58	6.11	4.8	4.98	3.1			
15	MAMMA1000621	18.37	26.27	42.33	24.96	17.41	18.13	16.86	13.76	19.28			
	MAMMA1000623	5.51	4.72	11.4	2.5	4.83	2.59	2.52	1.82	1.65			
	MAMMA1000625	3.19	6.18	12.95	3.95	4.29	3.37	3.1	1.01	2.69			
	MAMMA1000635	3.08	4.28	9.79	5.68	3.5	2.91	2.33	0.32	2.12			
	MAMMA1000643	3.16	4.8	8.96	4.43	4.19	14.5	3.27	1.73	4.43			
	MAMMA1000646	53.05	63.8	128.68	68.06	63.84	76.26	48.7	34.2	32.4			
20	MAMMA1000652	7.49	6.59	12.24	7.34	7.8	10.34	5.92	2.92	1.26			
	MAMMA1000657	4.53	4.12	7.44	5.71	2.66	4.08	1.96	2.59	1.6	*	-	
	MAMMA1000664	18.71	22.51	38.34	17.17	14.96	16	10.64	12.09	11.81			
	MAMMA1000667	8.69	17.36	17.2	3.58	6.25	8.92	3.77	5.36	2.7	*	-	
	MAMMA1000668	23.14	46.99	61.08	27.38	33.9	32.87	41.85	23.92	33.78			
	MAMMA1000669	3.03	3.5	9.1	2.2	6.51	1.81	2.38	2.13	1.46			
25	MAMMA1000670	4.89	6.68	9.53	5.24	3.91	6.43	9.4	3.5	1.93			
	MAMMA1000672	127	118.39	232.08	362.26	175.38	245.8	112.44	89.34	106.16			
	MAMMA1000681	42.17	56.4	66.57	28.1	10.46	18.45	7.15	8.3	5.57	*	**	-
	MAMMA1000684	6.35	5.06	11.76	8.34	4.22	4.13	4.18	2.86	3.12			
	MAMMA1000696	7.53	9.04	16.29	12.54	11.44	15.76	4.16	3.21	5.89			
	MAMMA1000702	2.37	2.75	7.2	4.27	3.94	4.85	2.38	1.14	1.76			
30	MAMMA1000706	7.11	13.17	13.46	6.85	13.62	11.39	5.11	2.82	4.43	*	-	
	MAMMA1000707	5.79	9.88	8.46	5.04	7.37	7.72	4.37	2.73	5.56			
	MAMMA1000713	13.18	25.83	23.83	10.07	8.95	6.62	3.02	4.1	4.74	*	*	-
	MAMMA1000714	21.05	29.79	38.76	24.92	18.64	21.26	20.38	21.53	20.97			
	MAMMA1000718	7.11	5.26	13.51	4.07	3.72	3	2.71	1.31	2.37			
	MAMMA1000720	56.24	56.67	100.19	108.88	65.38	82.83	53.41	37.73	50.75			
35	MAMMA1000723	83.95	62.78	122.37	158.83	112.68	140.59	85.25	48.89	63.98			
	MAMMA1000731	13.21	20.89	24.92	19.74	19.6	18.49	13.07	8.64	14.74			
	MAMMA1000732	4.13	6	9.07	5.99	9.97	7.96	4.16	1.33	3.64			
	MAMMA1000733	12.22	18.56	20.77	15.57	15.03	11.37	17.6	9.79	15.79			
	MAMMA1000734	4.23	6.43	10.91	7.98	3.73	6.91	3.13	3.72	3.43			
	MAMMA1000736	4.58	4.07	5.19	5.1	2.18	3.84	1.49	1.8	2.72	**	-	
40	MAMMA1000738	27.47	31.39	43.2	35.52	27.09	30.72	11.08	15.85	19.91	*	-	
	MAMMA1000744	11.43	16.18	20.32	9.63	9.84	10.4	16.64	15.89	17.27			
	MAMMA1000746	5.14	6.4	11.37	3.9	6.11	4.85	2.11	2.43	3.5			
	MAMMA1000748	2.95	3.98	9.11	2.66	4.26	3.02	2.63	1.16	2.48			
	MAMMA1000751	3.53	4.94	7.73	2.22	4.21	3.15	2.53	1.56	2.63			
	MAMMA1000752	9.18	9.76	16.46	16.7	13	12.37	10.17	5.29	10.03			
45	MAMMA1000757	17.77	21.89	38.71	25.58	19.94	21.44	12.48	15.54	20.02			
	MAMMA1000760	6.79	10.56	9.64	3.73	4.03	3.96	1.97	4.15	4.68	*	*	-
	MAMMA1000761	4.06	4.2	7.68	1.53	2.88	3.67	1.98	1.33	1.45	*	-	
	MAMMA1000775	4.12	5.64	14.4	7.07	2.94	5.07	2.8	2.71	4.1			
	MAMMA1000776	26.15	27.77	36.92	48.47	26.15	33.74	22.66	12.7	18.46	*	-	
	MAMMA1000778	38.93	73.17	60.3	15.58	59.91	40.66	15.6	19.11	12.75	*	-	
50	MAMMA1000781	10.71	16.72	21.46	6.1	15.65	13.14	10.25	9.83	6.19			
	MAMMA1000782	5.28	6.96	8.31	4.59	9.33	5.12	3.95	1.7	2.78	*	-	
	MAMMA1000784	12.93	21.78	27.25	9.87	8.6	8.24	5.41	7.95	18.83	*	-	
	MAMMA1000788	14.83	19.2	21.42	14.77	17.9	16.09	9.03	8.51	18.38			
	MAMMA1000798	10.63	12.91	13.99	6.66	4.6	7.92	6.32	3.01	7.59	*	*	-
	MAMMA1000802	10.59	10.38	19.17	11.33	9.98	8.79	5.57	3.43	5.21	*	-	
55	MAMMA1000810	6.03	6.16	13.72	6.5	6.85	7.38	2.82	2.22	3.59			
	MAMMA1000813	22.11	37.42	37.78	16.99	20.99	20.43	27.71	18.27	23.96			
	MAMMA1000814	1.64	5.26	13.69	2.27	7.88	1.6	3.8	1.06	1.8			

Table 394

	MAMMA1000824	52.75	82.46	54.98	22.75	86.37	46.11	53.27	21.38	20.22				
5	MAMMA1000827	3.29	5.2	12.5	6.91	5.04	2.83	2.54	1.96	3.02				
	MAMMA1000831	31.08	35.42	39.96	20.36	22.38	25.87	17.52	21.92	26.79	*	*	-	-
	MAMMA1000838	4.58	6.92	8.85	2.9	2.71	3.02	3.13	2.4	1.8	*	*	-	-
	MAMMA1000839	4.7	5.1	9.24	1.82	2.67	4.2	2.02	1.34	1.48		*		
	MAMMA1000841	4.43	2.78	9.96	2.71	2.83	2.07	3.01	0.81	2.24				
	MAMMA1000842	6.22	8.19	14.72	3.28	5.48	4.22	5.77	2.92	7.82				
10	MAMMA1000843	10.02	23.1	28.88	14.54	17.26	10.11	4.63	3.65	6.21	*		-	
	MAMMA1000845	2.57	2.89	10.34	0.88	3.81	2.04	1.66	1.53	3.4				
	MAMMA1000851	40.29	50.53	100.08	64.55	45.92	39.66	42.2	36.12	64.01				
	MAMMA1000854	3.86	5.86	8.12	2.91	1.76	3.56	1.11	0.53	1.24	*		-	
	MAMMA1000855	91.57	117.96	159.35	213.71	138.54	171.88	95.66	65.57	93.06				
	MAMMA1000856	3.13	2.69	5.73	1.9	1.05	2.66	1.82	0.46	1.81				
15	MAMMA1000859	3.59	5.65	10.37	1.76	1.83	1.2	3.38	1.09	1.24				
	MAMMA1000862	8.58	10.61	23.09	5.34	11.79	7.43	5.15	1.27	2.11				
	MAMMA1000863	17.14	20.47	45.55	14.36	24.31	16.09	24.81	12.68	16.34				
	MAMMA1000865	3.2	5.96	11.12	4.18	4.78	11.8	2.48	0	2.86				
	MAMMA1000867	12.55	18	37.97	18.03	16.36	15.97	9.25	8.53	14.8				
	MAMMA1000875	197.47	247.19	307.15	151.05	163.7	159.54	127.81	148.8	137.51	*	*	-	-
20	MAMMA1000876	4.29	6.54	6.75	2.84	2.75	3.43	2.51	1.58	2.61	*	*	-	-
	MAMMA1000877	2.84	3.61	4.96	2.05	1.13	1.68	2.93	0.77	2.2	*		-	
	MAMMA1000878	5.22	9.31	15.62	6.72	6.36	5.06	10.1	4.12	5.11				
	MAMMA1000880	13.15	18.7	32.08	12.61	12.85	8.92	10.54	7.92	11.52				
	MAMMA1000881	6.97	11.85	26.23	10.06	11.84	7.67	8.29	6.16	7.32				
	MAMMA1000883	11.76	21.56	31.01	16.67	19.82	18.1	18.77	10.78	19.11				
25	MAMMA1000897	18.89	25.07	44.99	26.44	17.53	21.31	17.58	14.36	19.92				
	MAMMA1000898	4.54	4.74	8.26	5.15	4.11	4	3.9	1.83	1.2				
	MAMMA1000905	19.81	46.58	24.87	13.58	12.04	12.03	17.95	11.63	11.81				
	MAMMA1000906	13.7	9.74	18.2	5.83	6.94	4.39	4.39	2.34	1.82	*	*	-	-
	MAMMA1000908	8.3	13.83	18.11	10.1	14.32	5.63	5.09	3.21	3.69	*		-	
	MAMMA1000911	13.12	16.04	26.46	13.81	12.11	7.57	12.29	5.96	12.25				
30	MAMMA1000914	2.41	3.47	11.09	1.11	2.25	1.29	1.59	0	0.87				
	MAMMA1000920	68.92	152.1	139.06	77.3	106.8	94.98	122.37	27.22	25.46				
	MAMMA1000921	3.68	5.93	12.67	7.11	6.12	6.97	3.45	2.44	2.92				
	MAMMA1000931	35.49	29.12	32.19	9.74	14.81	15.82	7.85	20.92	4.78	**	*	-	-
	MAMMA1000940	16.07	19.99	34.79	11.62	14.07	12.51	10.88	8.84	14.41				
	MAMMA1000941	36.94	28.9	55.32	14.85	46.69	25.1	44.15	31.17	20.09				
35	MAMMA1000942	19.99	18.82	58.05	28.3	25.6	20.38	16.91	16.31	24.51				
	MAMMA1000943	14.05	10.94	26.95	6.92	4.75	8.24	3.89	2.4	1.4	*		-	
	MAMMA1000952	3.98	5.7	16.6	3.37	4.97	3.51	7.54	1.89	3				
	MAMMA1000956	5.62	5.18	14.83	6.99	6.03	6.18	4.85	2.51	6.15				
	MAMMA1000957	0.61	0.47	2.13	0.38	0.27	1.52	0.16	0	0				
	MAMMA1000962	26.82	25.6	21.85	10.69	8.37	7.64	7.43	8.92	3.07	**	**	-	-
40	MAMMA1000966	13.96	15.32	18.62	3.18	4.77	5.42	5.48	5.55	2.07	**	**	-	-
	MAMMA1000968	3.82	3.17	8.04	2.19	4.04	1.69	2.56	0.98	1.54				
	MAMMA1000972	109.05	38.4	166	38.59	38.3	60.84	51.28	65.81	23.12				
	MAMMA1000973	4.24	3.6	8.43	1.16	3.43	2.39	3.18	1.23	1.88				
	MAMMA1000975	4.83	5.04	16.94	6.44	6.12	4.99	5.27	1.93	5.12				
	MAMMA1000976	10.4	12.69	31.13	7.88	10.7	11.37	8.68	4.42	4.88				
45	MAMMA1000979	15.33	18.37	49.49	29.29	22.41	26.44	15.03	8.9	16				
	MAMMA1000986	11.83	20.17	19.1	14.27	9.07	14.47	9.64	5.8	3.91	*		-	
	MAMMA1000987	35.85	39.55	84.06	67.43	62.8	61.8	46.73	25.89	38.89				
	MAMMA1000988	12.53	13.76	42.26	22.92	17.53	17.38	12.36	7.34	12.64				
	MAMMA1000994	6.93	10.09	26.01	16.14	13.54	12.99	6.56	3.79	6.83				
	MAMMA1000998	3.85	8.09	10.95	3.78	4.4	5.85	1.97	0.73	2.47	*		-	
50	MAMMA1001003	11.87	14.9	34.42	24.16	21.08	20.65	13.23	10.02	16.87				
	MAMMA1001007	4	4.13	6.2	3.14	6.73	3.28	4.14	1.49	4.79				
	MAMMA1001008	20.12	23.76	44.26	26.75	20.79	27.13	18.57	19.08	24.22				
	MAMMA1001013	9.3	12.99	14.08	13.97	3.4	7.56	6.85	5.46	5.5	*		-	
	MAMMA1001014	3.74	2.89	7.41	3.98	5.49	5.98	4.67	4.19	1.31				
	MAMMA1001021	58.82	76.19	93.74	67.98	54.85	51.75	72.35	45.95	58.5				
55	MAMMA1001024	88.7	92.15	131.2	139.16	94.51	99.4	87.98	68.05	106.24				
	MAMMA1001025	69.9	102.4	41.66	70.13	59.68	30.76	22.6	25.23	39.06				
	MAMMA1001028	80.18	111.56	110	73.96	84.44	72.45	97.15	91.69	100.75				

Table 395

	MAMMA1001030	7.4	11.72	12.89	11.66	7.79	10.11	7.28	6.15	7.3			
5	MAMMA1001035	39.22	53.03	74.6	50.1	27.34	38.76	23.51	31.74	38.44			
	MAMMA1001036	3.31	5.83	5.4	5.92	5.35	4.3	4.37	2.81	3.74			
	MAMMA1001037	24.23	31.03	53.22	27.23	25.26	31.34	28.91	17.23	25.45			
	MAMMA1001038	12.98	20.58	21.05	13.13	14.71	11.55	14.52	10.1	18.77			
	MAMMA1001041	1.54	2.15	5.75	4.24	4.69	7.8	3.02	1.22	2.08			
	MAMMA1001043	1.39	2.46	4.67	3.06	4.27	3.32	4.35	1.52	2.3			
10	MAMMA1001050	1.33	4.39	4.83	3.8	5.59	5.14	4.27	1.05	2.57			
	MAMMA1001054	19.75	24.03	50.38	32.02	21.79	27.11	13.83	16.21	20.46			
	MAMMA1001059	3.19	4.55	5.53	3.65	3.25	5.05	2.54	10.99	3.33			
	MAMMA1001066	5.02	4.16	8.84	5.66	2.95	3.72	1.82	2.25	3.08			
	MAMMA1001067	17.58	21.79	31.08	14.83	16.92	18.84	15.29	17.34	18.26			
	MAMMA1001072	2.53	1.88	3.3	1.93	1.68	2.41	2.3	1.25	2			
15	MAMMA1001073	0.84	2.27	6.85	1.01	1.41	5.24	0.75	4.07	1.61			
	MAMMA1001074	24.28	39.17	47.61	31.96	28.12	24.54	31.91	23.64	32.81			
	MAMMA1001075	1.48	5.48	8.44	3.99	4.91	2.99	2.44	2.09	3.72			
	MAMMA1001078	21.72	26.12	44.96	33.39	16.5	21.38	18.07	17.35	25.34			
	MAMMA1001080	12.04	17.72	15.6	14.26	12.06	16.7	6.39	6.97	11.08	*	-	
	MAMMA1001082	4.59	9.29	12.12	6.84	2.79	4.23	4.41	1.12	3.78			
20	MAMMA1001091	16.73	23.95	30.14	19.81	16.46	17.71	21.25	12.1	23.6			
	MAMMA1001092	7.81	11.13	15.6	7.44	8.17	6.28	7.18	4.54	7.68			
	MAMMA1001094	11.74	16.72	20.33	14.77	10.66	23.71	14.53	12.3	17.29			
	MAMMA1001105	45.26	57.55	66.73	41.25	47.01	32.75	30.09	24.22	28.58	*	-	
	MAMMA1001110	7.59	14.4	12.56	8.44	9.45	9.37	9.82	4.24	0.9			
	MAMMA1001126	37.56	44.85	64.49	49.13	34.88	37.49	24.63	36.31	49.73			
25	MAMMA1001133	5.76	9.31	8.87	3.28	3.01	4.08	2.64	5.37	6.55	*	-	
	MAMMA1001139	7.27	14.13	10.95	4.54	4.49	4.1	6.16	2.44	5.84	*	-	
	MAMMA1001141	6.69	8.3	15.1	2.9	4.24	4.06	2.47	2.3	5.32			
	MAMMA1001143	3.83	3.21	9.91	1.84	2.97	1.81	3.49	1.28	2.11			
	MAMMA1001145	2.22	12.54	14.95	2.6	3.58	6.73	2.4	2.76	3.58			
	MAMMA1001150	10.97	15.54	29.9	12.2	13.68	9.93	10.31	8.5	12.03			
30	MAMMA1001154	5.02	9.06	11.37	4.94	8.36	4.03	3.8	2.43	3.42			
	MAMMA1001159	6.91	7.68	15.13	5.63	3.35	4.72	2.34	2.78	4.72			
	MAMMA1001161	109.99	168.02	168.22	189.81	141.37	144.88	81.63	94.69	118.15			
	MAMMA1001162	7.19	5.58	7.65	7.64	5.6	5.96	4.02	2.29	5.78			
	MAMMA1001181	2.37	3.1	6.4	4.16	1.93	2.21	2.1	2.11	4.15			
	MAMMA1001186	3.02	2.01	9.14	2.7	2.02	2.05	2.34	0.77	3.58			
35	MAMMA1001189	17.92	24.89	44.3	19.97	22.86	16.26	24.9	14.32	18.92			
	MAMMA1001191	10.11	15.9	19.2	7.11	13.06	8.79	15.3	10.81	16.52			
	MAMMA1001198	4.68	8.28	11.96	3.49	7.28	5.15	6.52	2.84	2.49			
	MAMMA1001202	30.38	37.04	84.46	54.02	29.63	36.02	18.16	17.9	40.13			
	MAMMA1001203	8.99	12.77	20.34	10.56	11.45	9.96	10.07	8.3	11.49			
	MAMMA1001206	14.27	17.3	21.28	14.44	9.47	13.95	15.09	7.44	16.29			
40	MAMMA1001208	3.37	1.85	7.28	0.99	1.62	0.23	1.58	0.63	2.48			
	MAMMA1001215	12.57	20.58	26.01	4.39	17.55	6.44	10.98	8.12	6.27			
	MAMMA1001220	12.2	14.97	20.97	18.99	11.55	15.4	10.87	5.54	12.65			
	MAMMA1001222	13.14	15.27	54.43	12	15.72	10.61	17.61	13.51	15.3			
	MAMMA1001223	5.47	11.04	23.87	8.51	8.76	8.32	9.09	3.98	9.79			
	MAMMA1001232	5.9	6.27	10.44	10.05	4.68	7.4	3.45	2.12	5.89			
45	MAMMA1001234	78.47	62.1	106.68	104.09	22.14	88.22	44.43	81.83	25.73			
	MAMMA1001237	4.23	3.61	4.51	2.39	3.8	1.85	3.83	2.61	1.63			
	MAMMA1001243	26.51	33.45	37.19	22.72	19.97	20.13	13.4	8.73	6.36	*	**	-
	MAMMA1001244	3.29	3.23	5.47	2.05	2.81	0.99	2.32	0.99	1.85			
	MAMMA1001249	32.97	38.57	66.31	31.72	40.81	37.57	44.31	25.2	27.49			
	MAMMA1001256	13.8	15.37	22.1	10.86	16.44	20.14	15.27	12.69	11.49			
50	MAMMA1001259	3.58	4.73	9.83	2.71	2.66	1.74	5.81	0.4	3.31			
	MAMMA1001260	15.61	19.65	19.14	11.02	7.29	22.35	9.03	6.24	10.39	**	-	
	MAMMA1001262	8.3	48.53	16.27	15.78	7.11	6.47	9.48	5.41	7.71			
	MAMMA1001268	7.26	6.65	12.6	5.74	6.05	4.12	3.69	3.37	4.04			
	MAMMA1001271	4.99	4.56	6.83	2.12	3.55	3.26	4.68	2.4	2.94	*	-	
	MAMMA1001274	197.38	283.08	348.26	54.68	91.98	70.74	33.35	19.31	25.39	*	**	-
55	MAMMA1001280	10.76	14.33	28.14	10.36	11.35	10.7	14.52	8.71	14.89			
	MAMMA1001283	4.11	3.31	10.89	0.34	3.46	2.07	2.94	1.3	1.97			
	MAMMA1001284	6.24	6.15	16.76	7	6.77	4.3	3.05	1.61	4.29			



Table 396

	MAMMA1001286	29.08	30.31	35.52	8.75	7.01	14.48	10.18	16.99	22.31	**	*	-	-
5	MAMMA1001289	8.87	7.96	10.4	9.73	7.53	9	7.31	3.62	7.73				
	MAMMA1001292	24.97	44.07	66.64	9.34	36.59	35.11	13.77	28.43	10.4				
	MAMMA1001296	4	4.17	8.01	2.8	3.49	2.38	2.75	2.82	4.19				
	MAMMA1001298	7.53	9.89	10.46	2.88	6.46	2.62	5.34	3.84	1.86	*	*	-	-
	MAMMA1001305	3.74	4.35	13.81	2.61	4.06	3.12	3.76	5.53	2.5				
10	MAMMA1001309	10.42	15.14	31.52	12.87	13.99	9.19	10.23	3.68	9.96				
	MAMMA1001310	2.92	5.46	13.25	3.59	3.89	1.96	3.03	0.43	1.21				
	MAMMA1001322	2.17	2.64	6.93	3.3	2.91	2.5	1.12	1.37	2.03				
	MAMMA1001324	4.53	3.59	5.55	3.63	2.78	3	2.65	1.6	1.68	*		-	
	MAMMA1001330	4.9	5.1	12.68	7.84	4.19	4.82	3.36	2.64	3.18				
	MAMMA1001333	4.95	3.16	7.58	2.56	3.62	3.33	2.38	2.25	1.89				
15	MAMMA1001334	31.92	25.66	43.45	18.83	15.13	18.08	17.92	22.66	13.99	*		-	
	MAMMA1001337	4.26	3.84	13.74	3.62	4.64	5.34	4	3.29	3.16				
	MAMMA1001341	4.05	4.96	11.41	4.38	5.21	4.83	5.24	4.52	3.64				
	MAMMA1001343	2.73	5.65	10.8	3.22	4.68	4.2	3.94	1.64	3.95				
	MAMMA1001344	2.25	2.47	7.73	4.27	4.36	3.62	2.73	1.3	3.12				
	MAMMA1001346	5.84	6.71	17.37	10.65	9.35	8.33	6.74	3.26	6.06				
20	MAMMA1001383	6.99	8.47	18.39	14.27	8.27	9.89	7.45	4.12	6.12				
	MAMMA1001388	25.28	28.84	63.23	32.5	23.98	25.52	24.7	25.15	17.69				
	MAMMA1001396	15.94	20.37	30.49	14.54	24.62	26.46	14.45	46.08	11.25				
	MAMMA1001397	14.75	18.37	41.81	21.11	18.82	16.79	17.96	11.5	21.37				
	MAMMA1001401	2.94	3.12	6.56	1.21	2.62	3.02	2.46	0.76	2.89				
	MAMMA1001408	1.5	3.57	7.4	2.81	1.88	3.96	5.62	0.76	2.46				
25	MAMMA1001411	6.08	3.93	9.81	9.46	6.06	8.29	3.36	4.18	4.81				
	MAMMA1001414	6.51	7.32	14.7	23.79	6.86	10.67	5.51	4.82	6.45				
	MAMMA1001415	3.95	8.97	8.68	5.52	5.96	8.18	6.06	2.79	4.69				
	MAMMA1001418	8.77	9.1	12.47	12.83	10.06	11.32	13.03	7.4	7.63				
	MAMMA1001419	7.73	7.93	11.48	9.88	6.73	10.35	9.18	5.19	6.18				
	MAMMA1001420	5.14	4.76	6.97	10.23	6.22	6.56	5.34	3.95	4.64				
30	MAMMA1001426	5.19	7.71	9.63	5.55	8.11	6.73	7.6	4.91	8.87				
	MAMMA1001428	3.64	3.18	7.92	6.62	3.95	5.99	3.35	1.43	3.18				
	MAMMA1001432	12.35	13.88	21.83	18.83	11.53	18.33	8.1	11.28	14.53				
	MAMMA1001435	20.05	30.02	44.24	21.04	23.96	21.39	14.97	14.52	16.51				
	MAMMA1001442	6.94	7.75	11.08	5.53	5.57	7.7	6.68	4.54	7.44				
	MAMMA1001446	26.48	31.11	44.32	20.63	23.27	24.39	8.85	5.14	8.85	**		-	
35	MAMMA1001450	11.55	15.7	15.65	12.27	11.07	10.5	14.48	8.46	14.95				
	MAMMA1001452	4.86	7.91	8.36	9.2	4.08	6.24	7.72	3.93	6.05				
	MAMMA1001465	8.92	12.52	15.39	11.83	13.04	10.87	16.92	7.42	13.06				
	MAMMA1001476	132.51	144.85	285.99	418.67	194.96	350.68	82.5	94.08	100.24				
	MAMMA1001478	18.64	21.54	45.82	21.72	20.69	19.34	14.71	16.9	28				
40	MAMMA1001479	11.41	20.27	19.2	13.74	10.72	9.96	13.4	11.81	15.33				
	MAMMA1001487	48.7	29.91	87.89	41.22	44.32	54.61	29.8	35.15	13.96				
	MAMMA1001498	4.35	2.96	9.82	3.07	3.33	1.99	1.92	4.02	3.09				
	MAMMA1001501	4	5.27	10.62	3.92	4.81	5.08	4.06	2.78	3.9				
	MAMMA1001502	3.5	3.68	8.07	3.61	4.35	4.14	3.43	1.95	7.01				
	MAMMA1001510	11.46	20.55	16.62	13.12	12.05	13.04	13.33	7.96	10.37				
	MAMMA1001522	4.88	10.87	13.99	8.11	4.33	5	2.46	3.76	5.04				
45	MAMMA1001529	59.97	69.9	94.57	30.63	46.88	57.69	31.84	37.9	51.83	*		-	
	MAMMA1001532	28.38	37.51	51.46	23.78	26.52	23.49	26.6	24.11	41.98				
	MAMMA1001533	19.86	8.23	26.5	6.01	12.03	8.61	7.93	4.83	6.28				
	MAMMA1001534	11.45	13.72	20.66	6.58	8.79	8.61	9.6	5.71	8.05				
	MAMMA1001535	10.07	15.11	17.7	7.42	8.38	7	2.75	2.21	3.48	*	**	-	-
	MAMMA1001547	5.79	10.79	16.77	6.18	7.64	6.73	7.59	4.04	7.84				
	MAMMA1001551	1.79	3.35	10.09	2.36	3.75	2.54	3.47	0.46	2.39				
50	MAMMA1001569	5.44	7.64	12.53	5.97	3.18	5.89	2.71	3.74	6.78				
	MAMMA1001575	19.87	31.06	32.95	20.06	20.37	18.83	18.83	16.95	22.11				
	MAMMA1001576	4.97	13.68	9.34	4.55	6.26	3.49	1.76	5.49	4.16				
	MAMMA1001584	17.12	20.22	32.05	43.71	22.66	30.09	21.3	15.63	24.89				
	MAMMA1001586	3.44	2.63	9.42	2.75	2.52	1.44	2.63	0.98	2.02				
	MAMMA1001590	4.74	3.32	9.43	0.65	2.72	2.98	5.93	1.26	2.67				
55	MAMMA1001599	6.91	10.35	19.33	5.33	6.4	5.4	7.64	5.96	7.44				
	MAMMA1001600	12.56	24.27	25.25	10.57	15.9	13.61	21.16	12.02	17.72				
	MAMMA1001604	20.93	20.87	41.04	17.28	15.57	5.46	4.43	10.16	15.17				

Table 397

5	MAMMA1001606	37.25	38.33	44.14	13.41	26.09	29.22	7.5	16	15.16	*	**	-	-
	MAMMA1001609	2.18	4.53	5.97	1.87	1.39	1.8	4.17	2.27	1.51				
	MAMMA1001614	10.91	17.85	21.09	12.42	12.51	13.02	16.85	9.92	19.29				
	MAMMA1001615	1.95	3.17	11.55	2.77	2.24	1.36	2.33	1.46	2.06				
	MAMMA1001619	11.51	16.15	15.55	6.34	13.88	8.59	8.19	7.08	5.14	*		-	
	MAMMA1001620	4.59	6.42	11.46	1.77	3.88	3.43	3.11	1.71	4				
	MAMMA1001623	46.36	31	53.81	63.16	42.72	47.15	31.15	25.06	25.66				
10	MAMMA1001626	23.59	24.5	38.75	33.26	30.12	18.9	7.93	11.89	22.41				
	MAMMA1001627	23.89	43.37	29.47	17.73	21.82	12.9	6.43	10	7.98	*		-	
	MAMMA1001630	9.27	13.78	11.56	7.25	5.63	6.82	2.81	4.06	2.66	*	**	-	-
	MAMMA1001633	3.1	2.16	7.03	2.23	2.28	2.16	0.8	0.79	2.49				
	MAMMA1001634	3.53	6.28	9.01	3.76	4.19	2.88	3.9	2.94	2.79				
	MAMMA1001635	3.28	4.64	15.97	2.28	2.56	1.53	6.22	1.65	2.6				
15	MAMMA1001649	3.05	5.72	15.55	3.26	4.9	2.56	4.26	1.39	3.94				
	MAMMA1001654	4.23	5.9	13.55	3.26	5.84	3.8	3.63	1.4	2.71				
	MAMMA1001660	39.09	42.24	88.43	56.56	52.47	44.31	41.47	39	60.86				
	MAMMA1001663	8.52	11.06	11.71	10.2	6.57	5.19	7.96	6.94	8.33				
	MAMMA1001670	5.91	7.75	6.72	4.07	2.57	5.22	5.32	3.26	4.27	*	*	-	-
	MAMMA1001671	56.61	62.54	66.07	56.8	37.97	53.72	50.14	43.96	58.96				
20	MAMMA1001679	6.69	13.86	10.25	4.05	5.47	3.58	4.46	7.43	6.03				
	MAMMA1001683	15.6	21.19	31.72	12.85	17.62	10.3	18.14	10.49	14.57				
	MAMMA1001686	4.11	3.45	11.77	4.66	4.36	4.4	4.89	1.58	2.59				
	MAMMA1001688	4.96	5.41	15.23	3.79	4.7	4.42	2.65	1.46	3.58				
	MAMMA1001689	28.44	25.89	32.18	7.85	17.39	15.22	8.44	8.89	20.79	*	*	-	-
	MAMMA1001692	5.97	3.79	10.24	3.42	9.67	3.1	3.28	4.26	5.93				
25	MAMMA1001711	4.75	4.66	8.45	3.21	3.28	2.22	2.67	8.04	0.88				
	MAMMA1001715	4.22	4.73	9.43	3.9	2.04	3.47	3.76	4.11	2.61				
	MAMMA1001730	3.39	2.22	8.02	1.72	1.43	1.79	1.71	1.46	1.86				
	MAMMA1001735	8.81	9.96	22.03	12.16	11.12	10.37	6.84	5.43	7.1				
	MAMMA1001740	2.28	4.25	11.56	2.64	4.24	1.86	2.43	1.41	3.14				
	MAMMA1001743	10.52	18.5	19.92	5.55	7.23	6.37	6.45	1.87	3.83	*	*	-	-
30	MAMMA1001744	4.59	3.07	5.75	3.86	4	4.16	2.05	2.19	3.63				
	MAMMA1001745	12.62	11.29	21.77	12.13	11.56	10.5	13.92	9.55	13.74				
	MAMMA1001751	11.11	8.28	15.68	3.47	4.56	3.38	2.93	2.2	1.66	*	*	-	-
	MAMMA1001752	5.63	3.02	9.77	2.83	5.25	2.56	2.97	2.42	0.97				
	MAMMA1001754	23.39	32.69	51.88	31.96	35.9	26.06	34.24	24.41	25.71				
	MAMMA1001757	5.44	8.41	15.4	4.99	7.7	6.28	7.54	3.86	5.12				
35	MAMMA1001760	2.58	5.03	10.84	4.07	3.09	11.35	3.87	1.47	1.67				
	MAMMA1001764	1.11	5.18	12.27	3.88	5.02	2.55	4.09	0.44	2.15				
	MAMMA1001767	3.1	2.25	5.04	3.83	2.36	7.31	2.64	1.02	1.81				
	MAMMA1001768	11.92	10.35	26.44	10.9	12.51	10.66	12.91	3.89	9.69				
	MAMMA1001769	14.67	15.11	32.18	14.99	14.79	13.17	17.74	10.66	13.05				
	MAMMA1001771	5.81	5.01	9.7	5.52	6.04	4.42	3.1	4.15	2.2				
40	MAMMA1001773	40.73	46.88	88.4	41.31	38.76	36.3	25.57	21.1	22.63				
	MAMMA1001778	15.44	10.48	54.31	14.07	14.31	18.11	19.19	12.85	7.66				
	MAMMA1001783	12.5	12.45	33.56	11.62	10.75	17.89	7.63	5.83	3.14				
	MAMMA1001785	4.08	3.99	8.35	2.35	3.38	3.07	3.75	1.41	2.66				
	MAMMA1001788	6.1	6.55	20.74	18.01	10.68	15.67	7.37	4.2	7.06				
	MAMMA1001790	1.31	0.72	1.87	1.36	1.35	1.32	1.67	0.59	1.36				
45	MAMMA1001800	2.19	1.86	2.06	3.44	3.43	3.44	1.48	0.44	1.31	**	*	+	-
	MAMMA1001804	9.74	13.74	26.09	23.09	17.83	16.06	15.63	9.04	8.32				
	MAMMA1001806	15.42	15.2	24.16	21.08	16.33	17.7	13.08	11.61	12.4				
	MAMMA1001812	2.66	2.87	5.53	5.25	2.56	2.24	1.76	1.16	2				
	MAMMA1001815	0.82	1.33	4.14	2.35	1.64	0.9	2.33	0	1.04				
	MAMMA1001817	7.15	8.39	26.7	8.94	11.15	9.35	10.6	5.97	8.95				
50	MAMMA1001818	11.74	18.24	23.68	11.92	10.04	13.23	8.57	10.06	9.02				
	MAMMA1001819	15.72	24.34	43.46	17.35	11.3	16.16	12.64	12.63	16.41				
	MAMMA1001820	22.82	19.64	37.64	42.37	24.16	31.98	15.13	16.66	19.01				
	MAMMA1001824	8.99	12.77	18.28	12.69	14.09	15.06	12.72	9.76	11.95				
	MAMMA1001832	7.22	10.73	12.96	9.65	7.55	9.34	6.24	4.93	7.88				
	MAMMA1001836	9.42	23.13	19.47	21.69	15.29	10.85	11.8	5.71	11.11				
55	MAMMA1001837	3.6	4.29	8.23	5.89	6.7	8.36	4.62	1.11	4.3				
	MAMMA1001848	16.38	27.46	23.83	25.7	38.67	49.58	24.68	13.45	27.7				
	MAMMA1001850	4.58	4.63	5.94	6.14	2.91	3.96	4.34	2.05	2				

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	MAMMA1001851	3.04	3.08	4.42	3.11	3.54	2.54	2.52	0.56	2.38		
	MAMMA1001852	4.14	3.26	11.19	3.61	3.33	5.4	1.88	2.12	2.02		
5	MAMMA1001854	1.51	2.81	6.9	2.97	1.88	2.16	2.29	1.4	2.53		
	MAMMA1001858	19.51	21.77	35.8	19.05	16.81	16.88	15.59	11.41	20.06		
	MAMMA1001864	13.26	17.9	34.07	19.43	19.24	16.98	19.91	10.97	23.39		
	MAMMA1001868	36.41	51.95	37.39	27.02	32.06	24.02	38.47	28.02	40.25		
	MAMMA1001874	10.43	12.98	12.56	15.09	16.33	15.06	13.47	8	7.34	*	+
	MAMMA1001878	8.74	13.09	17.2	10.72	7.64	9.1	6.72	5.47	7.12		
10	MAMMA1001880	4.07	4.26	5.15	5.16	2.51	4.87	2.76	4.1	3.13		
	MAMMA1001885	11.53	16.59	20.89	11.02	9.99	7.12	10.84	10.3	12.47		
	MAMMA1001890	18	26.55	27.35	18.41	24.49	18.88	18.85	18.1	22.42		
	MAMMA1001893	9.74	13.29	21.33	8.06	11.26	12.34	13.42	8.15	13.42		
	MAMMA1001901	5.91	10.54	9.81	6.07	8.49	8.27	5.4	3.05	2.51	*	-
15	MAMMA1001907	2.61	3.62	7.04	35.62	7.01	7.16	2.77	1.6	2.87		
	MAMMA1001908	8.52	7.37	12.33	6.04	6.79	5.83	5.18	1.69	2.73	+	-
	MAMMA1001919	28.87	31.57	48.08	80.53	41.26	66.58	17.81	21.06	28		
	MAMMA1001931	5.05	3.95	9.8	4.52	3.24	2.79	3.04	5.51	2.52		
	MAMMA1001937	14.26	19.97	17.05	11.88	9.67	16.46	11.3	11.49	14.97		
	MAMMA1001951	10.03	11.71	22.7	11.88	9.84	10.7	11.47	12.01	12.62		
20	MAMMA1001956	993.12	926.97	1643.3	1427.1	1487.9	1519.7	1062.9	902.24	975.35		
	MAMMA1001957	5.28	8.16	19.85	8.48	7.2	6.6	6.19	4.02	7.97		
	MAMMA1001960	4.45	5.22	11.99	3.94	5.66	4.15	4.01	2.89	2.74		
	MAMMA1001963	9.87	14.96	20.98	14.68	14.73	14.4	8.07	6	3.43		
	MAMMA1001969	11.23	14.81	19.75	14.09	10.96	16.21	10.31	8.8	19.07		
	MAMMA1001970	4.02	5.46	5.52	3.48	4.15	15.31	4.95	4.07	2.18		
25	MAMMA1001978	13.78	19.86	26.28	16.09	13.28	16.86	13.67	12.24	23.16		
	MAMMA1001992	6	4.83	12.16	2.11	5.12	11.04	3.79	2.55	5.99		
	MAMMA1001994	4.27	7.76	10.55	16.33	8.69	5.41	3.19	4.78	5.52		
	MAMMA1002008	2.62	3.39	13.27	3.37	3.96	2.92	2.97	2.86	1.68		
	MAMMA1002009	3.5	5.4	13.89	4.02	6.32	3.6	2.53	1.71	1.09		
	MAMMA1002011	3.21	3.57	5.26	2.05	5.5	3.92	2.9	2.56	2.89		
30	MAMMA1002022	23.41	32.84	43.13	18.55	24.01	20.69	18.94	17.16	21.03		
	MAMMA1002024	4.69	8.48	7.51	4.82	3.7	4.18	3.88	2.33	4.09		
	MAMMA1002032	22.72	24.3	34.55	17.1	16.95	18.46	20.89	15.73	25.86		
	MAMMA1002033	5.27	4.69	9.29	4.37	4.11	4.75	8.94	7.94	5.81		
	MAMMA1002041	6.92	11.13	16.18	4.7	5.73	4.73	2.24	3.33	5.35		
	MAMMA1002042	4.21	5.9	12.97	1.93	6.7	3.65	5.79	7.29	5.48		
35	MAMMA1002045	3.58	4.86	12.3	4.27	5.48	4.41	3.9	4.78	2.67		
	MAMMA1002047	6.8	7.34	9.55	7.31	12.68	11.46	8.75	3.44	4.92		
	MAMMA1002056	2.57	2.86	6.49	3.74	3.21	3.7	1.38	1.89	2.78		
	MAMMA1002058	12.8	12.32	19.01	10.51	10.24	9.8	10.2	7.07	10.6		
	MAMMA1002060	3.44	2.98	10.21	3.91	3.36	3.73	4.39	1.38	3.75		
	MAMMA1002065	5.77	6.94	12.55	3.81	3.34	3.54	3.78	2.53	2.66		
40	MAMMA1002068	5.43	5.26	11.94	2.41	4.51	4.09	4.21	2.57	4.68		
	MAMMA1002070	3.38	5.43	10.65	2.42	2.8	1.57	1.88	0.34	3.17		
	MAMMA1002078	3.03	3.94	12.3	1.63	3.98	2.25	2.32	1.3	2.65		
	MAMMA1002080	11.92	16.79	18.92	3	9.03	5.76	7.02	2.85	4.16	*	**
	MAMMA1002082	8.32	5.53	12.97	8.62	3.65	5.55	2.81	1.42	4.34		
	MAMMA1002084	5.95	5.89	9.82	6.01	4.3	5.5	3.1	3.76	3.18	*	-
45	MAMMA1002087	4.18	2.51	5.36	3.1	3.55	1.79	2.57	2.24	1.51		
	MAMMA1002091	4.77	6.45	9.77	6.57	5.69	2.84	2.82	2.99	2.11	*	-
	MAMMA1002093	7.77	50.44	12.78	4.52	8.15	3.8	10.66	4.49	6.61		
	MAMMA1002095	2.07	3	10.99	1.29	1.85	0.7	1.89	0.49	1.88		
	MAMMA1002108	11.08	15.62	32.13	20.98	14.75	19.73	14.58	13.23	20.21		
	MAMMA1002112	11.23	16.95	26.2	16.44	15.29	9.14	16.6	9.46	11.52		
50	MAMMA1002118	15.81	20.81	31.7	25.23	19.06	12.25	11.43	15.5	24.54		
	MAMMA1002119	10	9.39	20.1	14.99	8.54	8.01	7.06	7.05	10.3		
	MAMMA1002125	8.81	6.62	15.53	7.95	7.53	5	5.63	5.81	8.41		
	MAMMA1002126	38.45	22.62	47.44	8.75	23.38	14.29	26.49	8	13.65		
	MAMMA1002128	9.97	18.56	26.22	10.58	12.77	9.47	19.63	7.42	11.63		
	MAMMA1002132	6.21	7.25	34.7	5.61	8.67	4.88	6.36	3.29	9.25		
55	MAMMA1002140	16.11	29.14	22.82	11.98	12.1	5.91	9.18	3.59	4.66	*	*
	MAMMA1002142	3.45	5.23	11.28	4.42	6.67	3.75	4.53	0.93	3.45		
	MAMMA1002143	16.35	16.97	31.08	20.92	14.17	21.18	9.45	9.06	16.49		

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	MAMMA1002145	59.23	60.84	77.53	26.62	46.01	14.01	21.49	27.44	27.68	*	**	-	-
5	MAMMA1002147	5.58	4.1	8.16	3.48	3.17	3.48	3.61	1.58	1.54				
	MAMMA1002153	2.82	4.71	7.06	3.26	5.54	4.01	3.33	4.14	1.01				
	MAMMA1002155	2.48	3.25	10.86	2.89	3.23	2.81	4.53	1.33	2.05				
	MAMMA1002156	1.89	5.51	11.57	0.4	3.84	3.05	2.17	1.45	3.44				
	MAMMA1002158	31.98	68.42	55.01	8.28	17.41	13.99	16.74	7.42	4.4	*	*	-	-
	MAMMA1002164	1.74	3.48	10.17	3.33	5.39	3.9	5.07	0.22	3.21				
10	MAMMA1002165	14.96	21.57	31.25	20.06	14.73	17.78	14.07	10.69	17.29				
	MAMMA1002170	22.65	29.54	35.22	10.64	9.2	7.67	9.57	17.6	7.86	**	*	-	-
	MAMMA1002174	5.6	8.95	10.45	5.64	4.66	7.45	4.49	3.82	4.25		*	-	
	MAMMA1002175	51.5	30.74	138.92	91.4	93.51	53.96	49.64	44.62	29.88				
	MAMMA1002180	26.41	35.57	64.21	33.73	28.48	23.51	38.7	27.33	38.33				
	MAMMA1002198	37.99	80.63	138.79	18.29	47.55	46.05	13.24	10.75	8.83				
15	MAMMA1002205	15.14	20.56	52.79	21.27	16.14	13.46	24.47	10.14	16.64				
	MAMMA1002206	2.93	3.59	10.31	2.52	3.96	2.18	3.53	0.98	3.24				
	MAMMA1002209	183.5	268.42	348.13	282.08	352.1	269.26	189.69	127.24	124.82				
	MAMMA1002215	24.38	31.33	40.05	29.39	28.67	24.47	25.62	23.02	20.25				
	MAMMA1002219	2.71	0.94	3.73	1.84	2.07	2.08	0.86	0.6	1.35				
	MAMMA1002224	15.23	8.24	19.36	12.34	12.12	11.67	6.61	10.38	6.31				
20	MAMMA1002229	16.46	14.44	27.79	9.51	10.83	11.84	7.32	11.92	8.59				
	MAMMA1002230	22	37.1	57.12	14.15	20.28	20.13	22.25	15.46	15.8				
	MAMMA1002233	70.38	89.47	122.68	8.19	33.96	39.69	218.52	154.84	147.67	*	*	-	+
	MAMMA1002234	7.92	8.85	12.79	4.92	10.39	5.68	11.44	4.89	8.58				
	MAMMA1002236	136.07	148.16	220.88	36.8	57.62	87.11	34.48	55.67	55.33	*	*	-	-
	MAMMA1002243	20.02	20.33	38.87	38.33	25.12	25.3	21.56	17.63	24.13				
25	MAMMA1002250	2.68	3.81	6.67	5.79	2.6	4.11	4.54	2.26	2.04				
	MAMMA1002253	0.57	1.7	6.1	2.21	1.65	3.98	2.62	1.41	1.86				
	MAMMA1002267	9.29	9.06	17.68	10.28	11.75	12.03	8.49	4.34	11.22				
	MAMMA1002268	0.57	3.72	6.93	16.18	7.45	4.5	3.59	1.73	3.92				
	MAMMA1002269	1.7	2.24	4.35	2.97	8.98	8.51	2.83	1.4	3.35				
	MAMMA1002282	2.86	3.76	4.32	2.98	7.03	4.77	3.56	5.53	5.39				
30	MAMMA1002292	15.43	25.26	45.69	33.39	19.64	22.84	15.48	15.23	21.7				
	MAMMA1002293	3.2	3.94	4.4	4.2	3.49	3.24	3.79	4.35	3.43				
	MAMMA1002294	9.41	6.68	12.5	3.33	7.99	10.5	5.31	8.44	4.21				
	MAMMA1002297	5.35	6.59	11.35	7.95	7.71	8	2.76	2.6	3.09				
	MAMMA1002298	3.44	2.01	8.19	4.11	4.61	4.39	2.48	2.96	3.08				
	MAMMA1002299	2.99	4.55	14.53	7.08	6.73	6.49	4.69	0.99	4.04				
35	MAMMA1002308	5.47	9.33	18.02	10.01	8.02	7.61	7.23	3.03	7.9				
	MAMMA1002310	9.13	10.94	18.01	13.86	17.88	11.7	14.2	7.14	10.5				
	MAMMA1002311	10.67	15.07	18.09	4.83	5.07	6.09	1.95	3.51	2.65	*	**	-	-
	MAMMA1002312	30.9	42.06	49.45	34.33	28.66	29.57	22.98	30.71	35.68				
	MAMMA1002317	5.72	5.28	10.29	3.9	3.7	4.94	4.31	4.41	4.7				
	MAMMA1002319	11.12	14.39	20.39	9.58	9.59	6.6	12.89	13.6	13.85				
40	MAMMA1002322	2.09	3.24	7.26	1.71	2.86	1.28	1.75	1.09	1.05				
	MAMMA1002329	17.33	19.74	32.38	18.64	18.47	17.53	19	10.56	17.8				
	MAMMA1002332	2.58	4.23	6.84	4.89	4.12	2.94	2.37	0.43	2.61				
	MAMMA1002333	1.45	2.08	7.07	4.55	5.97	6.64	2.39	0.64	2.14				
	MAMMA1002335	12.65	18.48	23.72	7.59	6.81	10.8	3.17	6.12	8.64	*	*	-	-
	MAMMA1002339	7.58	15	19.05	10.2	7.54	10.35	7.33	10.1	11.23				
45	MAMMA1002347	10.15	21.39	24.74	8.5	9.44	11.14	10.35	10.5	16.39				
	MAMMA1002351	7.61	10.35	21.39	9.12	8.67	7.13	7.44	4.46	10.65				
	MAMMA1002352	3.96	6.91	9.29	4.01	3.84	4.53	2.75	1.39	5.61				
	MAMMA1002353	8.39	10.78	23.6	6.39	12.46	12.35	7.8	9.12	7.88				
	MAMMA1002355	25.93	29.71	53.72	28.58	30.76	23.64	29.82	21.55	27.08				
	MAMMA1002356	28.68	42.92	56.16	40.53	46.92	35.69	34.66	27.13	37.63				
50	MAMMA1002359	9.7	13.9	19.55	15.93	13.24	12.52	6.92	6.02	14.49				
	MAMMA1002360	85.31	125.75	125.12	50.2	80.78	78.44	18.48	22.03	30.83	**		-	
	MAMMA1002361	4.68	5.33	13.4	6.92	5.11	6.08	3.35	2.61	7.85				
	MAMMA1002362	4.53	5.8	12.93	6.01	7	5.37	5.23	3.68	7.06				
	MAMMA1002367	13.67	17.12	24.55	7.42	11.11	9.42	8.07	3.62	6.96	*		-	
	MAMMA1002371	2.82	3.35	9.8	0.89	2.2	2.61	2.45	2.44	1.99				
55	MAMMA1002380	7.87	13.26	17.64	9.95	9.26	6.58	10	7.71	10.46				
	MAMMA1002384	91.44	168.34	87.56	61.83	126.23	76.47	56.65	15.61	10.22	*		-	
	MAMMA1002385	2.04	1.77	7.54	5.82	2.53	3.4	1.44	1.54	1.62				

Table 400

	MAMMA1002390	16.21	20.25	27.48	13.4	13.61	14.48	13.02	8.71	18.23			
	MAMMA1002392	4.77	2.83	6.02	7.9	2.39	4.12	3.41	2.08	4.6			
5	MAMMA1002396	2.99	1.82	9.4	2.48	1.34	2.01	2.08	1.84	0.91			
	MAMMA1002399	9.87	15.29	24.4	2.74	8.91	5.25	5.52	3.6	3.73		*	-
	MAMMA1002400	72.48	90.25	98.09	48.92	68.69	49.07	35.95	25.31	45.88	*	**	-
	MAMMA1002409	6.49	9.18	17.47	3.97	6.62	4.36	5.84	1.59	5.43			
	MAMMA1002411	9.51	7.57	20.49	9.69	12.54	10.88	11.51	6.91	7.16			
10	MAMMA1002413	34.97	38.81	65.44	49.38	40.42	34.55	32.31	27.95	41.66			
	MAMMA1002417	36.82	49.91	68.59	44.18	31.29	40.31	29.78	24.72	27.25			
	MAMMA1002427	6.8	10.05	17.81	10.58	7.31	11.82	13	6.65	9.6			
	MAMMA1002428	5.09	6.45	11.72	5.54	5.32	4.74	5.8	2.19	4.39			
	MAMMA1002433	14.18	24.47	33.83	12.49	14.56	9.41	13.05	9.04	12.93			
	MAMMA1002434	4.26	3.86	13.18	2.12	3.76	2.95	4.67	2.76	3.7			
15	MAMMA1002446	8.39	8.67	27.55	10.82	15.66	10.5	11.46	8.07	9.95			
	MAMMA1002447	4.71	6.42	13.3	4.25	7.94	6.39	4.34	1.12	6.19			
	MAMMA1002454	3.91	4.62	7.05	7.12	5.04	6.67	4.66	2.3	3.21			
	MAMMA1002461	27.3	34.86	56	30.05	20.73	23.5	29.37	22.7	32.72			
	MAMMA1002463	9.24	10.49	15.67	10.5	6.07	6.24	8.27	4.83	7.57			
	MAMMA1002464	3.98	2.85	5.66	1.75	3.24	1.37	1.77	2.41	1.96			
20	MAMMA1002466	4.86	7.93	15.75	8.06	8.89	6.34	6.75	3.95	4.7			
	MAMMA1002470	4.68	6.3	14.57	5.95	13.1	4.89	3.64	2.83	3.84			
	MAMMA1002475	17.39	22.9	40.72	24.51	29.14	16.55	20.39	12.61	16			
	MAMMA1002480	51.48	94.76	100.05	63.97	58.87	37.35	60.56	13.3	33.46			
	MAMMA1002485	19.11	15.89	43.85	26.44	20.15	19.25	16.32	13.38	18.32			
	MAMMA1002494	22.86	28.77	50.5	24.3	23.02	18.38	23.12	24.83	27.28			
25	MAMMA1002498	5.27	2.99	4.95	1.99	2.08	1.95	2.18	0.89	1.64	*	*	-
	MAMMA1002524	11.96	11.09	24.02	7.72	7.78	5.46	10.41	6.02	6.07			
	MAMMA1002530	277.32	388.85	679.97	473.31	550.87	394.12	467.12	251.99	328.81			
	MAMMA1002538	1.65	4.73	10.72	1.52	2.62	2.66	2.05	0.61	2.49			
	MAMMA1002545	2.59	2.37	13.88	1.77	4.03	1.39	1.68	0.09	1.93			
	MAMMA1002554	115.83	185.59	273.08	258.19	207.86	207.1	180.88	93.96	83.88			
30	MAMMA1002556	4.03	6.04	7.54	5.06	3.68	5.28	2.7	3.76	3.11			
	MAMMA1002561	15.67	18.37	24.06	5.72	9.69	8.96	6.7	7.18	2.52	*	**	-
	MAMMA1002565	20.13	19.37	64.78	24.22	20.52	19.19	20.48	14.5	21.19			
	MAMMA1002566	5.49	3.26	6.28	2.19	3.2	3.17	4.16	1.97	2.42			
	MAMMA1002571	12.97	18.44	36.1	16.95	12.11	12.28	16.66	10	13.05			
	MAMMA1002573	4.02	5.04	11.33	1.38	3.48	2.19	3.22	1.15	2.21			
35	MAMMA1002576	13.78	23.79	37.39	16.06	19.72	15.26	13.9	8.77	10.92			
	MAMMA1002584	9.21	12.39	27.02	16.71	13.29	9.15	13.96	6.48	12.24			
	MAMMA1002585	6.36	5.36	13.56	11.07	9.12	8.7	7.18	4.4	6.71			
	MAMMA1002586	21.75	21.37	47.64	26.29	19.9	20.88	19.88	14.32	18.17			
	MAMMA1002589	31.16	39.3	81.02	35.29	36.93	32.17	47.24	33.3	29.17			
	MAMMA1002590	8.65	6.16	15.55	9.32	8.84	9.26	5.06	3.24	4.01			
40	MAMMA1002593	8.47	7.53	30	8.1	8.37	7.45	8.63	8.66	8.47			
	MAMMA1002597	11.34	16.94	30.07	13.1	12.76	11.04	12.91	7.38	12.5			
	MAMMA1002598	9.23	11.39	26.12	15.11	13.9	10.6	14.04	4.47	10.54			
	MAMMA1002603	7.01	8.63	19.81	9.42	12.79	9.69	13.58	3.61	8.05			
	MAMMA1002612	0.64	0.54	1.4	4.76	2.04	2.86	2.1	0	0.92			
	MAMMA1002617	1.99	2.39	4.19	2.19	2.2	2.69	2.8	1.84	1.34			
45	MAMMA1002618	16.06	18.63	46.52	25.87	25.59	22.21	19.52	10.7	17.56			
	MAMMA1002619	7.62	6.62	18.84	13.61	11.83	9.5	6.72	6.93	5.26			
	MAMMA1002622	3.06	2.72	4.49	4.32	2.96	14.63	2.48	0.95	1.91			
	MAMMA1002623	2.38	2.14	3.99	2.64	2.39	1.68	1.62	0	1.12			
	MAMMA1002625	158.57	183.87	332.03	71.22	106.04	287.72	518.89	291.59	178.62			
	MAMMA1002627	6.48	11.48	14.86	11.21	19	9.56	12.93	6.03	9.03			
50	MAMMA1002629	20.19	19.33	33.94	25.61	18.48	21.46	13.72	14.18	19.09			
	MAMMA1002631	4.6	4.73	9.76	3.98	2.11	3.82	1.12	0.35	1.47	*	-	
	MAMMA1002633	64.25	69.26	104.49	122.15	95.76	107.58	86.41	60.3	67.07			
	MAMMA1002636	30.48	34.84	49.63	34.43	30.9	28.96	42.01	28.77	46.58			
	MAMMA1002637	2.95	5.14	7.06	4.15	3.68	2.57	4.18	1.82	4.8			
	MAMMA1002646	3.86	4.18	6.8	3.4	4.56	2.51	2.73	1.37	2.49			
55	MAMMA1002648	136.47	120.19	147.15	150.69	135.33	106.16	124.23	86.88	146.01			
	MAMMA1002650	1.26	1.85	1.15	1.57	0.72	1.64	0.26	0.46	0.54	*	-	
	MAMMA1002652	32.12	44.28	46.88	48.41	32.58	36.9	24.05	25.91	28.22	*	-	

Table 401

	MAMMA1002655	11.4	14.99	17.9	15.12	13.04	14.83	12.19	8.95	8.53			
5	MAMMA1002662	6.09	7.03	11.38	9.76	5.9	8.37	9.45	4.05	7.02			
	MAMMA1002665	45.5	69.25	89.49	54.25	62.78	56.03	66.39	47.78	71.4			
	MAMMA1002671	18.2	21.13	33.24	18.58	22.22	20.8	25.58	15.85	14.12			
	MAMMA1002673	11.32	15.65	15.97	11.87	13.24	9.54	13.67	9.79	13.55			
	MAMMA1002684	12.93	20.62	16.77	15.69	20.34	11.67	14.21	4.61	5.68			
	MAMMA1002685	5.98	5.53	9.57	4.13	4.23	3.62	3.38	2.66	3.46	*	*	-
10	MAMMA1002692	8.9	8.42	9.87	7.25	7.35	7.75	2.28	5.77	1.68	*	*	-
	MAMMA1002693	9.54	10.93	23.31	11.25	9.77	9.02	7.69	7.85	6.66			
	MAMMA1002698	6.28	7.75	12.56	8.05	7.51	8.6	5.96	6.56	6.22			
	MAMMA1002699	5.33	9.37	9.52	5.1	10.31	6.85	7.2	5.75	6.86			
	MAMMA1002701	26.1	32.61	44.74	24.49	33.98	29.72	36.76	18.9	37.16			
	MAMMA1002708	10.78	13.98	19.02	10.41	15.42	12.16	15.37	13.13	12.91			
15	MAMMA1002711	14.75	23.34	34.41	24.21	29.1	25.59	25.28	14.17	20.72			
	MAMMA1002712	11.97	12.21	14.44	7.62	10.08	13.25	6.69	8.26	7.29	**		-
	MAMMA1002716	4.68	7.56	7.57	4.77	4.14	4.42	3.66	3.97	3.59	*		-
	MAMMA1002721	14.39	14.75	20.55	11.28	10.99	13.97	10.36	11.19	14.35			
	MAMMA1002723	7.42	10.89	16.39	7.15	8.24	4.7	4.46	4.93	6.1			
	MAMMA1002727	5.86	7.13	17.65	5.65	6.92	6.82	4.72	3.49	6.01			
20	MAMMA1002728	203.39	279.55	292.72	297.21	297.38	218.05	240.28	159.35	257.9			
	MAMMA1002742	14.02	17.19	15.98	10.59	10.28	10.18	5.71	6.31	6.17	**	**	-
	MAMMA1002743	13.89	22.29	19.83	22.11	23.47	15.54	12.39	9.78	3.07			-
	MAMMA1002744	41.83	52.92	97.53	82.43	49.67	62.65	35.95	33.09	52.81			
	MAMMA1002746	1.97	3.26	4.93	1.96	3.41	2.27	2.78	1.33	2.98			
	MAMMA1002748	7.49	8.51	12.58	5.49	4.9	6.1	6.53	3.04	7			
25	MAMMA1002754	14.85	17.76	22.12	11.35	12.08	11.06	11.12	5.72	16.48	*		-
	MAMMA1002758	3.59	1.64	11.4	2.56	2.22	2.31	1.99	1.02	1.03			
	MAMMA1002762	132.2	159.47	185.48	173.16	185.47	170.91	152.23	100.87	138.71			
	MAMMA1002764	11.39	16.4	28.38	10.76	16.28	13.47	14.81	9.65	13.58			
	MAMMA1002765	7.34	7.13	16.56	5.42	10.33	6.06	7.41	3.51	6.05			
	MAMMA1002769	10.29	13.85	24.43	5.77	11.7	10.08	4.64	4.85	10.59			
30	MAMMA1002771	3.01	3.94	5.73	4.17	3.21	3.23	5.9	1.8	2.75			
	MAMMA1002775	37.45	33.73	58.09	84.46	48.03	62.49	34.89	23.26	53.34			
	MAMMA1002780	5.07	6.15	6.67	4.47	3.43	3.09	4.23	2.8	2.68	*	*	-
	MAMMA1002782	5.1	4.96	13.58	4.26	5.86	4.79	6.17	2.83	4.75			
	MAMMA1002795	4.5	6.79	10.64	2.77	4.7	2.89	3.8	0.29	3.67			
	MAMMA1002796	5.94	10.22	11.38	3.51	7	2.99	1.75	1.74	3.7	*		-
35	MAMMA1002805	7.95	9.3	18.26	5.36	11.22	10.66	9.08	3.61	6.4			
	MAMMA1002806	3.62	2.38	6.99	3.71	4.26	2.36	4.15	0.61	2.13			
	MAMMA1002807	18.13	22.17	39.72	27.6	21.23	23.03	24.44	17.51	32.38			
	MAMMA1002814	44.71	48.76	77.02	44.68	36.22	39.5	45.03	34.09	60.73			
	MAMMA1002817	3.99	4.65	7.4	2.69	1.42	2.37	1.9	1.38	3.31	*		-
	MAMMA1002820	8.85	7.77	12.62	4.45	5.02	3.82	4.58	3.34	5.96	*	*	-
40	MAMMA1002830	214.03	277.57	281.23	229.96	268.12	260.12	256.75	84.59	195.17			
	MAMMA1002833	35.45	43.35	56.35	30.19	48.83	31.33	58.07	31.41	58.94			
	MAMMA1002835	2.83	4.62	14.15	2.49	4.86	1.91	2.5	0.14	2.49			
	MAMMA1002838	11.11	14.42	31.43	18.22	13.58	15.03	12.7	4.89	21.91			
	MAMMA1002842	18.2	19.62	33.31	21.65	17.53	15.65	18.5	8.81	13.46			
	MAMMA1002843	8.38	8.96	10.43	6.56	6.63	6.17	6.89	4.51	5.73	*	*	-
45	MAMMA1002844	7.03	7.49	9.64	4.13	4.73	3.32	3.78	1.87	4.09	*	*	-
	MAMMA1002845	2.68	3.31	8.62	2.22	3.45	1.79	1.92	0.92	2.1			
	MAMMA1002857	706.2	952.23	1146	1100.2	1170.5	914.39	1224.8	597.31	410.7			
	MAMMA1002858	2294.5	2940.8	1870.4	2372.6	1763.7	1167.7	3253.7	1423.1	844.59			
	MAMMA1002863	7.34	6.7	14.07	6.73	7.47	6.7	10.22	2.68	6.73			
	MAMMA1002868	37.22	42.58	112.8	66.03	44.4	46.77	34.24	23.46	47.24			
50	MAMMA1002869	27.07	27.29	44.22	74.9	47.13	42.55	24.18	21.4	25.44			
	MAMMA1002871	14.38	15.38	24.35	3.88	5.79	4.67	3.41	1.65	2.57	*	**	-
	MAMMA1002875	10.61	9.93	8.16	4.59	5.33	3.55	2.05	0.93	2.17	**	**	-
	MAMMA1002879	85.9	153.46	165.38	90.95	121.6	91.59	134.87	73.22	108.93			
	MAMMA1002880	3.99	4.47	13.13	3.43	2.59	1.91	2.37	0	2.3			
	MAMMA1002881	8.75	7.92	17.49	5.86	8.28	6.29	10.75	4.45	6.2			
55	MAMMA1002885	3.52	4.77	10.68	3.3	3.4	4.24	2.69	0.63	2.73			
	MAMMA1002886	26.73	26.24	71.16	37.73	28.68	31.72	26.26	17.17	36.38			
	MAMMA1002887	4.31	6.26	14.8	6.26	3.45	6.36	3.77	1.7	3.28			

Table 402

	MAMMA1002890	11.31	9.48	18.16	8.56	8.49	19.82	9.15	5.95	8.48		
	MAMMA1002892	13.36	11.62	14.89	12.15	11.02	9.05	7.92	7.62	11.8		
5	MAMMA1002893	8.64	14.35	13.28	7.89	13.97	5.96	10.13	7.23	1.86		
	MAMMA1002895	3.34	5.32	14.4	3.46	5.81	1.87	4.28	2.34	3.5		
	MAMMA1002898	4.08	5.01	17.31	2.16	5.01	1.78	3.17	0.38	2.02		
	MAMMA1002905	4	11.4	20	7.75	8.82	9.71	6.71	1.7	4.46		
	MAMMA1002906	2.68	1.92	5.05	4.09	2.8	3.58	1.97	0.54	1.64		
10	MAMMA1002908	14.98	16.18	26.75	12.12	15.62	14.31	16.05	8.69	18.72		
	MAMMA1002909	30.34	34.63	68.19	28.69	18.89	22.65	34.89	20.01	32.36		
	MAMMA1002918	13	10.64	27.29	16.01	18.07	12.45	12.7	8.75	10.42		
	MAMMA1002925	49.1	23.96	62.42	27.59	36.92	32.28	67.91	43.67	13.09		
	MAMMA1002926	25.41	28.93	57.26	38.61	37.53	35.54	28.57	14.19	28.89		
	MAMMA1002930	27	34.75	73.56	25.58	25.59	23.42	47.23	26.24	37.21		
15	MAMMA1002937	65.34	59.27	78.68	106.43	76.67	71.14	57.91	26.1	50.41		
	MAMMA1002938	1.94	2.84	7.68	5.03	4.18	4.4	2.05	0.91	2.65		
	MAMMA1002941	7.09	6.07	17.41	12.34	8.56	8.04	6.56	3.92	5.66		
	MAMMA1002947	16.06	20.72	33.43	32.88	25.81	27	19.39	13.57	20.15		
	MAMMA1002964	14.52	21.96	48.58	29.27	22.13	24.66	18.71	13.88	18.49		
	MAMMA1002967	6.96	4.19	15.96	5.47	7.15	5.12	3.82	5.07	4.36		
20	MAMMA1002970	16.09	29.77	65.22	27.91	25.08	19.79	28.99	12.64	23.95		
	MAMMA1002971	4.02	4.7	8.35	3.51	4.7	2.27	5.82	2.89	2.46		
	MAMMA1002972	3.94	3.63	9.75	6.43	4.91	5.11	4.27	0.9	3.28		
	MAMMA1002973	20.96	22.17	31	24.13	16.86	22.18	16.66	11.21	13.94	*	-
	MAMMA1002979	129.92	194.32	219.31	151.08	71.59	113.43	55.53	74.31	23.22	*	-
	MAMMA1002982	2.18	1.25	7.22	2.29	3.22	3.34	5.33	0.9	3.23		
25	MAMMA1002987	10.35	12.2	15.88	9.6	9.29	9.6	13.48	8.42	11.93		
	MAMMA1003003	10.92	12.48	21.55	9.72	10.82	10.86	12.69	9.52	10.22	*	-
	MAMMA1003004	9.35	12	11.41	6.36	11.7	10.34	5.34	4.84	8.09		
	MAMMA1003007	5.35	7.51	8.39	5.22	6.88	6.35	8.36	3.78	6.7		
	MAMMA1003011	3.33	3.62	5.57	4.14	2.91	4.01	2.44	1.93	2.62		
	MAMMA1003013	52.58	50.01	73.47	127.57	69.44	113.36	42.21	37.2	47.45		
30	MAMMA1003015	4.4	9.22	10.22	6.68	9.17	6.66	6.79	4.74	5.08		
	MAMMA1003019	6	3.52	10.72	6.3	3.92	5.12	4.27	1.82	2.44		
	MAMMA1003020	9.29	17.63	21.88	11.76	13.24	12.14	9.04	4.99	7.31		
	MAMMA1003026	2.19	2.41	7.93	1.47	3.27	2.09	1.98	0.75	2.98		
	MAMMA1003031	12.83	17.1	23.06	9.93	17.27	14.35	13.73	7.28	15.8		
	MAMMA1003033	7.59	11.58	13.68	6.87	12.75	8.45	8.32	3.56	9.08		
35	MAMMA1003035	14.44	18.88	35.58	17.37	11.86	13.06	6.41	9.44	10.62		
	MAMMA1003039	5.57	9.4	15.11	7.17	7.63	9.67	4.3	4.16	6.95		
	MAMMA1003040	22.42	25.75	39.61	22.72	19.76	23.47	30.8	25.19	32.64		
	MAMMA1003044	23.58	26.13	43.98	21.92	19.68	21.85	23.01	22.17	23.66		
	MAMMA1003047	25.89	30.87	33.12	18.34	23.66	19.64	30.18	18.74	28.8	*	-
	MAMMA1003049	2.33	2.17	8.04	1.08	1.14	1.06	1.63	0.08	1.3		
40	MAMMA1003055	17.22	25.14	35.08	23.45	17.28	15.29	23.26	16.76	22.03		
	MAMMA1003056	1.24	3.89	8.92	1.85	1.6	1.77	4.37	0	1.6		
	MAMMA1003057	7.01	11.35	14.1	7.31	6.88	7.83	3.86	5.43	8.7		
	MAMMA1003066	16.42	21.28	30.29	14.08	16.97	16.54	12.01	11.17	25.5		
	MAMMA1003075	6.07	7.85	12.07	6.85	6.1	6.14	7.15	5.26	7.72		
	MAMMA1003089	37.69	44.94	70.13	31.56	35.51	31.8	38.3	22.85	38.78		
45	MAMMA1003092	2.7	6.77	9.29	2.59	2.39	2.86	1.65	0.84	2.49	*	*
	MAMMA1003095	11.71	16.36	22.28	5.96	7.13	4.55	3.24	2.25	2.45		
	MAMMA1003099	12.83	14.7	25.29	10.89	15.86	9.22	14.89	11.45	12.15		
	MAMMA1003102	3.77	5.08	9.09	1.68	4.54	2.6	2.97	0.85	1.92		
	MAMMA1003104	2.23	3.23	4.66	5.3	4.9	4.18	1.01	1.61	4.75		
	MAMMA1003113	12.38	25.98	27.12	11.65	17.89	10.18	7.19	8.58	13.27		
50	MAMMA1003126	20.48	25.06	25.6	15.4	13.83	15.96	10.44	8.97	17.98	**	*
	MAMMA1003127	11.67	12.89	22.02	11.38	12.69	10.66	9.71	8.8	11.4		
	MAMMA1003131	8.9	14.73	17.42	6.88	7.18	8.51	7.06	3.18	4.59	*	-
	MAMMA1003135	3.06	2.9	10.48	1.24	2.69	1.3	3	1.87	1.55		
	MAMMA1003140	5.46	6.32	15.55	2.89	4.63	3.63	3.24	3.7	5.1		
	MAMMA1003146	4.31	6.5	9.12	2.65	6.5	3.58	4.41	3.82	3.28		
55	MAMMA1003150	4.32	7.47	10.56	5.78	4.99	3.76	3.2	3.41	5.87		
	MAMMA1003154	2.93	3.77	5.99	2.37	2.94	2.85	2.68	0.86	2.1		
	MAMMA1003155	35.26	33.7	28.41	18.29	14.13	13.99	27.83	12.47	20.55	**	-

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	MAMMA1003157	9.8	11.92	16.49	8.35	7.14	7	5.32	5.07	5.53	*		-
	MAMMA1003163	6.69	5.07	11.11	7.07	6.08	5.54	2.67	4.3	4.05			
5	MAMMA1003164	9.65	8.42	12.05	4.3	5.95	3.77	2.65	1.16	3.38	*	**	-
	MAMMA1003166	13.16	17.5	21.96	14.35	15.87	10.73	8.74	5.62	7.88	*		-
	NB9N31000010	22.17	30.34	35	8.06	26.76	14.32	17.42	5.42	10.61	*		-
	NB9N31000016	6.11	10.91	22.1	11.04	8.39	6.1	4.87	1.93	11.92			
	NB9N31000043	10.01	15.51	20.02	13.55	11.04	7.12	6.17	3.99	7.07	*		-
10	NB9N31000045	170.84	205.1	142.2	172.26	138.41	173.74	84.94	88.64	18.56	*		-
	NB9N31000054	36.72	46.14	51.85	45.82	42.67	36.97	50.28	31.68	29.41			
	NB9N31000076	7.95	11.11	16	8.53	7.69	7.72	11.59	4.88	6.85			
	NB9N31000086	4.15	2.68	11.91	2.36	4	2.05	3.15	0.81	2.03			
	NT2RM1000001	7.05	9.84	23.41	7.46	11.26	6.73	9.81	4.19	5.49			
	NT2RM1000018	6.2	11.24	12.18	4.32	8.37	5.02	4.96	1.12	2.49	*		-
15	NT2RM1000032	6.17	20.65	14.02	3.2	3.21	6.55	7.1	3.44	6.93			
	NT2RM1000035	5.32	12.32	11.65	5.42	4.73	4.54	3.82	4.31	2.73			
	NT2RM1000037	6.94	9.49	8.81	3.59	2.53	4.32	3.57	2.25	1.49	**	**	-
	NT2RM1000039	17.35	20.78	18.95	11.31	10.08	7.38	8.83	5.7	8.35	**	**	-
	NT2RM1000042	285.1	504.24	359.39	438.78	386.15	125.88	306.06	229.38	295.8			
	NT2RM1000055	3.2	5.45	10.27	2.35	2.5	0.71	3.16	1.31	1.79			
20	NT2RM1000059	6.89	5.26	12.3	2.6	4.12	1.14	3.74	1.4	3.81			
	NT2RM1000062	3.25	17.72	14.57	2.77	4.02	2.38	6.97	0.66	3.27			
	NT2RM1000065	129.93	146.35	187.39	51.11	120.84	109.9	91.66	120.6	204.01			
	NT2RM1000066	8.15	10.03	11.93	3.29	5.25	5.44	3.51	4.17	3.47	*	**	-
	NT2RM1000071	663.12	662.77	828.24	110.41	580.78	259.28	351.73	417.5	139.33	*		-
25	NT2RM1000080	24.34	23.12	24.37	3.56	11.29	8.21	9.27	5.24	4.03	**	**	-
	NT2RM1000086	10.86	12.97	11.53	2.83	5.32	3.9	5.64	4.4	2.88	**	**	-
	NT2RM1000092	20.13	29.95	35.15	36.08	29.43	24.61	19.3	14.65	20.49			
	NT2RM1000118	1.37	1.52	9.04	0	0.67	0	0.36	0	0.79			
	NT2RM1000119	1.84	9.53	13.52	3.77	3.18	2.59	3.62	0	1.09			
	NT2RM1000121	4.53	3.89	4.67	2.15	3.4	5.49	1.08	0.78	1.77	**		-
30	NT2RM1000122	12.06	9.02	14.76	4.72	5.56	4.77	3.17	7.39	6.45	*	*	-
	NT2RM1000127	4.86	3.09	8.85	2.65	2.99	2.48	1.52	1.46	1.57			
	NT2RM1000131	2.61	0.69	3.44	0.91	1.56	0.43	1.25	0.9	1.02			
	NT2RM1000132	14.01	8.86	18.39	14.15	9.4	7.78	17.49	15	6.09			
	NT2RM1000153	5.01	3.78	14.31	1.42	4.08	2.81	5.68	1.59	2.53			
	NT2RM1000184	281.4	361.08	212.97	228.94	161.22	121.63	212.54	317.63	41.9			
35	NT2RM1000186	2.47	4.7	12.56	1.93	2.64	2.03	5.08	0.92	2.79			
	NT2RM1000187	13.51	16.82	27.58	4.35	7.1	11.13	3.58	3.22	6.78	*		-
	NT2RM1000199	2.37	2.51	5.33	3.1	3.18	3.27	2.76	0.66	1.97			
	NT2RM1000213	14.38	13.17	27	9.3	8.17	9.61	8.4	3.99	3.63			
	NT2RM1000215	127.65	93.55	105.56	47	125.55	90	93.27	92.32	37.71			
	NT2RM1000218	17.5	12.81	37.21	8.7	7.66	13.12	12.93	9.58	4.51			
40	NT2RM1000224	38.8	21.38	99.03	21.96	23.06	30.11	56.22	41.03	10.49			
	NT2RM1000236	128.23	106.27	224.67	36.44	158.46	117.76	233.25	180.75	49.09			
	NT2RM1000242	0.21	0.74	2.56	0	1.12	0	0.56	0	0.76			
	NT2RM1000244	7.07	7.69	14.14	11.09	6.96	9.63	3.01	2.46	3.87	*		-
	NT2RM1000252	3.63	3.86	6.34	5.75	3.24	4.11	5.02	2.57	2.44			
	NT2RM1000256	13.89	13.11	17.86	12.49	12.19	15.55	9.96	9.49	3.8	*		-
	NT2RM1000257	7.26	4.79	22.28	12.27	7.82	12.93	3.88	4.6	1.41			
45	NT2RM1000260	44.37	50.35	69.11	33.91	47.16	50.17	26.8	25.27	25.69	*		-
	NT2RM1000269	4.48	3.66	6.5	3.35	3.23	4.63	2.09	1.54	1.92	*		-
	NT2RM1000271	2.07	1.72	5.77	1.75	2.06	0.52	0.83	0.09	0.38			
	NT2RM1000272	93.8	125.17	184.07	85.39	186.36	110.41	166.71	67.77	97.63			
	NT2RM1000273	44.49	55.95	63.71	32.07	31.24	23.66	15.32	26.55	33.94	*	*	-
	NT2RM1000274	455.63	719.55	944.44	916.81	390.33	402.82	570.68	746.39	848.53			
50	NT2RM1000280	6.37	12.22	16.78	15.15	6.91	15.12	10.36	3.5	4.59			
	NT2RM1000295	0.98	1.35	3.23	1.46	0.9	2.46	0.9	0.93	3.62			
	NT2RM1000300	6.74	6.95	12.1	10.61	8.44	10.7	5.89	3.63	7.13			
	NT2RM1000304	737.06	1023.4	718.47	1038.7	1097.8	469.75	946.67	780.24	888.74			
	NT2RM1000314	4.57	4.01	6.01	3.26	3.98	4.08	4.92	1.32	3.56			
	NT2RM1000318	421.37	294.99	289.4	315.7	574.37	386.7	448.45	209.13	302.89			
55	NT2RM1000335	11.96	11.64	18.91	9.64	8.09	12	6.06	5.29	8.48	*	*	-
	NT2RM1000341	1.94	1.67	2.31	1.53	0.88	0.82	1.64	0.39	2.21	*		-
	NT2RM1000350	8.91	10.88	13.15	11.12	8.93	9.83	7.57	4.14	7.11	*		-



Table 404

	NT2RM1000354	0.4	1.68	2.48	0.51	1.02	0.95	0.87	0.21	0.21			
	NT2RM1000355	18.03	21.12	26.82	24.57	24.38	11.58	16.5	8.01	13.65			
5	NT2RM1000361	2.57	1.81	2.89	1.57	3.04	3.2	2.49	0.23	2.67			
	NT2RM1000365	0.53	2.31	3.79	0	3.39	1.9	2.3	0	1			
	NT2RM1000372	55.88	63.08	56.77	80.59	90.54	75.31	135.63	66.87	19.91	**	+	
	NT2RM1000377	29.22	32.95	43.33	46.89	24.42	30.81	18.03	18.61	14.45	*	-	
	NT2RM1000388	3.72	3.27	4.82	4.15	1.73	3.91	2.28	2.59	2.31	*	-	
10	NT2RM1000394	1.56	1.31	3.56	1.15	0.93	0.79	1.9	2.42	1.43			
	NT2RM1000399	5.42	3.53	8.67	4.2	3.61	3.12	6.84	2.24	2.92			
	NT2RM1000407	1.68	1.87	7.64	2.01	1.44	1.69	2.06	1.13	3.04			
	NT2RM1000421	0.74	0.94	3.14	1.35	1.14	2	1.61	0	0.06			
	NT2RM1000422	134.24	176.38	156.33	143.97	232.16	154.32	116.71	110.46	75.99	*	-	
	NT2RM1000430	4.06	4.21	6.87	5.11	7.78	3.82	6.49	1.64	1.64			
15	NT2RM1000462	17.49	21.49	23.94	21.57	15.84	20.24	13.6	12.18	18.48			
	NT2RM1000499	11.77	14.5	12.66	4.08	5.8	6.16	2.2	2.63	4.58	**	**	-
	NT2RM1000512	50.79	65.54	89.54	15.65	74.29	59.09	19.69	52.23	55.59			
	NT2RM1000519	108.54	108.15	106.36	60.23	134.25	94.69	58.45	58.56	60.96	**	-	
	NT2RM1000527	51.37	48.34	68.1	100.86	64	65.36	54.81	19.74	44.25			
	NT2RM1000539	19.83	27.84	33.74	35.02	28.56	31.96	16.52	8.8	16.69			
20	NT2RM1000542	2.91	2.41	11.46	0.76	1.72	0.95	1.66	0.17	0.24			
	NT2RM1000553	49.27	35.57	63.05	73.97	60.28	58.45	40.5	24.9	19.69			
	NT2RM1000555	85.13	121.39	124.03	87.28	76.76	74.83	41.33	57.49	77.7	*	-	
	NT2RM1000558	26.75	25.54	23.49	36.55	31.73	36.63	21.2	19.34	35.09	**	+	
	NT2RM1000563	9.05	10.86	14.09	10.89	9.42	9.24	7.48	6.52	10.32			
	NT2RM1000566	6.73	8.38	15.32	6.55	8.24	9.4	8.98	6.08	9.24			
25	NT2RM1000570	125.7	201.18	105.25	41.82	195.51	106.3	185	132.56	153.14			
	NT2RM1000571	50.08	74.69	65.76	14.46	84.43	39.98	43.45	24.14	6.89	*	-	
	NT2RM1000574	2.53	1.65	9.83	1.89	3.52	1.98	1.99	0.19	1.58			
	NT2RM1000580	7.86	7.46	8.12	4.52	12.24	4.74	8.38	3.22	4.57			
	NT2RM1000620	22.3	25.58	42.74	35.73	32.55	28.94	25.27	21.57	27.34			
	NT2RM1000623	1.13	1.82	2.51	0.54	0.62	1.17	0.35	0.18	1.57			
30	NT2RM1000630	3.11	2.76	5.89	2.21	1.76	2.12	2.49	0.75	1.9			
	NT2RM1000633	91.32	89.94	117.97	56.97	108.85	75.65	98.98	107.05	51.97			
	NT2RM1000634	11.16	13.34	24.68	9.79	14.73	9.21	12.08	6.93	12.7			
	NT2RM1000642	12.72	15.83	20.12	6.07	8.95	6.42	3.63	2.38	4.98	*	**	-
	NT2RM1000647	58.32	165.39	134.62	67.85	112.06	61.29	71.96	52.24	87.23			
	NT2RM1000648	7.26	13.24	8.89	5.57	12.68	6.6	14.52	3.49	7.15			
35	NT2RM1000650	6.62	9.44	9.46	2.83	6.47	6.87	3.69	5.63	4.1	*	-	
	NT2RM1000661	15.88	18.26	26.1	21.53	19.01	24.34	8.08	7.55	8.54	*	-	
	NT2RM1000666	1.96	1.18	6.92	1.86	1.52	1.45	0.88	0.27	0.92			
	NT2RM1000669	17.26	18.78	20.02	4.09	4.91	3.69	2.13	1.18	2.17	**	**	-
	NT2RM1000672	13.67	18.24	42.69	19.37	17.89	17.56	7.45	2.82	5.99			
	NT2RM1000681	9.08	16.58	18.31	9.41	17.68	12.92	13.31	5.99	9.03			
40	NT2RM1000691	4.68	7.55	17.93	4	7.1	7.03	5.99	3.47	5.58			
	NT2RM1000698	12.42	13.98	20.53	4.92	32.5	5.23	15.99	3.16	6.38			
	NT2RM1000699	5.67	7.09	9.09	7.34	5.78	7.37	2.45	1.86	3.56	*	-	
	NT2RM1000702	25.96	30.69	39.69	30.16	23.23	32.77	24.6	18.35	22.21			
	NT2RM1000703	32.53	88.64	53.23	36.64	56.43	43.04	42.73	50.17	17.73			
	NT2RM1000704	43.17	84	45.95	47.88	42.53	19.03	39.69	25.24	10.87			
45	NT2RM1000726	5.67	6.22	17.4	3.29	4.23	3.21	4.45	0.93	1.78			
	NT2RM1000731	21.17	21.67	40.88	23.29	32.82	14.51	24.97	11.69	10.31			
	NT2RM1000741	3.88	5.18	10.63	4.4	7.39	2.14	6.17	0	1.39			
	NT2RM1000742	28.88	28.51	36.7	38.75	29.44	32.74	34.48	36.03	27.02			
	NT2RM1000744	18.57	21.62	27.17	23.44	20.36	17.29	20.61	18.9	23.17			
	NT2RM1000746	7.85	8.11	11.72	4.17	4.62	5.27	5.53	3.03	1.14	*	*	-
50	NT2RM1000747	30.16	38.37	65.95	28.71	33.95	34.03	30.94	18.08	23.76			
	NT2RM1000752	6.43	11.58	14.15	3.61	7.68	5.76	4.96	2.69	4.73			
	NT2RM1000767	82.05	87.93	86.38	98.35	104.39	73.49	112.1	59.62	78.42			
	NT2RM1000770	9.08	11.59	19.18	5.23	6.92	2.95	3.61	2.19	4.43	*	-	
	NT2RM1000772	0.81	1.85	7.5	1.21	3.6	1.86	2.53	0	2.7			
	NT2RM1000779	107.98	131.01	176.51	63.61	94.24	109.72	76.84	69.35	114.65			
55	NT2RM1000780	6.52	7.85	9.21	2.66	6.05	5.1	2.74	1.38	1.99	**	-	
	NT2RM1000781	6.79	4.22	9.28	1.5	2.8	0.61	2.07	1.26	0.75	*	*	-
	NT2RM1000789	63.83	77.27	95.07	93.46	102.47	101.3	60.5	47.17	81.09			

Table 405

	NT2RM1000800	8.8	11.31	17.21	5.12	7.9	6.45	6.62	2.19	3.3	*	-
	NT2RM1000802	37.09	50.36	74.58	36.6	34.84	28.86	14.15	4.56	9.84	*	-
5	NT2RM1000811	12.36	9.86	24.52	8.71	10.02	9.58	14.12	5.95	8.7		
	NT2RM1000826	30.88	47.18	81.3	44.32	50.77	35.09	43.27	14.54	16.43		
	NT2RM1000829	19.85	28.15	42.49	15.46	18.32	22.11	18.5	10.73	22.04		
	NT2RM1000831	641.62	637.04	913.82	275.83	388.75	407.08	509.83	541.98	267.92	*	-
	NT2RM1000833	131.01	121.94	243.56	117.55	172.46	143.86	179.55	110.44	138.22		
	NT2RM1000834	26.33	24.31	2.89	0	0.65	2.02	26.66	20.39	19.97		
10	NT2RM1000841	24.25	46.24	73.12	11.51	14.12	14.5	18.59	16.34	8.01		
	NT2RM1000848	14.13	26.98	37.82	13	21.43	18.99	20.71	11.34	13.28		
	NT2RM1000850	24.68	26.73	36.64	21.15	32.91	25.01	46.02	20.2	29.9		
	NT2RM1000852	13.97	15.95	23.78	18.75	27.94	15.23	31.21	18.1	21.46		
	NT2RM1000853	4.2	3.72	6.66	7.37	4.53	5.05	3.89	2.23	2.94		
	NT2RM1000855	68.98	71.69	82.2	36.85	37.1	51.79	74.89	42.55	21.65	**	-
15	NT2RM1000857	18.68	28.42	44.59	21.2	21.59	23.12	20.54	14.01	19.44		
	NT2RM1000858	19.44	18.6	24.07	17.38	13.26	16.79	12.93	7.9	10.41	*	-
	NT2RM1000867	47.06	39.97	81.53	51.39	22.67	30.69	24.25	41.66	28.02		
	NT2RM1000874	15.53	21.9	42.18	11.95	15.55	12.17	9.14	4.05	6.39		
	NT2RM1000882	8.95	14.01	25.71	7.66	9.72	9.63	17.06	6.72	11.92		
20	NT2RM1000883	14.26	11.55	31.41	10.17	21.02	6.37	28.25	10.83	25.46		
	NT2RM1000885	24.96	25.3	31.55	8.98	10.57	16.46	9.36	11.69	11.59	**	-
	NT2RM1000893	28.28	40.4	46.33	35.83	16.57	27.75	26.99	25.66	21.62		
	NT2RM1000894	11.16	14.78	12.12	9.67	5.22	9.03	7.62	4.24	5.7	**	-
	NT2RM1000898	16.49	18.47	21.09	20.98	15.98	15.23	9.37	6.69	9.26	**	-
	NT2RM1000899	5.15	4.63	7.57	5.14	7.26	5.6	4.73	2.38	2.79		
25	NT2RM1000905	294.53	321.81	294.85	264.7	213.45	208.71	204.71	142.52	169.18	*	-
	NT2RM1000910	73.69	67.82	69.43	87.95	125.51	72.31	61.51	49.51	44.37	*	-
	NT2RM1000914	51.65	67.13	49.73	46.16	55.8	39.43	58.15	36.24	73.81		
	NT2RM1000919	31.63	34.55	49.42	11.97	21.16	18.78	16.17	26.42	28.42	*	-
	NT2RM1000921	6.87	9.33	11.95	7.94	8.86	8.21	8.17	4.59	6.66		
	NT2RM1000922	13.29	8.81	21.03	4.57	14.42	11.98	8.29	7.63	6.27		
30	NT2RM1000924	4.71	2.79	7.57	4.61	10.85	2.89	2.79	1.75	0.64		
	NT2RM1000927	6.24	8.21	11.68	5.06	6.28	6.3	9.48	6.11	7.76		
	NT2RM1000951	43.38	31.87	51.83	47.29	42.21	49.1	23.28	12.15	25.07	*	-
	NT2RM1000956	14.05	17.39	13.26	12.15	19.17	13.5	7.97	3.02	6.22	**	-
	NT2RM1000960	27.19	36.09	41.59	49.18	53.65	39.11	40.71	16.46	20.8		
	NT2RM1000961	31.7	37.01	55	10.53	21.75	21.52	13.1	26.97	26.19	*	-
35	NT2RM1000962	27.85	38.63	33.9	11.13	12.72	11.99	4.23	8.24	8.72	**	-
	NT2RM1000973	43.5	24.74	82.26	40.71	70.49	56.15	24.22	34.19	11.88		
	NT2RM1000978	0.68	0.64	4.81	0	0.42	0.84	0.61	2.06	0.63		
	NT2RM1000982	16.77	17.99	20.27	10.66	18.58	11.05	7.48	6.36	6.54	**	-
	NT2RM1000991	7.55	12.77	12.19	10.81	11.04	11.17	5.79	6.02	8.13		
	NT2RM1000994	39.31	47	23.95	9.37	52.07	40.12	12.98	9.18	11.27	*	-
40	NT2RM1001002	32.74	42.78	50.1	43.61	48.24	33.17	37.45	15.22	13.9		
	NT2RM1001003	22.14	23.85	35.08	16.55	19.31	27.31	8.71	13.75	14.54	*	-
	NT2RM1001008	2.98	2.17	4.26	1.07	1.49	2.65	1.82	2.32	1.41		
	NT2RM1001011	24.49	19.42	39.5	9.16	16.59	21.83	7.1	5.35	13.23	*	-
	NT2RM1001013	7.58	6.4	15.54	3.26	7.12	6.38	8.21	10.22	6.35		
	NT2RM1001017	2.99	2.36	7.63	0.68	1.65	2.36	1.32	0	2.89		
45	NT2RM1001018	389.38	678.69	541.36	131	345.59	266.19	206.53	225.12	141.21	*	-
	NT2RM1001026	7.53	12.1	18.29	9.07	8.15	5.48	3.88	1.52	2.01	*	-
	NT2RM1001028	4.9	7.17	9.41	6.47	12.06	5.7	11.7	4.86	5.5		
	NT2RM1001043	26.98	28.41	30.47	32.28	26.93	18.1	7.33	9.19	17.19	**	-
	NT2RM1001044	13.61	15.79	12.73	5.11	11.55	9.29	6.83	6	8.45	**	-
	NT2RM1001059	17.62	17.16	21.39	29.41	18.53	17.53	21.59	10.53	22.05		
50	NT2RM1001063	4.42	2.79	10.14	1.51	2.68	1.95	3.55	2.61	2.37		
	NT2RM1001066	5.44	6.05	11.22	3.97	4.37	2.62	5.3	2.25	4.68		
	NT2RM1001072	2.1	2.09	9.94	0.59	2.67	1.88	2.14	0.14	1.84		
	NT2RM1001074	4.98	10.47	11.14	5.42	6.47	3.23	4.47	1.73	1.4	*	-
	NT2RM1001076	7.28	10.41	10.61	10.91	16.92	6.26	16.73	6.71	6.46		
	NT2RM1001082	15.79	21.18	26.04	16.26	13.72	10.05	11.58	9.75	14.56		
55	NT2RM1001085	1.82	1.24	5.39	0.21	0.47	1.19	1.3	0.55	1.17		
	NT2RM1001092	38.97	56.81	56.39	54.52	49.61	49.24	59.76	48.35	50.33		
	NT2RM1001102	10.81	9.79	17.74	9.01	8	8.42	8.99	8.26	5.92		

Table 406

	NT2RM1001103	12.11	14.64	19.71	7.84	12.92	9.54	14.04	7.04	13.96			
	NT2RM1001105	4.22	7.99	12.4	1.52	4.66	3.36	1.61	1.94	3.34			
5	NT2RM1001112	5.26	6.44	10.76	4.28	9.37	3.52	5.38	1.59	3.46			
	NT2RM1001115	7.42	6.2	16.09	7.99	9.99	7.63	6.92	3.96	3.94			
	NT2RM1001122	13.95	16.42	25.8	14.65	15.41	13.67	7.73	7.37	13.09			
	NT2RM1001136	4.38	9.14	8.72	2.16	2.27	3.09	2.35	0.89	0.34	*	*	-
	NT2RM1001139	10.44	16.1	18.58	8.95	9.3	8.97	8.52	6.5	7.34	*	*	-
	NT2RM2000003	3.68	3.81	8.36	4.11	1.99	1.48	3.39	1.06	1.76			
10	NT2RM2000006	19.96	26.87	32.42	17.36	19.88	13.64	34.18	15.67	16.17			
	NT2RM2000010	13.11	32.27	43.36	20.14	26.86	16.98	10.37	4.84	2.67			
	NT2RM2000013	111.85	65.82	177.02	150.21	118.48	155.88	73.81	57	69.05			
	NT2RM2000030	47.5	43.12	78.78	78.26	63.56	52.76	55.62	28.2	43.38			
	NT2RM2000032	27.93	34.32	46.51	34.09	25.35	35.27	22.38	22.42	18.15			
	NT2RM2000039	15.44	18.82	11.91	10.78	6.19	11.58	11	10.28	4.44			
15	NT2RM2000042	22.91	29.95	35.12	39.39	23.39	35.58	21.42	15.87	21.82			
	NT2RM2000092	3.58	4.4	7.65	2.5	2.61	1.79	2.27	5.17	2.19			
	NT2RM2000093	9.7	29.83	14.41	14.47	18.41	7.29	12.45	10.38	11.19			
	NT2RM2000101	92.12	99.66	118.62	114.91	128.83	118.95	69.62	52.13	78.59	*	*	-
	NT2RM2000104	62.95	69.41	129.33	110.95	90.54	74.09	72.52	52.94	63.78			
20	NT2RM2000124	8.36	13.36	22.64	10.6	20.3	10.85	19.19	7.38	15.25			
	NT2RM2000155	8.61	19.1	14.45	7.85	7.12	5.48	4.06	1.65	4.16	*	*	-
	NT2RM2000191	45.98	51.15	77.89	79.82	71.61	59.62	35.22	25.83	44.53			
	NT2RM2000192	4.72	2.97	6.83	2.91	2.72	2.95	2.76	1.61	1.47			
	NT2RM2000239	13.1	14.91	17.36	3.56	5.21	3.86	9.92	3.36	2.39	**	*	-
	NT2RM2000241	10.79	19.6	19.09	8.89	13.98	6.49	11.46	3.01	8.51			
25	NT2RM2000250	5.15	5.11	16.92	5.37	6.41	3.58	6.45	1.4	5.59			
	NT2RM2000259	7.84	17.03	22.56	4.92	6.83	6.63	8.62	2.03	2.42			
	NT2RM2000260	9.47	10.65	9.59	4.97	5.31	6.44	6.43	4.5	4.7	**	**	-
	NT2RM2000265	1.13	1.27	5.15	0.34	1.13	1.33	1.14	0	0.82			
	NT2RM2000287	47.66	55.1	96.28	31.39	36.17	31.93	36.1	33.17	17.11			
	NT2RM2000306	66.48	31.19	72.95	23.2	54.18	20.2	25.43	22.47	8.61			
30	NT2RM2000312	32.44	17.61	49.51	8.46	13.33	15.12	25.48	21.27	10.02			
	NT2RM2000322	7.99	6.33	16.54	4.19	5.04	3.2	3.47	0.77	1.48			
	NT2RM2000343	85.23	93.06	177.62	122.74	138.14	108.3	83.09	46.31	57.15			
	NT2RM2000359	6.22	10.59	23.8	9.56	9.52	5.13	12.03	2.74	6.22			
	NT2RM2000362	121.28	140.62	246.7	173.62	223.63	249.97	108	78.11	121.29			
	NT2RM2000363	3.84	6.52	9.96	6.57	3.72	4.83	5.89	2.02	2.82			
35	NT2RM2000368	26.44	19.81	43.02	11.49	11.34	10.46	8.57	3.39	3.24			
	NT2RM2000371	547.25	508.14	752.99	148.13	425.69	273.34	355.28	228.93	135.68	*	*	-
	NT2RM2000374	12.96	13.63	33.5	14.47	12.05	8.49	18.75	11.86	10.92			
	NT2RM2000387	30.78	60.24	91.33	10.11	11.64	24.36	10.29	9.16	3.11	*	*	-
	NT2RM2000393	10.16	9.5	18.93	3.77	7.23	5.64	6.78	3.44	2.74			
	NT2RM2000395	3.42	4.7	7.68	4.26	7.48	3.65	6.98	2.09	2.77			
40	NT2RM2000402	19.66	22.97	34.41	26.49	10.93	25.33	8.72	3.41	2.72	*	*	-
	NT2RM2000405	3.7	3.95	7.31	4.5	3.17	3.25	3.78	1.94	0.68			
	NT2RM2000407	6.18	7.05	11.03	8.23	7.83	7.22	4.36	3.58	3.42	*	*	-
	NT2RM2000410	6.69	5.24	14.77	10.81	8.59	8.57	4.92	7	5.39			
	NT2RM2000420	12.46	12.68	20.53	7.85	6.53	12.66	7.69	6.33	9.37			
	NT2RM2000422	13.42	17.5	14.12	8.88	9.58	15.24	10	8.21	5.9	*	*	-
45	NT2RM2000423	15.54	22.01	50.31	29.73	23.33	19.31	31.02	12.98	24.15			
	NT2RM2000452	3.39	4.23	12.53	5.47	7.75	4.42	5.91	1.75	4.57			
	NT2RM2000469	3.15	2.51	7.63	7.05	2.6	1.83	2.99	3.89	3.38			
	NT2RM2000490	12.63	13.33	17.91	18.49	9.81	12.7	9.63	10.71	10.64			
	NT2RM2000497	6.31	3.98	9.54	8.32	2.31	5.44	4.36	6.15	6.13			
	NT2RM2000502	7.65	10.01	17.15	15.2	7.83	12.64	18.37	19.29	16.37			
50	NT2RM2000504	8.62	13.61	12.8	14.35	8.61	11.65	11.39	5.05	12.11			
	NT2RM2000514	3.24	4.13	6.05	5.11	2.16	2.21	3.1	2.79	1.66			
	NT2RM2000522	0.79	1.87	2.28	5.66	1.51	1.86	2.44	0.56	1.28			
	NT2RM2000540	36.37	16.56	24.89	25.09	10.1	17.62	15.11	17.92	16.53			
	NT2RM2000565	10.96	7.91	19.23	7.94	6.73	6.21	4.49	7.85	6.72			
	NT2RM2000566	35.88	29.95	48.96	40.83	31.02	33.77	42.8	32.01	34.75			
55	NT2RM2000567	5.01	5.28	9.14	7.2	2.55	2.31	2.41	4.02	2.26			
	NT2RM2000569	11.75	12.7	16.59	10.42	10.16	8.54	12.04	11.54	10.63			
	NT2RM2000577	23.09	36.16	46.55	20.42	16.61	17.63	9.65	9.61	18.29	*	*	-

Table 407

	NT2RM2000581	16.64	23.76	26.4	16.81	10.83	8.04	10.45	10.74	12.79	*	-
	NT2RM2000582	34.62	16.91	29.03	32.54	12.57	23.96	20.07	22	22.14		
5	NT2RM2000588	206.96	155.13	213.15	202.22	154.41	234.16	169.86	193.16	204.6	*	-
	NT2RM2000589	21.73	20.45	25.51	21.73	16.89	13.34	11.8	15.99	14.79		
	NT2RM2000594	3.88	3.97	9.16	5.31	1.87	1.58	2.08	3.22	2.03		
	NT2RM2000599	23.3	37.43	42.86	41.55	34.51	20.59	19.28	20.01	29.72		
	NT2RM2000609	11.28	11.34	20.18	17.86	7.32	5.53	10.38	8.31	8.85		
10	NT2RM2000612	12.76	13.34	15.09	12.28	9.14	7.94	10.91	11.84	11.22	*	-
	NT2RM2000622	141.09	153.93	193.67	159.94	144.1	158.9	186.97	168.17	180.75		
	NT2RM2000623	10.1	4.92	12.51	17.89	6.76	12.96	6.19	8.79	10.66		
	NT2RM2000624	40.95	32.48	53.61	29.49	39.42	24.44	20.09	35.85	21.95		
	NT2RM2000632	4.22	16.93	13.59	10.55	4.72	5.77	3.71	9.75	42.27		
	NT2RM2000635	17.3	14.29	24.16	11.9	11.44	7.82	6.12	9.2	22.13		
15	NT2RM2000636	8.64	6.1	10.92	8.1	4.79	4.03	4.23	7.12	5.02	*	**
	NT2RM2000639	12.38	11.39	15.28	10.66	6.59	7.7	5.72	6.03	7.49	*	**
	NT2RM2000649	21.7	22.5	30.17	18.52	14.23	12.19	12.61	12.94	13.29	*	*
	NT2RM2000658	32.82	43.08	46.86	26.73	41.37	32	30.61	19.44	22.2	*	*
	NT2RM2000660	14.51	13.27	29.92	14.04	12.55	16.72	10.13	15.37	13.11		
	NT2RM2000669	10.87	10.69	21.85	10.05	8.58	6.66	4.07	7.21	13.35		
20	NT2RM2000689	95.32	133.69	72.27	57.73	75.12	39.22	34.72	103.73	96.38		
	NT2RM2000691	8.29	7.99	12.66	7.17	5.02	1.98	1.67	3.91	3.3	*	-
	NT2RM2000714	22.27	18.36	27.51	17.39	20.26	19.54	14.42	10.68	9.4	*	-
	NT2RM2000718	7.47	11.22	8.73	7.49	4.21	3.74	6.42	4.3	4.39	*	-
	NT2RM2000732	30.31	39.24	31.84	16.98	20.8	19.07	19.55	19.14	20.81	**	**
	NT2RM2000735	9.9	11.53	13.44	9.07	5.38	4.22	4.93	3.86	5.02	*	**
25	NT2RM2000740	6.93	5.88	14.03	10.18	2.3	7.44	6.84	7.79	7.93		
	NT2RM2000743	6.68	6.8	14.3	6.91	4.28	3.65	5.06	3.56	3.44		
	NT2RM2000772	27.24	33.91	37.64	22.25	28.4	15.62	5.89	15.75	8.53	**	-
	NT2RM2000773	52.46	53.2	70.82	31.56	39.87	27.02	30.18	38.39	37.45	*	*
	NT2RM2000776	68.74	76.62	73.41	45.06	64.43	20.51	36.77	44.34	50.74	**	-
	NT2RM2000784	15.31	17.83	22.47	11.93	15.96	6.63	6.13	10.15	9.45	*	-
30	NT2RM2000795	27.14	19.23	31.28	19.3	19.19	9.44	22.75	21.68	23.6		
	NT2RM2000796	7.18	4.13	6.34	5.73	2.37	1.38	4.64	1.74	1.29		
	NT2RM2000798	220.92	157.62	241.6	287.45	173.39	313.04	164.61	215.06	234.9		
	NT2RM2000801	206.47	181.87	250.93	201.4	210	276.53	117.76	135.99	178.08		
	NT2RM2000821	19.71	21.75	22.88	13.91	8.23	8.65	3.33	5.35	4.94	**	**
	NT2RM2000829	32.72	37.9	42.47	37.61	27.12	23.67	12.82	16.2	13.46	**	-
35	NT2RM2000837	12.85	10.7	21.49	8.33	5.59	2.89	4.75	4.19	3.96	*	-
	NT2RM2000924	66.24	48.22	89.49	72.54	62.16	39.92	33.79	29.08	40.4		
	NT2RM2000930	48.55	63.69	52.84	46.58	51.6	35.79	27	25.97	35.7	**	-
	NT2RM2000937	31.8	58.4	47.42	22.54	35.77	15.38	12.6	7.67	4.38	**	-
	NT2RM2000939	6.62	8.62	14.57	7.32	3.05	3.47	2.42	2.17	3.83	*	-
	NT2RM2000942	734.65	670.2	631.32	344.25	467.07	301.87	150.27	478.62	381.55	**	*
40	NT2RM2000951	4.26	4.86	13.05	5.55	2.39	1.46	1.13	1.84	1.19		
	NT2RM2000952	9.67	43.75	19.11	12.99	13.49	9.68	6.64	9	6.45		
	NT2RM2000966	187.94	165.71	228.75	214.51	217.85	161.14	133.25	108.26	108.39	*	-
	NT2RM2000973	104.1	257.68	179.14	123.46	180.6	103.68	80.15	78.39	82.31		
	NT2RM2000983	44.05	48.21	49.47	28.35	25.15	19.95	21.95	14.49	14.64	**	**
	NT2RM2000984	14.04	16.71	14.65	9.74	5.64	4.75	5.34	3.15	3.97	**	**
45	NT2RM2000994	36.03	29.02	31.03	22.45	13.36	11.64	9.34	22.92	20.85	*	*
	NT2RM2001004	87.18	99.34	120.85	105.48	104.79	118.66	75.52	78.54	88.2		
	NT2RM2001022	465.07	829.81	488.65	279.37	461.13	292.23	411.29	508	337.91		
	NT2RM2001035	119.48	128.64	135.94	69.22	98.88	76.14	85.64	92.65	116	*	*
	NT2RM2001038	30.1	53.09	55.15	35.29	31.06	27.29	33.8	26.97	56.89		
	NT2RM2001043	17.78	17.9	22.19	14.07	14.29	12.96	14.08	13.2	13.27	*	*
50	NT2RM2001050	16.36	10.75	11.34	9.74	5.11	3.09	5.76	4.31	3.75	*	*
	NT2RM2001055	7.49	7.2	8.19	5.79	2.69	1.59	3.42	2.92	3.04	*	**
	NT2RM2001065	18.94	19.43	21.19	16.28	10.87	7.49	3.44	9.8	10.97	*	**
	NT2RM2001075	352.66	309.42	355.51	314.53	188.83	298.2	178.61	439.36	452.62		
	NT2RM2001083	7.08	9.84	12.58	9.39	11.2	5.35	8.46	10.07	4.34		
	NT2RM2001100	132.53	127.49	140.57	168.49	157.74	186.39	108.36	105.08	125.06	*	*
55	NT2RM2001105	19.7	23.88	18.02	9.87	6.9	7.5	7.31	7.33	7.99	**	**
	NT2RM2001109	20.13	43.33	44.99	10.64	14.91	10.34	19.4	14.81	19.72	*	-
	NT2RM2001110	32.89	28.37	36.47	39.19	23.1	32.21	27.03	23.61	20.38	*	-

Table 408

	NT2RM2001126	10.89	14.19	16.02	9.38	4.33	6.54	7.81	4.58	5.85	*	*	-	-
	NT2RM2001131	35.31	23.37	27.48	39.22	24.25	32.19	17.26	18.93	15.18		*	-	-
5	NT2RM2001141	23.07	16.72	24.48	15.15	8.42	15.3	16.57	25.01	24.73		**	-	-
	NT2RM2001152	7.28	6.36	6.81	7.22	2.67	4.03	3.72	4.85	2.92		*	-	-
	NT2RM2001177	16.43	13.33	22.76	9.09	9.55	10.29	11.03	12.82	14.78	*	*	-	-
	NT2RM2001194	18.95	35.2	33.45	15.63	10.75	13.96	9.18	10.24	10.12	*	*	-	-
	NT2RM2001195	22.22	32.77	41.71	19.89	14.02	10.87	14.76	17.07	21.12	*	*	-	-
10	NT2RM2001196	12.18	14.33	14.56	8.23	2.8	2.96	2.65	3.74	5.12	**	**	-	-
	NT2RM2001201	112.26	151.54	152.39	113.21	71.67	129.08	182.51	124.84	110.23		*	-	-
	NT2RM2001221	15.16	10.19	12.98	12.97	6.39	8.39	4.13	7.92	7.64		*	-	-
	NT2RM2001238	7.02	4.76	7.61	7.38	2.47	4.7	2.6	3.8	3.66		*	-	-
	NT2RM2001243	28.44	25.47	29.19	20	12.3	9.83	7.01	16.89	8.25	*	**	-	-
	NT2RM2001244	14.84	14.77	26.94	13.43	7.79	12.02	6.46	7.21	5.59		*	-	-
15	NT2RM2001247	149.17	156.12	167.83	262.88	153.51	292.21	159.18	102.66	137.39		*	-	-
	NT2RM2001256	12.96	15.03	17.12	8.24	5.02	5.55	4.85	4.32	6.34	**	**	-	-
	NT2RM2001269	10.95	13.1	12.53	11.07	7.62	4.32	9.04	9.38	5.97		*	-	-
	NT2RM2001278	10.38	10.85	11.45	12.61	4.01	9.04	14.51	13.94	16.53	**	*	+	-
	NT2RM2001291	8.24	5.62	12.69	7.3	4.57	5.55	4.22	4.08	3.96		*	-	-
	NT2RM2001294	64.54	65.77	111.27	63.88	47.1	58.52	73.02	74.33	85.75		*	-	-
20	NT2RM2001295	8.24	9.79	14.29	5.61	3.8	3.62	3.42	2.36	2.25	*	*	-	-
	NT2RM2001302	3.39	6.85	11.75	6.43	3.29	2.51	3.71	3.87	1.57		*	-	-
	NT2RM2001306	11.41	14.23	14.66	11.73	5.3	7.08	5.43	5.34	3.99		**	-	-
	NT2RM2001312	3.55	4.56	12.72	6.28	2.54	2.63	4.61	2.59	2.39		*	-	-
	NT2RM2001319	5.86	9.67	14.24	9.42	5.49	4.3	4.35	3.58	2.75		*	-	-
	NT2RM2001324	18.95	7.8	13.76	18.03	4.46	12.42	10.21	14.53	14.86		*	-	-
25	NT2RM2001345	28.65	21.37	24.71	26.89	8	18.65	5.12	14.99	21.21		*	-	-
	NT2RM2001360	17.92	12.3	24.16	13.81	8.68	10.67	6.5	8.95	13.99		*	-	-
	NT2RM2001370	10.29	7.05	19.66	11.56	5.81	4.36	5.18	4.87	5.67		*	-	-
	NT2RM2001391	7.29	4.99	11.62	6.8	2.82	5.45	4.23	6.86	5.98		*	-	-
	NT2RM2001393	12.33	6.71	15.2	11.88	7.78	6.57	5.84	9.03	6.99		*	-	-
	NT2RM2001420	8.12	9.09	13.52	7.85	4.31	5.05	3.66	4.14	3.54		*	-	-
30	NT2RM2001423	17.63	16.34	28	15.84	12.17	12	10.06	5.58	6.91	*	*	-	-
	NT2RM2001424	27.85	17.9	24.35	16.51	10.81	12.46	10.74	18.59	16.89	*	*	-	-
	NT2RM2001482	8.67	6.53	15.28	13.75	6.43	10.52	8.21	10.88	32.33		*	-	-
	NT2RM2001499	6.83	5.56	14.66	6.11	6.28	4.16	4.43	4.99	9.08		*	-	-
	NT2RM2001504	10.92	6.52	14.65	8.66	7.17	4.96	4.36	8.69	6.66		*	-	-
	NT2RM2001524	14.94	10.41	10.01	10.19	8.66	6.87	5.54	6.7	4.33		*	-	-
35	NT2RM2001530	3.04	4.86	7.01	5.84	1.95	3.09	2.61	3.78	1.3		*	-	-
	NT2RM2001533	31.06	33.52	48.05	22.65	24.5	20.86	46.4	35.86	44.09		*	-	-
	NT2RM2001540	13.31	12.86	17.79	14.39	9.31	10.73	9.68	7.65	7.91		*	-	-
	NT2RM2001544	6.59	3.7	12.06	6.73	1.95	5.1	3.34	3.2	4.05		*	-	-
	NT2RM2001547	17.98	17.35	32.25	17.06	12.78	13.61	10.07	14.99	28.06		*	-	-
	NT2RM2001558	3.53	3.66	12.29	5.32	1.92	2.05	1.78	3.67	4.24		*	-	-
40	NT2RM2001575	12.53	9.85	20.98	9.37	6.51	6.57	9.69	11.4	8.27		*	-	-
	NT2RM2001582	18.86	18.39	26.78	16.91	11.16	8.85	13.11	10.99	13.56		*	-	-
	NT2RM2001588	33.5	33.04	38.62	26.73	19.6	15.21	19.42	19.94	22.31	*	**	-	-
	NT2RM2001592	8.06	9.31	10.24	8.08	7.97	5.3	6.26	2.96	5.52		*	-	-
	NT2RM2001603	18.68	34.48	37.52	19.83	12.18	16.75	16.12	15.01	10.86		*	-	-
	NT2RM2001605	2.46	1.84	10.05	3.68	0.89	3.29	1.27	2.06	1.52		*	-	-
45	NT2RM2001611	8.26	11.08	21.04	8.21	4.42	4.61	5.24	5.95	7.18		*	-	-
	NT2RM2001613	31.23	41.23	53.28	26.42	31.28	14.27	16.42	46.76	35.82		*	-	-
	NT2RM2001626	7.76	5	11.59	5.79	3.19	1.08	2.56	3.93	1.62		*	-	-
	NT2RM2001632	12.51	10.55	19.26	10.94	8.41	4.21	3.48	2.87	3.67		*	-	-
	NT2RM2001633	9.38	12.28	13.2	7.51	9.17	4.14	3.74	4.79	3.89		**	-	-
	NT2RM2001635	8.99	10.05	10.56	5.7	4.03	2.66	6.33	4.93	5.79	**	**	-	-
50	NT2RM2001636	13.44	12.39	18.22	10.09	11.69	6.86	5.49	5.27	4.75		*	-	-
	NT2RM2001637	5.38	4.7	11.19	6.81	1.81	3.12	2.09	2.96	1.51		*	-	-
	NT2RM2001639	12.13	12.21	20.77	10.63	8.64	7	4.1	7.5	7.85		*	-	-
	NT2RM2001641	8.65	5.25	15	6.44	4.6	3.79	6.08	10.65	9.66		*	-	-
	NT2RM2001643	13.92	14.16	22.25	10.74	7	2.7	2.29	4.88	4.18		*	-	-
	NT2RM2001648	39.15	45.91	36.48	26.92	23.84	12.46	22.53	23.65	32.08	*	*	-	-
55	NT2RM2001652	12.26	10.35	14.74	6.98	5.99	3.53	3.25	2.26	3.06	*	**	-	-
	NT2RM2001659	16.4	10.95	13.51	8.64	9.21	1.42	3.18	2.99	3.04		**	-	-
	NT2RM2001660	10.08	9.77	12.95	6.57	5.46	2.86	2.55	2.98	2.6	*	**	-	-

Table 409

	NT2RM2001664	5.02	5.48	16.95	8.08	4.37	8.84	2.47	6.43	6.78				
5	NT2RM2001668	15.06	19.03	25.63	5.79	6.13	6.44	2.42	3.93	2.92	*	**	-	-
	NT2RM2001670	5.32	7.34	15.89	6.82	2.18	2.28	5.04	5.37	3.96				
	NT2RM2001671	8.87	8.86	12.78	9.4	4.31	5.72	3.03	4.34	3.98	**		-	-
	NT2RM2001675	5.39	3.86	9.7	4.63	1.07	1.86	1.29	1.4	0.96	*		-	-
	NT2RM2001681	10.15	3.72	7.87	6.68	2.43	1.75	3.17	2.29	1.77				
	NT2RM2001685	5.99	4.42	4.61	4.4	0.95	1.7	1.76	0.44	1.52	**		-	-
10	NT2RM2001688	7.35	10.19	21.96	10.5	8.43	4.5	8.27	2.69	4.73				
	NT2RM2001695	21.84	15.61	27.76	16.05	12.1	18.2	12.98	24.27	27.96				
	NT2RM2001696	11.41	12.78	17.34	10.47	4.47	6.07	3.84	8.22	8.43	*		-	-
	NT2RM2001698	4.46	5.04	9.55	6.62	3.5	2.86	2.2	3.3	2.08				
	NT2RM2001699	9.41	7.54	15.28	7.73	5.45	4.44	4.63	5.76	3.45				
	NT2RM2001700	6.01	3.92	15.92	7.19	8.76	1.93	1.65	2.78	1.4				
15	NT2RM2001704	15.56	11	13.6	7.65	5.94	5.33	7.22	3.63	5.28	**	**	-	-
	NT2RM2001706	17.58	13	15.93	12.4	7.58	8.26	9.21	8.02	9.01	*	**	-	-
	NT2RM2001714	6.57	6.52	7.48	5.63	2.25	2.43	2.36	2.21	2	*	**	-	-
	NT2RM2001716	8.11	6.76	8.16	6.9	3	2.28	1.75	4.87	3.64	*		-	-
	NT2RM2001718	5.27	4.14	10.17	6.69	1.77	2.4	3.07	2.63	3.19				
	NT2RM2001723	7.52	14.9	19.44	7.99	8.79	1.56	2.66	6.02	4.35				
20	NT2RM2001727	13.96	15.14	20.23	10.17	9.39	6.64	16.21	10.41	9.88	*		-	-
	NT2RM2001730	19.9	22.32	24.32	11.37	7.04	10.08	9.63	10.59	8.89	**	**	-	-
	NT2RM2001738	24.21	32	34.82	11.52	20.69	8.94	10.25	6.51	7.37	*	**	-	-
	NT2RM2001743	11.04	12.3	13.73	7.4	4.32	2.84	7.29	5	5.26	**	**	-	-
	NT2RM2001753	33.97	33.52	45.06	27.22	20.28	23.67	19.89	16.73	21.61	*	*	-	-
	NT2RM2001755	5.43	4.23	7.05	6	2.04	4.11	2.32	3.16	2.92	*		-	-
25	NT2RM2001760	42.97	46.84	32.99	27.92	15.82	19.33	23.92	44.69	49.12	*		-	-
	NT2RM2001765	3.06	3.62	6.89	4.79	2.41	2.93	4.69	3.78	2.64				
	NT2RM2001767	156.3	123.32	123.27	161.08	199.81	185.95	99.49	113.99	123.4	*		+	-
	NT2RM2001768	10.21	7.85	24.02	6.47	5.49	3.96	2.75	3.87	3.14				
	NT2RM2001771	8.46	12.44	14.25	6.18	3.66	4.08	3.36	4	3.1	*	**	-	-
	NT2RM2001778	7.68	9.54	13.49	7.21	3	4.06	5.69	4.22	4.13	*		-	-
30	NT2RM2001782	8.45	16.26	12.43	10.97	4.91	8.55	7.19	5.67	4.31				
	NT2RM2001784	2.33	3.38	2.94	5.28	0.42	1.26	1.88	3.54	2.58				
	NT2RM2001785	26.54	25.99	26.3	14.79	12.05	14.71	11.42	23.99	14.87	**		-	-
	NT2RM2001792	9.85	6.48	8.81	6.44	5.86	3.8	3.68	3.95	3.88	*		-	-
	NT2RM2001795	6.29	3.46	12.45	6.74	1.68	4.68	1.95	2.66	2.03				
	NT2RM2001797	5.8	5.87	12.89	5.74	3.15	4.35	4.29	3.75	2.07				
35	NT2RM2001800	8.98	9.98	12.02	6.5	3.87	3.21	3.89	2.41	4.66	*	**	-	-
	NT2RM2001803	9.13	11.59	12.8	14.78	5.7	4.76	5	4.99	6.43	**		-	-
	NT2RM2001805	5.23	4.93	4.93	5.77	2.81	1.86	2.38	1.02	1.76	**		-	-
	NT2RM2001806	9.59	8.37	10.47	8.03	2.61	4.16	1.45	2.5	1.61	**		-	-
	NT2RM2001813	4.64	2.78	4.37	7.6	3.08	5.69	2.05	4.02	2.1				
	NT2RM2001814	4.12	2.59	2.69	6.32	1.65	3.13	2.04	1.23	1.1	*		-	-
40	NT2RM2001818	2.04	2.24	0.99	4.82	0.99	0.95	0.43	0.73	1.2				
	NT2RM2001823	3.33	1.51	3.32	5	0.06	3.46	1.75	2.14	2.76				
	NT2RM2001825	18.28	14.86	18.88	21.81	10.23	18.33	13.27	20.99	16.7				
	NT2RM2001832	8.66	8.97	9.59	7.39	2.65	5.19	2.03	4.44	3.08	*	**	-	-
	NT2RM2001839	39.76	56.2	55.7	17.75	23.24	41.75	69.27	61.03	74.92				
	NT2RM2001840	16.73	9.83	12.67	16.44	10.4	10.16	11.51	19.3	18.18				
45	NT2RM2001851	13.19	13.13	16.5	15.12	5.82	6.1	7.33	10.63	8.57	*		-	-
	NT2RM2001855	24.09	22.55	30.11	14.9	11.35	11.17	11.7	10.3	11.91	**	**	-	-
	NT2RM2001867	4.7	5.27	10.74	7.68	2.21	3.72	3.8	4.17	5.58				
	NT2RM2001869	150.4	263.47	450.85	333.27	292.69	360.02	366.03	265.55	360.35				
	NT2RM2001879	4.5	3.92	9.65	7	2.4	3.74	3.05	3.17	3.3				
	NT2RM2001883	0.5	1.23	3.35	4.6	1.17	2.06	2.26	1.81	2.31				
50	NT2RM2001886	5.2	8.33	7.95	8.22	4.29	6.46	4.42	3.66	6				
	NT2RM2001887	10.27	7.46	19.23	10.21	4.91	6.33	4.19	5.06	5.45				
	NT2RM2001896	1909.2	1304.9	1706.8	669.09	517.88	706.49	508.04	455.61	977.52	**	*	-	-
	NT2RM2001902	4.57	4.04	12.43	5.26	2.22	2.22	1.58	3.18	2.3				
	NT2RM2001903	63.33	63.93	80.39	57.98	54.4	31.36	55.94	50.98	47.6	*		-	-
	NT2RM2001930	4.16	7.96	10.97	7.26	3.74	5.15	3.87	4.57	4.22				
55	NT2RM2001935	6.31	7.33	13.94	7.14	3.83	4.76	3.89	3.34	2.47				
	NT2RM2001936	4.31	7.8	13.64	6.57	5.23	5.41	6.76	3.21	3.62				
	NT2RM2001939	1.41	2.6	6.02	7.8	3.89	3.31	3.06	4.67	3.29				

Table 410

	NT2RM2001941	6.04	4.24	11.07	8.57	3.76	4	3.69	5.77	3.42			
	NT2RM2001950	10.88	9.24	13.32	9.74	3.68	5.38	5.27	9.54	12.08			
5	NT2RM2001952	5.22	5.96	18.37	6.97	3.67	2.12	3.56	5.93	8.5			
	NT2RM2001976	43.9	27.85	44.8	42.85	38.56	26.62	16.38	23.06	20.86	*		-
	NT2RM2001982	3.43	5.03	6.82	6.99	3.67	2.56	3.51	3.09	3.63			
	NT2RM2001983	12.18	15.12	21.04	15.68	19.01	6.03	9.47	6.45	4.73	*		-
	NT2RM2001984	20.37	33.54	33.12	16.47	10.56	10.16	8.25	7.86	3.8	**		-
	NT2RM2001989	3.86	5.39	6.78	8.98	3.51	2.63	4.78	3.3	2.04			
10	NT2RM2001996	16.29	18.4	29.01	16.49	15.54	12.47	7.55	13.49	15.15			
	NT2RM2001997	11.71	10.41	18.16	7.7	4.63	5.51	3.14	5.18	8.39	*		-
	NT2RM2001998	9.82	8.18	17.59	8.92	5.29	6.42	2.82	8.96	6.36			
	NT2RM2001999	18.02	20.28	27.06	10.57	9.9	5.15	3.81	3.98	3.66	*	**	-
	NT2RM2002003	50.92	53.27	55.93	27	36.02	21.81	18.72	19.18	19.35	**	**	-
	NT2RM2002004	4.18	6.17	7.32	5.72	2.78	2.44	2.58	3.1	3.84			
15	NT2RM2002009	12.24	20.57	21.82	12.13	12.36	8.91	7.8	3.92	5.72	*		-
	NT2RM2002014	2.73	6.1	5.88	8.11	3.54	6	6.1	6.78	3.31			
	NT2RM2002019	125.13	124.6	184.05	89.22	90.25	54.05	33.48	56.11	68.43	*	*	-
	NT2RM2002029	13.94	31.19	27.2	28.59	19.23	17.84	11.48	35.39	33.05			
	NT2RM2002030	16.61	18.25	22.39	8.8	11.56	5.36	5.58	12.47	9.07	*	*	-
20	NT2RM2002034	58.72	73.27	50.5	59.63	56.44	27.9	21	20.77	37.34	*		-
	NT2RM2002049	21.26	22	23.61	14.68	15.64	11.74	6.05	9.95	7.32	**	**	-
	NT2RM2002055	3.27	6.4	6.36	5.47	2.96	2.6	3.63	3.29	2.55			
	NT2RM2002072	40.82	52.88	39.93	24.05	29.78	18.81	18.47	15.25	18	*	**	-
	NT2RM2002088	82.31	80.35	97	73.51	51.16	68.26	90.62	55.31	84.87			
	NT2RM2002091	22.22	21.11	34.44	9.76	9.27	5.82	2.71	4.2	5.17	*	**	-
25	NT2RM2002100	12.27	9.78	20.49	8.79	6.55	5.99	3.91	6.96	6.5			
	NT2RM2002109	4.21	5.64	16.28	7.68	3.73	3.18	3.74	2.46	4.42			
	NT2RM2002126	27.51	39.25	34.46	33.04	40.35	13.28	17.62	8.06	21.42	*		-
	NT2RM2002128	4.47	5.67	11.09	4.57	2.71	1.5	2.22	2.89	1.62			
	NT2RM2002129	22.51	19.86	17.11	13.35	16.48	7.76	5.96	8.88	6.92	**		-
	NT2RM2002142	23.72	27.99	22.69	11.44	14.47	7.07	5.7	5.27	5.78	**	**	-
30	NT2RM2002144	5.53	4.42	5.98	7	2.78	3.75	3.22	1.93	3.5	*	*	-
	NT2RM2002145	12.68	17.57	21.16	8.81	4.88	6.47	2.77	6.22	7.99	*	*	-
	NT2RM2002153	10.64	8.88	12.47	8.77	5.52	6.62	3.59	3.26	3.47	**		-
	NT2RM2002163	3.34	3.58	10.5	5.65	2.59	1.58	0.8	1.56	1.92			
	NT2RM2002170	9.23	12.24	23.46	10.21	7.83	3.14	3.4	4.81	4.17			
	NT2RM2002178	9.54	6.98	11.63	5.56	4.58	2.92	3.63	2.57	1.48	*	**	-
35	NT2RM2002179	8.2	10.06	9.02	7.04	6.34	2.72	2.79	2.76	2.85	**		-
	NT2RM2002270	5.65	6.66	8.96	6.13	3.31	1.8	2.35	2.99	1.98	*		-
	NT2RM2002326	8.26	5.94	6.26	7.55	3.63	3.3	2.53	3.14	5.2	*		-
	NT2RM2002337	9.91	15.68	18.49	12.85	7.23	4.54	5.02	6.94	5.77	*		-
	NT2RM2002339	6.62	10.73	17.92	7.67	6.02	5.59	3.93	4.03	4.49			
	NT2RM2002345	12.28	11.64	16.5	11.35	8.87	6.37	4.6	5.99	5.18	**		-
40	NT2RM2002368	11.9	12.43	21.01	8.78	6.6	5.66	4.97	7.35	7.34	*		-
	NT2RM2002381	5.04	4.54	7.61	5.17	3.68	1.33	2.23	2.48	3.79			
	NT2RM2002424	6.19	9.87	12.12	6.06	3.81	1.42	2.55	2.13	2.39	*		-
	NT2RM2002450	5.83	4.84	6.17	9.5	2.45	2.17	3.24	2.41	1.89	**		-
	NT2RM2002482	6.57	3.99	6.22	7.86	2.37	2.81	5.1	2.33	2.52			
	NT2RM2002492	115.88	159.06	153.05	67.65	86	93.3	108.8	133.63	153.04	*		-
45	NT2RM2002575	8.81	10.86	19.91	10.34	8.51	6.85	6.71	8.36	8.38			
	NT2RM2002580	12.81	11.63	17.51	7.68	4.03	7.15	4.84	5.41	5.92	*	**	-
	NT2RM2002592	30.1	60.89	57.77	16.85	24.42	15.38	23.91	11.59	15.71	*	*	-
	NT2RM2002608	107.02	108.16	125.35	69.13	83.62	75.26	86.4	51.95	98.01	**		-
	NT2RM2002615	21.13	24.19	16.26	10.72	11.75	7.36	11.09	7.92	5.92	*	*	-
	NT2RM2002622	37.43	55.62	40.03	34.45	40.44	21.34	16.57	11.49	8.97	**		-
50	NT2RM2002630	17.23	13.55	15.45	18.01	9.28	15.57	19.85	13.91	16.46			
	NT2RM2002634	10.84	11.13	17.05	9.62	2.19	5.41	7.89	7.53	7.31			
	NT2RM2002645	19.66	20.09	27.47	17.63	14.57	10.2	9.86	18.1	25.3			
	NT2RM2002646	40.87	51.15	69.9	15.35	22.28	15.25	17.48	14.11	15.62	*	*	-
	NT2RM2002647	50.8	59.26	54.64	17.81	19.82	20.32	24.11	18.36	23.98	**	**	-
	NT2RM2002652	15.86	23.36	17.16	10.87	6.59	8.39	7.1	6.49	11.22	*	*	-
55	NT2RM2002692	6.96	5.59	6.84	5.88	3.32	1.36	2.92	2.3	3.51	**	**	-
	NT2RM2002721	65.28	100.72	114.83	36.62	27.49	27.32	87.26	32.69	72.44	*		-
	NT2RM2002748	96.93	107.15	111.07	119.35	46.49	100.69	117.84	48.85	124.45			

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	NT2RM2002764	5.49	12.15	7.39	6.52	3.1	7.78	2.89	4.03	5.76				
5	NT2RM2002772	29.76	33.25	38.82	20.56	12.45	9.21	4.96	16.05	9.09	**	**	-	-
	NT2RM2002811	16.39	25	25.21	9.15	15.71	3.55	6.58	8.61	10.62	*	*	-	-
	NT2RM2002818	20.34	18.56	21.22	13.83	9.54	15.73	17.66	20.72	25.61	*		-	-
	NT2RM2002879	25.35	30.35	32.28	9.31	5.54	8.46	5.48	6.4	6.89	**	**	-	-
	NT2RM2002979	45.6	67	65.04	29.24	39.73	11.12	45.71	18.88	50.67	*		-	-
	NT2RM2002981	6.39	5.25	5.04	5.13	2.8	1.9	2.21	1.27	2.8		**	-	-
10	NT2RM2002995	4.58	2.61	3.97	7.89	1.25	3.74	3.35	2.92	4.03			-	-
	NT2RM2003031	4.98	5.14	6.7	6.97	3.27	6.19	2.14	4.35	4.33			-	-
	NT2RM2003042	32.29	28.58	51.11	28.69	7.79	11.66	9.6	10.82	7.31	*		-	-
	NT2RM2003044	5.51	2.76	2.92	6.07	1.88	3.64	2.44	2.91	3.92			-	-
	NT2RM2003090	15.51	15.57	25.03	16.18	8.25	19.49	18.74	20.12	15.75			-	-
	NT2RM2003095	23.07	26.27	29.36	22.31	14.66	13.94	29.67	24.13	25.38	*		-	-
15	NT2RM2003116	19.38	32.85	27.63	12.52	9.52	10.31	6.49	8.73	7.15	*	**	-	-
	NT2RM2003222	4.03	3.37	4.48	6.23	1.12	2.42	2.91	3.67	3.87			-	-
	NT2RM2003224	23.91	19.9	24.52	18.14	9.42	15.36	24.57	16.25	13.82	*		-	-
	NT2RM2003250	119.92	69.2	166.74	153.09	107.43	107.61	63.52	77.81	74.98			-	-
	NT2RM2003258	14.27	11.09	23.88	11.45	8.67	5.92	4.04	5.75	7.4			-	-
	NT2RM2003262	13.63	6.96	21.6	7.07	3.47	2.7	6.15	5.4	5.15			-	-
20	NT2RM4000023	16.25	15.39	24.54	14.62	6.88	9.36	9.34	7.69	6.58	*		-	-
	NT2RM4000024	5.57	7.1	11.59	9.02	4.21	3.87	3.82	4.08	2.65			-	-
	NT2RM4000027	4.73	3.54	9.85	6.85	4.18	2.53	4.65	2.99	2.04			-	-
	NT2RM4000030	5.72	8.1	11.8	8.56	5.42	3.94	5.02	4.04	3.02			-	-
	NT2RM4000033	5.95	4.77	7.64	13.08	3.98	7.38	10.23	6.96	6.85			-	-
	NT2RM4000034	14.03	8.95	17.36	14.71	7.52	11.06	7.66	12.11	11.07			-	-
25	NT2RM4000046	5.52	5.71	10.27	5.43	2.75	2.16	4.42	4.99	3.5			-	-
	NT2RM4000052	3.65	3.61	9.75	4.88	2.31	3.26	1.99	3.02	2.4			-	-
	NT2RM4000054	24.72	16.37	22.59	16.92	16.99	12.56	13.57	15.39	11.37	*		-	-
	NT2RM4000061	2.45	2.46	7.19	5.03	3.91	3.49	2.41	2.69	0.75			-	-
	NT2RM4000074	109.94	111.99	162.79	132.85	134.31	127.91	155.38	114.81	153.05			-	-
	NT2RM4000085	16.76	26.39	27.87	18.47	15.63	12.58	12.15	6.78	9.96	*		-	-
30	NT2RM4000086	5.66	6.66	7.88	8.93	4.39	5.02	8.75	6.18	6.29			-	-
	NT2RM4000100	33.67	23.83	35.82	31.94	18.51	25.58	27.68	38.43	48.27			-	-
	NT2RM4000101	24.08	19.83	27.89	18.1	9.03	12.06	10.92	15.22	16.58	*	*	-	-
	NT2RM4000102	31.73	28.52	43	29.96	36.82	28.28	11.54	34.43	29.82			-	-
	NT2RM4000104	12.56	10.41	15.15	10.13	9.81	7.37	8.35	10.19	9.76			-	-
	NT2RM4000115	5.71	9.33	11.32	11.36	6.79	5.37	7.68	7.13	8.99			-	-
35	NT2RM4000129	2.55	5.58	5.12	5.02	4.24	3.57	3.26	2.78	3.18			-	-
	NT2RM4000139	5.53	8.52	11.67	6.45	6.29	5.11	4.73	4.33	5.31			-	-
	NT2RM4000149	3.74	4.09	4.62	8.9	2.03	3.09	4.1	3.49	3.35			-	-
	NT2RM4000155	17.15	10.36	17.5	14.41	8.06	9.43	4.52	7.7	6.79	*		-	-
	NT2RM4000156	43.23	34.65	52.17	33.06	31.74	35.59	32.83	34.2	32.88			-	-
	NT2RM4000167	5.13	4.59	12.54	4.2	2.19	0.82	1.69	2.03	1.71			-	-
40	NT2RM4000169	116.9	136.33	190.06	211.72	166.35	130.17	146.08	152.04	180.53			-	-
	NT2RM4000191	10.04	6.72	12.84	9.1	7.11	6.9	7.89	7.38	7.91			-	-
	NT2RM4000197	3.31	6.64	7.83	5.96	3.1	2.95	2.4	2.51	3.17			-	-
	NT2RM4000198	13.19	12.13	17.78	14.45	8.75	9.44	12.48	10.4	9.17			-	-
	NT2RM4000199	3.72	4.46	6.47	8.34	4.51	5.35	6.27	5.09	6.45			-	-
	NT2RM4000200	3.27	5.32	11.6	5.66	2.52	4.69	3.52	3.66	3.02			-	-
45	NT2RM4000202	7.07	4.86	13.64	7.53	1.78	3.26	4.51	5.82	5.86			-	-
	NT2RM4000210	5.45	5.44	15.45	6.67	3.23	1.92	1.86	2.7	2.32			-	-
	NT2RM4000215	8.8	9.1	12.69	7.49	4.69	2.59	3.73	4.19	3.48	*	**	-	-
	NT2RM4000220	21.3	15.96	19.47	12.48	9.78	7.44	10.31	10.33	6.87	*	**	-	-
	NT2RM4000229	4.29	6.1	7.3	4.96	2.64	1.79	2.82	2.26	3.55	*		-	-
	NT2RM4000231	12.18	22.17	22.16	12.3	13.79	7.12	11.29	7.48	7.64	*		-	-
50	NT2RM4000233	21.08	19.41	23.05	29.48	16.53	15.89	23.49	16.8	20.56			-	-
	NT2RM4000244	7.04	6.33	12.22	6.72	4.83	3.85	2.65	5.84	4.45			-	-
	NT2RM4000251	8.01	7.64	14.53	7	8.84	3.91	3.55	5.44	5.4			-	-
	NT2RM4000255	8.99	6.74	14.46	7.34	5.4	4.93	3.56	3.66	2.79	*		-	-
	NT2RM4000265	13.77	11.08	20.66	10.54	8.41	4.23	9.98	13.42	10.55			-	-
	NT2RM4000283	213.58	220.77	174.14	136.23	205.5	145.83	158.43	132.77	224.43			-	-
55	NT2RM4000284	85.27	81.74	108.73	78.21	81.89	45.3	89.45	84.2	83.7			-	-
	NT2RM4000290	13.22	11	18	10.81	6.15	3.95	7.71	6.59	6.44	*		-	-
	NT2RM4000295	9.32	6.67	7.61	11.47	5.8	4.29	6.42	5.34	6.78			-	-



Table 412

	NT2RM4000306	39.39	31.22	45.45	18.05	17.89	26.02	12.1	14.22	20.93	*	**	-	-
	NT2RM4000307	10.91	9.3	17.74	9.83	6.51	5.04	4.55	5.59	9.36				
5	NT2RM4000309	6.25	6.98	13.33	6.03	3.16	3.04	0.89	2.68	1.25	*		-	
	NT2RM4000313	8.25	9.27	15.88	8.4	4.79	4.48	3.48	4.24	4.11	*		-	
	NT2RM4000318	7.74	12.3	19.97	11.61	7.91	4.9	8.74	11.58	10.87				
	NT2RM4000324	7.02	4.79	7.97	5.66	2.78	1.11	2.3	1.61	0.69	**		-	
	NT2RM4000326	9.61	6.92	8.36	6.7	2.41	2.62	3.8	2.41	1.32	**		-	
	NT2RM4000327	10.62	7.04	10.88	10.24	4.86	9.97	11.64	7.37	9.72				
10	NT2RM4000344	28.12	43.85	37.76	23.98	18.35	22.38	19.35	25.83	27.75	*		-	
	NT2RM4000349	54.86	44.05	74.07	45.06	38.46	49	53.73	62.48	76.26				
	NT2RM4000354	3.83	4.95	10.6	6.31	1.75	1.8	2.77	2.77	2.79				
	NT2RM4000356	5.03	3.65	9.35	5.42	1.79	2.58	1.32	3.38	0.81				
	NT2RM4000366	170.18	124.74	186.28	108.07	122.86	98.86	143.05	122.68	104.4				
	NT2RM4000368	16.94	13.21	17.9	9.95	5.92	5.45	9.44	7.79	10.81	*	*	-	-
15	NT2RM4000373	32.64	29.04	37.96	31.16	21.65	24.87	33.11	24.62	25.87				
	NT2RM4000386	6.62	6.28	8.3	8.65	4.71	4.93	6.02	2.91	5.23				
	NT2RM4000395	10.95	13.82	15.83	10.78	7.59	9.02	5.57	7.71	10.22	*		-	
	NT2RM4000414	4.69	4.37	11.16	5.76	0.91	3.43	2.88	1.6	3.45				
	NT2RM4000417	11.27	10.89	8.84	6.8	4.15	6.41	8.68	3.94	4.92	*		-	
	NT2RM4000421	10.28	10.99	14.3	8.17	4.31	2.7	2.33	2.02	4.78	*	**	-	-
20	NT2RM4000425	91.24	92.57	106.69	64.91	58.82	58.32	76.16	70.13	74.53	**	*	-	-
	NT2RM4000433	6.13	6.12	8.53	7.28	5.88	4.18	2.6	4.18	3.51	*		-	
	NT2RM4000436	18.9	19.36	27.32	20	14.51	11.77	15.16	14.79	15.69				
	NT2RM4000444	18.5	21.83	23.5	27.88	22.92	21.75	22.28	13.95	20.52				
	NT2RM4000457	13.16	19.12	21.52	10.27	6.05	7.18	7.2	10.64	8.19	*	*	-	-
	NT2RM4000471	11.07	11.03	12.38	8.14	9.49	4.57	3.84	6.85	3.58	**		-	-
25	NT2RM4000472	19.66	22.31	17.4	12.44	15.19	12.8	11.64	22.04	27.4	*		-	
	NT2RM4000486	10.68	18.04	19.73	11.41	9.93	10.39	10.79	12.22	9.89				
	NT2RM4000490	14.19	17.43	15	9.61	4.76	5.97	7.87	5.19	5.16	**	**	-	-
	NT2RM4000496	4.23	6.24	5.23	3.18	0.15	0.92	1.52	0.44	1.12	*	**	-	-
	NT2RM4000505	107.79	139.53	149.56	114.44	75.32	107.4	136.82	107.52	141.57				
	NT2RM4000511	73.01	84.21	82.3	77.22	39.83	88.6	83	54.31	48.26				
30	NT2RM4000514	15.58	17.06	20.66	15.1	9.63	16.07	11.41	15.96	14.62				
	NT2RM4000515	15.97	18.43	19.43	7.56	4.12	3.43	3.77	6.97	4.37	**	**	-	-
	NT2RM4000517	351.24	469.1	440.94	138.38	381.29	140.48	205.12	297.92	317.1	*		-	
	NT2RM4000520	3.56	5.44	6.75	6.2	2.43	4.29	3.06	2.99	1.91				
	NT2RM4000531	7.21	6.94	9.49	7.75	2.88	4.52	5.61	3.99	4.45	*		-	
	NT2RM4000532	6.55	5.58	4.11	7.27	2.1	1.72	3.22	3.22	3.25	*		-	
35	NT2RM4000533	5.69	4.73	4.92	6.83	1.35	2.87	3.57	2.18	3.55	*		-	
	NT2RM4000534	4.83	3.29	2.48	5.97	1.61	1.76	3.52	3.71	3.07				
	NT2RM4000563	23.61	15.27	21.44	28.24	15.01	45.63	27.71	31.71	29.82	*		+	
	NT2RM4000566	9.4	6.65	10.24	13	4.81	13.26	8.88	9.31	9.58				
	NT2RM4000568	24.52	13.96	20.25	24.28	11.25	22.83	7.78	15.36	11.01				
	NT2RM4000585	3.91	1.91	3.08	7.76	1.73	4.77	2.79	4.1	3.39				
40	NT2RM4000587	7.59	6.74	8.76	10.89	3.52	5.69	7.38	7.94	10.18				
	NT2RM4000590	2.8	2.23	4.43	6.82	1.35	3.31	2.85	3.67	2.59				
	NT2RM4000593	8.21	5	10.19	8.56	3.29	5.21	6.43	4.7	4.53				
	NT2RM4000595	4.79	4.42	3.36	7.11	6.02	3.43	4.16	2.82	3.87				
	NT2RM4000603	5.4	2.57	9.66	6.3	2.52	2.39	2.28	2.67	2.18				
45	NT2RM4000611	28.57	18.91	36.37	25.67	15.39	24.58	19.91	19.95	26.79				
	NT2RM4000616	9.69	7.13	13.2	7.2	3.11	4.07	2.46	3.02	2.66	*		-	
	NT2RM4000621	3.69	1.04	7.35	6.04	1.52	1.99	3.47	3.26	2.31				
	NT2RM4000648	7.93	5.22	9.62	8.39	3.12	4.35	6.48	5.01	6.06				
	NT2RM4000649	4.41	3.44	7.74	6.28	2.95	1.85	3.85	1.71	2.41				
	NT2RM4000658	5.46	6.14	9.39	8.84	2.67	4.42	4.63	4.69	4.24				
50	NT2RM4000661	15.52	9.28	15.4	13.03	7.61	7.72	5.33	7.59	7.97	*		-	
	NT2RM4000673	13.87	8.93	21.18	9.61	6.09	5.58	4.94	6.04	10.95				
	NT2RM4000674	33.39	14.79	28.45	15.54	18.31	16.46	9.71	12.48	12.12				
	NT2RM4000689	13.32	8.68	20.09	9.6	6.2	5.32	9.33	7.16	5.74				
	NT2RM4000698	3.25	4.45	8.82	7.51	4.65	2.16	4.55	4.72	3.77				
	NT2RM4000700	9.2	12.82	18.94	9.98	10.71	10.66	5.56	6.11	5.56	*		-	
55	NT2RM4000701	37.49	38.63	57.82	37.22	35.87	38.99	50.37	52.92	48.89				
	NT2RM4000712	26.37	34.47	28.93	18.91	14.79	13.59	9.02	8.85	10.91	**	**	-	-
	NT2RM4000717	24.65	10.07	20.07	21.94	7.33	18.21	17.18	23.49	18.21				

Table 413

	NT2RM4000733	9.25	6.15	14.75	8.98	6.63	6.77	4.25	7.21	11			
	NT2RM4000734	6.83	6.23	12.29	7.58	4.56	3.67	3.75	5.75	9.29			
5	NT2RM4000741	13.34	10.33	15.73	9.84	9.36	7.54	6.59	7.87	3.9	*	-	
	NT2RM4000744	885.53	451.3	1241	1383.2	1506.5	707.31	777.95	717.55	894.48			
	NT2RM4000749	51.3	49.81	57.77	49.46	44.79	42.49	59.41	56.25	54.64			
	NT2RM4000751	10.01	10.59	16.02	7.97	7.75	5.05	5.19	5.27	4.04	*	-	
	NT2RM4000752	14.18	16.62	13.54	10.44	6.55	5.76	8.04	11.07	5.33	*	*	-
10	NT2RM4000760	66.66	27.61	44.38	43.74	22.69	40.29	50.15	65.89	60.41			
	NT2RM4000761	19.9	12.95	27.34	11.59	8.66	7.67	5.75	12.58	17.06			
	NT2RM4000764	28.14	13.4	30.32	14.61	9.8	20.16	18.5	24.69	24.19			
	NT2RM4000768	91.29	73.54	83.67	77.4	70.39	93.31	63.42	64.16	68.6	*	-	
	NT2RM4000778	8.24	6.22	8.88	7.38	4.94	5.13	2.54	2.81	2.48	**	-	
	NT2RM4000779	13.14	10.85	20.24	8.82	8.68	7.51	2.45	7.69	5.22	*	-	
15	NT2RM4000787	15.66	16.22	17.04	13.21	10.45	11.66	11.77	12.92	11.34	**	**	-
	NT2RM4000790	2620.9	2248.3	2489	2090	3251.6	2752.2	3676.2	1775.7	1256.3			
	NT2RM4000795	7.92	4.23	13.52	7.6	3.13	5.92	6.03	8.23	6.4			
	NT2RM4000796	26.78	15.24	27.73	18.41	12.57	18.03	14.45	19.92	38.07			
	NT2RM4000798	7.01	8.1	18.9	8.2	4	6.33	3.86	7.47	8.07			
	NT2RM4000800	5.35	6.72	10.01	6.15	1.63	3.53	2.61	2.89	3.11	*	-	
20	NT2RM4000813	11.25	10	13.48	6.95	4.25	5.74	3.76	4.39	3.13	**	**	-
	NT2RM4000820	26.13	26.55	28.07	22.17	20.99	17.91	22.8	23.35	20.32	**	*	-
	NT2RM4000827	10.03	14.9	13.91	7.34	7.52	5.34	7.29	6.84	3.6	*	*	-
	NT2RM4000830	12.07	12.08	13.71	8.9	8.35	9.39	11.27	7.81	7.47	**	*	-
	NT2RM4000833	11.24	7.17	16.3	8.57	3.24	6.92	2.5	5.31	5.24			
	NT2RM4000841	12.98	15.96	14.24	9.21	12.52	7.68	4.07	5.69	5.39	**	-	
25	NT2RM4000846	9.5	7.99	19.32	10.93	5.53	8.29	6.17	10.68	8.48			
	NT2RM4000848	7.99	8	13.35	6.98	3.66	2.79	2.7	4.77	2.57	*	-	
	NT2RM4000852	14.87	14.63	15.93	7.89	7	3.89	3.95	4.67	2.59	**	*	-
	NT2RM4000855	6.4	5.44	7.14	5.82	2.45	2.19	1.77	2.66	1.11	**	-	
	NT2RM4000859	16.62	15.67	16.78	13.33	8.27	6.7	12.27	10.96	12.51	*	**	-
	NT2RM4000868	19.91	23.16	23.62	14.39	12.92	10.23	4.82	6.2	3.98	**	**	-
30	NT2RM4000870	13	13.65	19.75	13.98	14.72	8.66	5.75	8.62	12.86			
	NT2RM4000879	41.44	32.18	43.25	14.78	13.02	16.56	3.72	8.51	8.81	**	**	-
	NT2RM4000882	15	11.7	22.42	13.18	7.01	7.9	5.18	5.53	4.92	*	-	
	NT2RM4000887	41.97	33.25	51.62	36.36	23.39	28.87	18.02	26.87	25.16	*	-	
	NT2RM4000895	26.8	20.11	33.05	17.45	16.12	7.46	11.88	6.83	10.98	*	-	
	NT2RM4000897	9.87	8.53	11.07	8.99	4.54	3.34	4.8	3.39	4.04	**	-	
35	NT2RM4000901	10.96	12.11	11.53	7.56	7.1	4.42	5.41	4.23	6.77	**	**	-
	NT2RM4000950	9.78	8.98	10.35	8.13	5.43	3.19	2.51	2.31	1.79	*	**	-
	NT2RM4000965	28.19	32.79	35.21	15.2	12.26	17.85	6.17	10.47	12.16	**	**	-
	NT2RM4000971	97.81	77.57	101.74	132.86	95.27	155.13	87.73	92.85	108.16			
	NT2RM4000979	6.96	6.06	14.84	8.87	6.06	5.77	4.88	5.81	4.09			
	NT2RM4000987	998.76	831.62	1103.5	625.74	1156.8	778.33	1010.1	1262.3	668.26			
40	NT2RM4000989	20.87	13	27.71	19.07	13.82	14.2	14.36	15.32	14.94			
	NT2RM4000991	41.92	23.13	35.75	37.46	31.48	28.64	21.97	22.75	24.51			
	NT2RM4000992	10.32	6.68	8.53	6.07	2.23	2.13	3.02	2.16	2.78	*	**	-
	NT2RM4000996	22.09	29.46	18.01	12.6	11.82	10.41	9.81	3.95	3.92	*	*	-
	NT2RM4000997	28.21	30.93	25.95	19.16	13.92	19.47	16.5	21.62	24.11	**	*	-
	NT2RM4001001	7.63	6.6	15.15	9.35	5.11	5.88	3.96	7.75	5.13			
45	NT2RM4001002	459.98	441	503.26	494.01	440.37	522.33	521.26	628.75	590.54	*	+	
	NT2RM4001016	19.09	20.3	24.95	12.05	10.46	13.91	10.42	12.83	14.8	*	*	-
	NT2RM4001025	6.64	7.24	14.2	7.08	5.08	3.26	5.04	3.42	2.59			
	NT2RM4001027	4.69	5.86	4.64	4.07	1	1.53	1.18	1	1.23	*	**	-
	NT2RM4001032	13.63	13.78	6.47	6.13	6.41	2.73	4.98	2.77	2.21	*	-	
	NT2RM4001047	17.2	23.07	17.27	11.83	13.43	8.74	14.05	4.88	2.78	*	*	-
50	NT2RM4001049	14.8	12.01	16.43	12.47	5.42	11.65	9.35	13.4	14.12			
	NT2RM4001051	23.07	23.96	19.46	18.43	11.09	9.95	3.77	14.4	12.67	*	*	-
	NT2RM4001052	9.72	6.17	11.79	8.32	6.45	2.86	8.57	9.7	6.4			
	NT2RM4001053	8.35	8.46	10.92	7.64	6.3	5.31	6.88	7.16	3.68			
	NT2RM4001054	15.68	17.03	15.78	11.07	4.7	7.63	9.63	9.71	11.5	*	**	-
	NT2RM4001059	5.24	11.23	8.09	5.5	2.85	2.53	2.48	2.39	3	*	-	
55	NT2RM4001071	23.88	28.79	33.58	18.66	9.28	10.59	17.49	15.69	16.83	*	*	-
	NT2RM4001084	12.62	12.59	13.06	12.4	5.97	9.54	14.16	9.85	15.23			
	NT2RM4001092	7.67	7.08	7.41	8.26	5.02	4.62	2.05	6.72	4.2			

Table 414

	NT2RM4001100	10.34	6.97	14.94	8.81	5.31	8.81	7.75	11.53	7.75			
	NT2RM4001116	6.46	5.43	9.66	8.08	5.44	5.9	5.27	4.35	5.99			
5	NT2RM4001119	4.41	2.95	6.53	4.88	4.54	2.33	3.03	2.56	2.24			
	NT2RM4001140	6.58	8.81	10.22	5.74	2.39	2.78	3.27	2.64	2.47	*	**	-
	NT2RM4001148	77.43	82.01	87.89	109.01	92.69	80.91	71.63	54.14	60.54	*		-
	NT2RM4001151	25.3	23.87	22.4	14.14	12.5	10.51	24	19.61	17.03	**		-
	NT2RM4001155	7.7	10.96	9.45	14.26	6.55	9.63	8.68	7.88	7.8			
10	NT2RM4001157	4.69	2.46	3.77	5.35	1.74	4.67	1.85	2.85	2.34			
	NT2RM4001160	10.13	5.87	8.44	9.04	3.06	4.73	3.63	6.09	4.88			
	NT2RM4001163	8.69	6.99	8.41	6.85	4.09	5.89	3.57	3.78	3.99	**		-
	NT2RM4001187	15.55	10.66	18.41	9.39	4.2	6.99	4.74	5.75	3.81	*	*	-
	NT2RM4001191	6.6	5.61	4.99	6.79	10.14	6.02	8.39	4.7	8.34			
	NT2RM4001200	2.58	2.46	3.46	4.38	3.72	1.51	1.91	2.35	0.33			
15	NT2RM4001203	6.43	5.54	5.53	5.95	1.89	1.97	3.96	4.4	1.73	*		-
	NT2RM4001204	9.94	10.43	11.48	7.05	1.89	2.44	3.49	2.67	2.11	*	**	-
	NT2RM4001217	24.69	17.41	30.8	23.78	12.47	18.57	27.41	26.41	29.34			
	NT2RM4001245	156.95	84.48	149.16	130.37	116.53	157.67	151.03	141.35	178.46			
	NT2RM4001247	4.65	4.91	11.8	4.49	3.5	3.11	6.79	3.17	2.29			
	NT2RM4001256	9.61	7.67	12.78	9.59	5.91	6.14	7.73	8.06	8.51			
20	NT2RM4001258	70.47	64.71	70.52	44.98	46.66	50.08	53.38	45.51	40.98	**	**	-
	NT2RM4001267	5.89	4.4	10.4	6.42	2.33	2.85	4.9	3.94	4.52			
	NT2RM4001273	1.34	2.22	3.89	5.02	1.41	1.99	4	2.5	2.16			
	NT2RM4001281	8.06	5.61	14.03	10.91	4.33	7.34	4.05	7.62	5.35			
	NT2RM4001286	51.19	32.28	36.36	29.23	18.59	18.64	13.09	20.76	31.46			
	NT2RM4001290	8.38	5.81	13.36	7.76	4.34	4.65	5.33	4.36	7.29			
25	NT2RM4001309	98.2	68.64	139.85	90.19	105.33	108.01	85.7	73.37	76.26			
	NT2RM4001313	6.16	7.7	10.44	8.55	3.72	5.52	2.76	5.94	3.03			
	NT2RM4001316	10.67	13.16	19.79	13.68	8.94	6.99	6.58	5.71	5.93	*		-
	NT2RM4001320	20.75	22.22	27.83	18.9	15.02	17.67	25.16	19.45	25.01			
	NT2RM4001321	3.2	9.27	5.51	7.64	4.65	3.21	6.77	5.74	7.05			
	NT2RM4001325	6.99	10.29	13.71	11.04	4.07	7.04	5.14	7.06	21.4			
30	NT2RM4001333	11.2	7.57	11.93	8.81	7.22	5.3	2.36	6.09	14.33			
	NT2RM4001340	59.12	52.84	78.91	69.02	66.75	67.91	59.71	47.75	38.99			
	NT2RM4001344	6.4	4.63	10.13	7.69	4.29	5.37	3.9	5.77	3.72			
	NT2RM4001347	414.8	327.64	302.6	368.33	392.69	323.06	333.75	373.98	353.9			
	NT2RM4001357	6.26	7.97	8.82	6.78	6.02	4.63	3.22	2.89	2.9	**		-
	NT2RM4001360	8.63	8.04	10.78	8.59	6.1	3.5	4.75	7.61	3.39			
35	NT2RM4001371	15.56	11.85	10	11.21	16.5	13.92	36.9	13.45	6.6			
	NT2RM4001377	21.16	11.62	19.22	16.27	7.45	12.65	8.88	10.18	9.45			
	NT2RM4001382	16.22	9.22	22.97	11.49	7.37	7.19	3.28	8.65	16.08			
	NT2RM4001384	4.53	5.9	14.13	5.13	2.13	2.71	2.62	2.27	2.98			
	NT2RM4001400	10.43	9.23	12.46	8.14	5.92	4.37	4.37	6.39	3.72	*	**	-
	NT2RM4001409	4.67	5.55	8.19	6.09	3.26	2.83	3.17	3.27	3.39			
40	NT2RM4001410	6.89	14.26	12.51	8.64	5.38	3.51	3.98	6.53	3.24			
	NT2RM4001411	25.9	30.99	34.06	31.33	32.6	28.51	31.72	28.52	32.83			
	NT2RM4001412	825.39	1226.8	1011.2	1004.1	804.98	983.25	1210.2	810.05	943.27			
	NT2RM4001414	12.79	6.6	16.28	6.35	2.72	5.16	2.14	4.73	3.09	*		-
	NT2RM4001436	63.2	35.96	69.06	56.83	54.08	67.38	42.65	35.42	49.83			
	NT2RM4001437	26.18	27.89	39.17	20.31	15.52	18.05	16.35	28.68	22.74	*		-
45	NT2RM4001444	3.41	3.61	9.9	6.98	3.02	1.89	2.57	2.59	2.26			
	NT2RM4001454	19.23	20.25	21.89	16.73	15.4	12.09	15.71	18.45	13.57	*	*	-
	NT2RM4001455	5.88	19	6.35	4.26	2.07	3.65	1.94	1.57	2.98			
	NT2RM4001483	8.69	16.03	11.64	7.61	4.41	5.78	3.96	3.81	3.42	*		-
	NT2RM4001489	12.59	12.07	8.74	5.56	6.34	2.86	4.94	5.52	3.23	*	**	-
	NT2RM4001495	36.43	24.24	20.4	12.41	16.18	17.63	5.62	16.36	11.58			
50	NT2RM4001499	22.29	18.15	30.48	16.01	14.05	14.71	4.23	11.08	11.85	*		-
	NT2RM4001515	6.81	5.91	14.18	6.91	2.64	4.03	2.9	4.57	2.36			
	NT2RM4001519	8.21	4.24	9.85	5.65	1.45	0.78	1.08	3.15	1.34	*		-
	NT2RM4001522	8.19	6.53	12.02	6.15	2.52	1.81	2.28	3.64	1.62	*		-
	NT2RM4001523	73.84	75.98	71.57	35.61	37.16	20.7	26.91	23.43	33.3	**	**	-
	NT2RM4001550	10.75	6.21	9.98	6.43	6.16	2.2	5.6	2.68	8.03			
55	NT2RM4001553	11.94	9.8	11.96	9.12	5.14	4.64	3.81	2.93	3.19	*	**	-
	NT2RM4001554	151.86	72	141.69	164.83	103.78	171.98	80.79	76.13	147.24			
	NT2RM4001557	51.14	42.32	58.99	56.35	49.65	76.92	34.69	30.81	38.74	*		-

Table 415

	NT2RM4001565	12.7	17.39	26.89	14.14	12.4	12.69	7.45	6.92	4.69	*	-
	NT2RM4001566	17.21	11.12	20.03	22.75	14.87	13.43	10.31	12.88	15.08		
5	NT2RM4001569	3.45	2.79	9.43	4.65	1.24	1.1	2.19	2.38	1.74		
	NT2RM4001579	7.75	7.8	9.32	7.49	3.8	1.35	2.94	2.54	2.36	**	-
	NT2RM4001582	6.95	5.09	5.63	5.76	1.73	2.34	1.66	1.19	2.1	**	-
	NT2RM4001589	113.7	167.05	103.64	41.43	57.6	46.23	27.72	15.73	11.4	* **	-
	NT2RM4001592	6.17	5.42	14.24	6.52	2.18	4.41	4.13	6.42	4.93		
10	NT2RM4001594	386.49	313.56	285.69	287	185.32	238.47	160.25	299.69	275.08		
	NT2RM4001597	6.23	6.27	13.54	6.73	3.64	4.25	2.96	4.23	3.88		
	NT2RM4001605	16.38	18.33	22.25	14.56	11.19	8.87	10.5	12.13	9.23	* *	-
	NT2RM4001609	23.54	15.9	22.4	13.71	9.55	9.27	6.4	7.54	6.99	* **	-
	NT2RM4001610	10.55	8.52	11.74	9.35	5.13	4.46	6.11	6	5.63	*	-
	NT2RM4001611	14.22	14.7	15.89	10.73	7.27	6.47	6.73	5.19	3.38	** **	-
15	NT2RM4001618	13.74	16.13	14.23	8.24	4.82	5.02	4.84	2.49	3.4	** **	-
	NT2RM4001622	5.3	5.16	10.27	7.37	3.16	3.66	2.49	3.88	1.85		
	NT2RM4001624	7.85	5.37	11.44	5.27	1.81	3.96	3.07	2.98	3.67	*	-
	NT2RM4001625	8.28	12.41	10.38	15.36	14.48	2.63	7.15	9.31	10.39		
	NT2RM4001629	14.67	21.52	22.9	19.11	13.87	22.31	12.28	12.44	12.55	*	-
	NT2RM4001632	325.71	457.93	338.97	242.41	290.06	370.51	594.61	333.67	482.68		
20	NT2RM4001642	5.97	4.92	5.47	4.64	2.19	2.19	0.94	2.25	0.91	* **	-
	NT2RM4001647	18.42	12.21	17.82	18.58	14.27	17.66	13.87	14.03	11.49		
	NT2RM4001650	27.91	31.97	47.33	36.24	30.14	33.6	22.2	16.78	26.83		
	NT2RM4001662	12.58	10.55	10.99	18.39	7.75	15.61	11.98	12.75	8.09		
	NT2RM4001666	7.92	11.39	9.77	4.29	5.85	7.46	4.49	4.14	4.36	* **	-
	NT2RM4001670	25.82	19.71	20.86	17.87	11.22	17.38	19.89	23.01	24.94		
25	NT2RM4001682	8.89	10.21	10.73	7.71	7.31	3.19	3.94	4.22	3.18	**	-
	NT2RM4001710	8	9.89	13.67	6.48	2.86	3.01	1.39	4.38	1.64	* *	-
	NT2RM4001712	6.13	6.94	9.77	4.06	2.96	2.15	2.17	4.16	1.89	* *	-
	NT2RM4001714	18.44	20.46	18.31	8.4	3.92	5.06	6.84	3.44	4.9	** **	-
	NT2RM4001715	22.24	32.3	32.67	17.97	6.58	16.35	15.07	7.8	8.58	* *	-
	NT2RM4001727	17.83	12.1	16.99	14.9	8.57	19.16	13.54	13.69	14.31		
30	NT2RM4001731	9.18	5.56	7.2	4.83	1.9	3.44	2.33	4	3.02	* *	-
	NT2RM4001735	15.03	8.65	13.3	10.72	9.69	6.1	6.95	9.42	9.18		
	NT2RM4001739	3.31	4.05	7.1	6.51	1.7	2.71	2.2	2.1	1.76		
	NT2RM4001741	5.03	6.39	6.03	4.45	2.85	1.9	3.44	3.9	2.72	* **	-
	NT2RM4001746	27.18	35.45	35.48	20.34	15.62	12.62	17.33	16.68	21.57	** *	-
	NT2RM4001754	47.9	62.7	56.46	79.4	39.53	40.99	48.7	37.13	39.56		
35	NT2RM4001757	4.77	10.74	3.2	6.77	1.73	2.53	2.83	4.79	2.31		
	NT2RM4001758	8.89	8.75	6.1	8.32	3.51	5.38	5.98	8.51	9.88		
	NT2RM4001768	3.37	0.36	1.12	5.36	1.88	2.21	0.35	1.5	0.9		
	NT2RM4001775	6.53	3.93	5.59	8.91	3.97	5.25	4	3.54	3.16		
	NT2RM4001776	28.42	28.92	28.25	33.08	15.74	17.3	19.26	20.43	19.52	**	-
	NT2RM4001783	4.96	4.55	4.74	5.37	2.6	3.32	2.42	2.8	2.84	**	-
40	NT2RM4001793	14.95	13.94	19.52	14.23	7.85	12.31	14.46	13.31	17.08		
	NT2RM4001810	23.52	24.77	30.47	26.07	19.33	20.51	34.17	38.53	24.95		
	NT2RM4001813	9.51	6.59	9.34	11.22	3.7	8.5	12.3	12.03	14.87	*	+
	NT2RM4001818	4.65	1.67	8.39	7.01	2.88	5.12	5.55	5.88	5.41		
	NT2RM4001819	80.16	35.79	68.43	71.44	40.61	80.22	41.62	48.42	47.06		
	NT2RM4001823	10.42	6.03	12.1	10.8	5.46	5.65	5.68	8.09	6.63		
45	NT2RM4001828	3.57	2.82	6.95	5.66	1.65	1.21	2.42	1.92	2.31		
	NT2RM4001835	4.94	4.42	12.73	8.71	1.8	3.96	4.63	4.11	5.11		
	NT2RM4001836	5.12	3.81	8.12	5.95	1.63	1.85	2.61	3.45	2.12		
	NT2RM4001841	6.73	6.82	10.79	10.33	4.39	6.34	6.7	6.45	7.77		
	NT2RM4001842	2.89	4.82	4.7	7.5	2.83	2.4	3.82	3.29	2.69		
	NT2RM4001843	48.57	28.12	59.83	46.07	40.73	45.97	28.16	28.11	29.49		
50	NT2RM4001856	14.1	14.11	19.35	11.87	5.04	7.86	7.47	6.5	8.37	* *	-
	NT2RM4001858	20.02	12.7	24.11	14.43	7.61	10.18	17.09	15.78	20.13		
	NT2RM4001861	14.08	10.48	18.84	13.72	9.53	5.84	12.28	18.05	13.36		
	NT2RM4001863	27.15	15.67	30.03	15.24	18.38	17.87	16.63	16.94	11.79		
	NT2RM4001865	8.03	9.87	15.29	7.44	8.43	5.34	6.68	5.7	6.95		
	NT2RM4001869	12.34	16.35	21.36	13.19	9.35	9.55	19.86	14.54	12.88		
55	NT2RM4001873	6.51	9.79	10.96	7.15	2.28	3.17	4.21	4.29	2.39	*	-
	NT2RM4001876	13.28	10.02	39.33	14.58	13.74	11.65	8.08	13.34	13.31		
	NT2RM4001880	22.41	18.46	28.54	18.91	14.09	15.45	13.74	18.99	19.02		

Table 416

	NT2RM4001885	71.31	49.62	81.98	53.98	43.04	45.93	68.83	64.57	48.87			
	NT2RM4001889	10.85	7.93	15.01	8.59	4.29	4.67	4.77	6.73	3.99			
5	NT2RM4001894	30.62	32.08	44.07	33.7	34.28	35.89	33.56	30.42	25.18			
	NT2RM4001897	8.76	10.37	11.73	7.79	4.55	4.65	3.35	3.47	2.33	*	**	-
	NT2RM4001899	4.19	5.18	10.36	7.76	5.5	4.54	4.99	5.17	3.45			
	NT2RM4001905	8.04	9.67	9.34	12.13	4.62	8.49	17.26	7.42	9.7			
	NT2RM4001922	10.52	7.5	13.46	10.13	4.31	4.77	4.26	7.33	9.75			
10	NT2RM4001930	42.04	27.93	35.21	26.34	18.3	24.57	35.05	37.8	24.49			
	NT2RM4001938	11.86	11.93	17.44	9.19	6.81	6.54	7.09	10.88	7.99	*		-
	NT2RM4001940	40.15	39.79	42.12	29.48	25.03	26.5	19.62	21.25	18.41	**	**	-
	NT2RM4001942	7.8	8.46	12.88	6.27	3.74	4.54	3.46	2.56	2.64	*		-
	NT2RM4001953	2.56	5.71	6.3	5.41	2.95	2.84	2.21	3.3	2.4			
	NT2RM4001965	9	9.88	11.74	9.82	12.01	7.33	7.4	10.04	8.64			
15	NT2RM4001966	51.68	52.74	61.28	70.45	40.89	59.05	88.01	53.06	72.22			
	NT2RM4001969	9.53	10.35	15.87	9.41	5.57	8.09	5.17	7.89	12.14			
	NT2RM4001974	12.36	21.98	16.69	16.74	8.35	12.5	5.35	17.32	22.51			
	NT2RM4001979	23.89	19.24	22.43	14.04	16.93	18.71	17.76	22.69	22.51			
	NT2RM4001980	94.16	97.18	94	64.27	69.09	81.77	75.44	72.18	71.63	*	**	-
	NT2RM4001984	9.67	8.39	11.58	7.27	4.78	4.84	2.35	4.35	2.8	*	**	-
20	NT2RM4001987	7.05	10.61	11.42	5.92	3.18	5.3	2.56	4.02	2.33	*	**	-
	NT2RM4002013	15.54	16.72	17.68	12.71	8.41	7.52	18.32	10.81	11.68	*		-
	NT2RM4002018	18.51	18.01	18.38	23.63	14.06	15.67	18.72	13.95	13.04			
	NT2RM4002033	6.2	4.97	12.78	7.92	4.07	6.05	2.33	3.53	3.27			
	NT2RM4002034	9.06	7.36	15.25	10.05	4.49	7.82	4.17	10.89	9.93			
	NT2RM4002044	29.35	20.58	32.58	18.82	16.22	17.19	21.2	22.06	24.1			
25	NT2RM4002047	20.66	17	25.07	17.46	15.74	9.49	16.1	15.14	16.08			
	NT2RM4002054	31.19	30.54	36.08	20.52	17.55	11.13	16.47	15.97	19.8	**	**	-
	NT2RM4002055	21.78	18.7	21.85	12.08	11.37	8.76	14.04	16.74	17.09	**	*	-
	NT2RM4002059	10.36	12.77	15.52	6.8	7.53	3.99	4.33	4.04	2.53	*	**	-
	NT2RM4002061	9	11	9.24	10.93	6.62	5.33	6.65	4.88	4.34	**		-
	NT2RM4002062	97.19	68.62	99.9	109.04	77.98	163.08	52.62	59.12	71.01			
30	NT2RM4002063	8.61	5.55	11.75	8.31	3.06	3.95	4.25	4.81	4.94			
	NT2RM4002066	7.96	8.56	22.27	12.72	22.89	4.97	2.38	10.48	2.89			
	NT2RM4002067	10.87	18.12	21.45	11.17	10.75	7.5	4.23	11.4	5.44			
	NT2RM4002073	34.87	29.49	32.35	16.42	15.53	13.85	5.51	8.53	5.15	**	**	-
	NT2RM4002074	13.13	16	13.48	9.5	9.68	8.27	2.81	4.16	5.74	**	**	-
	NT2RM4002075	12.66	9.69	13.41	10.12	6.41	6.32	4.7	4.84	4.77	**		-
35	NT2RM4002076	5.05	4.42	4.84	7.24	1.99	2.02	1.56	2.18	1.6	**		-
	NT2RM4002078	61.79	41.41	62.13	44.43	23.08	49.45	46.13	69.55	79.59			
	NT2RM4002081	12.47	11.63	21.52	11.3	5.46	8.36	4.38	5.75	7.06	*		-
	NT2RM4002082	28.78	23.31	28.71	31.25	27.4	16.48	17.58	15.02	15.49	**		-
	NT2RM4002093	9.61	9.51	12.26	11.79	5.58	6.25	5.84	7.44	5.28	*		-
	NT2RM4002109	5.91	6.93	10.41	8.11	5.84	4.18	3.3	3.14	2.63	*		-
40	NT2RM4002115	9.41	7.3	7.03	6.27	4.66	1.89	3.74	1.98	2.7	**		-
	NT2RM4002118	37.45	58.41	50.21	20.19	26.02	17.58	13.66	5.39	8.55	*	**	-
	NT2RM4002128	8.86	5.7	4.74	7.73	3.31	3.74	6.06	4.03	5.02			
	NT2RM4002137	10.72	7.46	13.29	9.5	3.57	7.97	5.86	8.61	6.51			
	NT2RM4002139	4.03	2.83	9.32	5.97	2.53	3.54	2.11	4.86	1.91			
	NT2RM4002140	13.52	11.7	18.78	14.09	10.76	8.24	10.97	13.55	10.92			
45	NT2RM4002145	9.85	17.52	15.66	7.49	7.31	6.12	9.29	8.25	6.8	*		-
	NT2RM4002146	53.03	50.09	60.28	48.49	40.37	39.91	51.33	53.96	59.3	*		-
	NT2RM4002161	42.85	50.59	52.56	30.41	24.15	28.58	27.02	24.86	21.9	**	**	-
	NT2RM4002174	10.01	10.09	12.11	7.53	4.92	3.2	3.7	2.29	3.16	*	**	-
	NT2RM4002178	12.55	13.35	13.21	15.19	8.36	11.5	9.67	9.09	6.99	**		-
	NT2RM4002180	29.73	19.51	29	18.7	7.96	18.84	13.92	22.12	26.06			
50	NT2RM4002185	43.79	41.64	55.35	22.67	17.47	26.66	26.11	42.39	45.09	**		-
	NT2RM4002189	7.67	6.99	10.29	5.96	5.23	2.74	5.92	2.8	1.53	*		-
	NT2RM4002194	41.77	35.89	39.22	19.41	14.19	21.77	29.88	28.52	30.53	**	**	-
	NT2RM4002198	65.16	103.48	83.23	24.68	28.75	36.65	24.56	34.17	38.68	**	*	-
	NT2RM4002205	10.02	12.63	11.47	6.5	3.78	3.22	4.61	2.19	6.22	**	**	-
	NT2RM4002213	21.88	23.22	24.09	13.45	7.91	12.62	20.89	17.99	21.66	**		-
55	NT2RM4002216	7.77	7.03	5.96	10.01	6.36	6.33	6.06	4.45	5.36			
	NT2RM4002226	41.57	37.46	37.46	67.73	42.88	64.51	42.92	35.21	34.67			
	NT2RM4002237	7.28	7.73	10.06	4.52	3.54	3.6	2.94	7.15	4.84	**		-

Table 417

	NT2RM4002240	41.31	33.08	34.96	23.86	21.39	33.98	42.08	38.96	43.61			
	NT2RM4002251	3.39	3.69	6.47	4.89	3.61	2.4	2.93	2.15	17.6			
5	NT2RM4002256	4.28	3.3	5.05	4.37	2.61	2.38	2.35	2.33	1.46	*	-	-
	NT2RM4002262	25.4	21.79	26.58	14.04	9.23	12.13	20.41	14.34	24.05	**	-	-
	NT2RM4002266	32	29.71	28.68	24.62	15.02	21.58	34.67	32.96	37.69	*	+	+
	NT2RM4002276	14.45	13.71	15.67	14.53	13.36	16.53	16.37	10.08	9			
	NT2RM4002278	18.11	14.14	14.01	7.25	7.14	10.52	3.65	6.03	7.88	*	-	-
10	NT2RM4002281	9.29	5.59	12.79	12.53	4.74	10.06	6.18	9.79	8.22			
	NT2RM4002287	17.77	15.59	14.41	11.94	5.05	12.57	14.23	12.4	14.92			
	NT2RM4002294	5.99	6.14	6.14	5.51	2.38	5.99	3.64	2.35	2.91	**	-	-
	NT2RM4002298	64.75	62.55	58.47	42.58	28.72	43.54	69.57	64.59	61.46	**	-	-
	NT2RM4002301	3.57	3.23	3.63	6.49	2.3	3.07	3.59	2.99	3.21			
	NT2RM4002306	25.86	19.13	24.79	14.02	9.84	17.37	30.57	32.67	35.82	*	+	+
15	NT2RM4002323	7.61	6.27	5.98	7.59	3.26	7.4	8.04	6.9	4.8			
	NT2RM4002334	14.45	6.6	16.75	21.2	9.98	15.23	10.19	12.3	13.22			
	NT2RM4002339	36.85	25.91	51.52	34.79	27.9	40.82	21.13	20.38	29.16			
	NT2RM4002344	17.19	8.04	22.21	10.94	8.27	8.93	15.04	14.72	15.42			
	NT2RM4002345	7.58	5.39	12.54	5.63	3.79	3.52	2.31	4.45	2.41			
	NT2RM4002352	44.06	33.96	54.03	33.98	35.28	37.69	25.21	30.31	27.97			
20	NT2RM4002362	39.95	26.35	45.23	28.03	24.7	27.77	28.92	25.64	24.85			
	NT2RM4002373	9.44	6.99	7.1	8.69	3.38	4.42	5.88	3.57	3.37	*	-	-
	NT2RM4002374	0.94	1.53	2.98	5.8	0.19	1.91	2.19	2.71	2.57			
	NT2RM4002376	14.29	7.3	14.66	12.48	5.38	11.68	12.33	14.05	16.09			
	NT2RM4002383	5.57	4.67	12.54	5.61	3.39	2.94	3.24	5.28	5.45			
	NT2RM4002390	8.2	7.31	15.14	6.97	3.2	6.3	4.57	6.71	7.54			
25	NT2RM4002398	16.51	8.98	16.5	15.05	12.49	8.92	7.11	8.76	5.38			
	NT2RM4002409	3.91	1.86	5.55	4.87	1.55	2.44	2.22	2.93	0.87			
	NT2RM4002414	18.86	15.16	32.88	21.65	23.59	21.32	20.36	19.06	17.22			
	NT2RM4002438	3.96	4.99	8.08	7.18	3.61	4.94	4.85	4.1	2.07			
	NT2RM4002440	32.39	17.01	28.92	38.22	20.77	30.03	30.94	26.11	25.22			
	NT2RM4002446	10.16	7.87	12.29	14.29	6.56	8.04	5.21	8.63	33.19			
30	NT2RM4002450	5.69	5.77	10.55	7.51	2.92	4.53	1.81	3.53	7.42			
	NT2RM4002452	15.3	12.15	20.1	12.34	7.95	8.52	9.04	11.33	9.95			
	NT2RM4002457	5.93	4.98	9.2	5.51	3.34	2.74	3.42	3.45	3.16			
	NT2RM4002458	5.3	7.18	9	7.94	5.54	4.54	4.93	4.05	3.12			
	NT2RM4002460	5.82	9.3	10.61	8.18	6.55	6.42	6.02	6.26	3.91			
	NT2RM4002464	5.03	6.81	7.71	5.37	2.82	2.94	2.52	3.29	2.23	*	-	-
35	NT2RM4002479	40.28	37.05	46.08	41.61	24.81	36.24	37.84	34.54	34.16			
	NT2RM4002482	13.66	18.31	28.36	15.72	10.35	15.81	9.15	8.99	19.35			
	NT2RM4002489	15.44	12.03	20.84	12.49	8.35	8.73	7.84	10.26	14.04			
	NT2RM4002493	8.53	4.66	11.35	5.77	2.46	3.69	1.55	3.88	3.31			
	NT2RM4002499	16.96	15.44	26.91	11.24	8.53	18.09	18.09	16.97	14.06			
	NT2RM4002504	24.74	20.57	17.4	17.01	12.22	12.67	5.73	8.11	7.63	**	-	-
40	NT2RM4002506	9.92	11.26	12.04	6.45	4.68	4.22	2.88	4.99	2.98	**	-	-
	NT2RM4002510	17.14	20.34	27.62	13.7	8.64	11	8.3	5.68	5.29	*	-	-
	NT2RM4002527	5.27	5.32	5.24	9.73	2.73	4.8	7.63	6.1	4.65			
	NT2RM4002532	2.04	3.38	12.81	3.92	2.01	0.75	2.59	1.83	2.16			
	NT2RM4002534	6.24	4.2	12.1	6.74	2.8	3.26	1.86	3.47	2.45			
	NT2RM4002535	9.02	8.87	16.41	7.91	3.99	2.92	0.97	4.02	2.94	*	-	-
45	NT2RM4002554	6.47	7.38	8.92	4.87	2.87	2.29	2.04	1.83	1.15	**	-	-
	NT2RM4002558	10.72	10.21	14.55	8.7	6.67	5.1	5.89	7.82	7.9	*	-	-
	NT2RM4002565	7.12	9.02	9.26	6.37	4.46	3.35	5.55	4.05	5.46	*	-	-
	NT2RM4002567	8.35	6.05	12.48	6.62	4.6	3.2	2.87	5.5	6.18			
	NT2RM4002571	3.38	3.03	4.65	5.3	2.26	1.53	2.86	1.83	1.84			
	NT2RM4002572	3.42	1.92	7.29	5.02	1.66	0.9	0.78	0.74	1.09			
50	NT2RM4002577	17.78	12.61	20.74	8.52	7.02	10.13	3.18	8.47	5.97	*	-	-
	NT2RM4002583	26.66	37.71	48	24.28	17.87	13.18	6.06	13.66	11.34	*	-	-
	NT2RM4002584	24.55	35.28	41	25.45	15.38	14.04	7.11	11.26	5.72	**	-	-
	NT2RM4002593	13.18	11.32	14.62	7.42	4.85	4.9	3.83	4.05	2.43	**	-	-
	NT2RM4002594	17.08	15.66	20.52	11.9	10.96	5.12	3.63	4.19	2.45	*	-	-
	NT2RM4002604	8.24	6.88	8.88	5.84	3.74	2.95	2.65	0.99	1.52	*	-	-
55	NT2RM4002614	14.57	8.99	9.81	12.06	5.4	4.41	5.49	5.87	6.71	*	-	-
	NT2RM4002616	31.41	23.47	38.09	26.19	21.94	0.64	13.84	17.54	27			
	NT2RM4002623	6.22	6.78	13.92	7.63	3.69	4.81	3.87	5.8	5.63			

Table 418

	NT2RM4002634	8.22	4.99	13.16	9.11	4.37	3.31	1.21	3.45	2.39			
	NT2RM4002636	6.59	6.68	10.88	5.63	3.08	3.09	2.42	3.32	2.29	*	-	
5	NT2RP1000002	38.84	33.13	45.9	29.04	32.42	26.61	13.28	16.85	17.96	**	-	
	NT2RP1000006	16.16	12.37	15.85	10.42	5.99	5.72	9.46	7.81	8.28	*	**	-
	NT2RP1000015	7.32	9.13	12.92	6.24	3.84	1.22	4.29	2.29	4.19	*	-	
	NT2RP1000018	7.99	5.66	4.74	10.16	3.74	4.75	7.93	7.02	6.47			
	NT2RP1000034	93.68	89.94	88.11	64.65	53.66	86	72.54	94.51	102.97			
10	NT2RP1000035	18.17	13.62	22.35	15.17	8.64	11.35	7.31	9.51	10.39	*	-	
	NT2RP1000040	16.4	12.21	23.34	12.38	8.64	8.09	5.04	9.39	4.11	*	-	
	NT2RP1000042	3.77	4.47	8.66	6.24	2.47	2.4	1.5	1.51	0.43	*	-	
	NT2RP1000048	11.21	13.33	14.61	8.93	8.14	5.51	8.58	7.29	5.06	*	*	-
	NT2RP1000050	5.73	12.28	7.67	5.34	2.29	5.33	2.26	2.09	1.81	*	-	
	NT2RP1000056	13.77	17.86	17.27	9.41	8.14	4.91	6.92	3.33	2.85	**	**	-
15	NT2RP1000058	2.7	2.41	1.36	4.8	0.95	2.39	2.76	1.39	2.38			
	NT2RP1000063	17.16	17.65	11.27	8.7	3.73	4.52	5.36	8.5	8.3	*	*	-
	NT2RP1000068	29.14	23.7	36.49	16.13	16.83	12.51	21.73	27.58	32.86	*	-	
	NT2RP1000072	39.99	32.45	48.63	26.8	23.08	25.9	35.59	35.1	31.66	*	-	
	NT2RP1000073	30.81	35.89	43.46	17.05	9.38	10.22	9.08	9.67	9.54	**	**	-
	NT2RP1000078	9.27	9.25	12.57	6.24	5.48	5.5	2.69	7.89	4.73	*	*	-
20	NT2RP1000079	5.69	6.1	5.36	5.53	2.36	2.02	2.99	2.23	1.19	**	-	
	NT2RP1000080	8.49	8.44	8.35	6.53	2.81	2.65	4.1	3.05	2.07	*	**	-
	NT2RP1000086	8.5	9.4	9.89	12.4	14.28	6.92	7.93	6.49	7.97	*	-	
	NT2RP1000087	90.2	68.37	62.22	84.59	56.96	88.52	51.31	53.27	70.97			
	NT2RP1000089	42.88	33.03	33.53	24.16	25.57	29.27	22.12	38.13	29.4	*	-	
	NT2RP1000090	36.01	34.5	36.9	42.34	38.64	45.67	26.7	26.11	29.29	*	**	+
25	NT2RP1000100	842.61	1542.2	1396.7	306.69	827.1	384.76	1509.9	896.88	763.21	*	-	
	NT2RP1000101	35.43	98.15	94.63	31.12	33.53	50.26	29.26	23.54	17.24			
	NT2RP1000111	7.76	7.95	10.33	5.26	2.18	1.26	2.31	1.62	2.57	*	**	-
	NT2RP1000112	23.37	50.82	42.64	24.98	11.61	20.15	18.5	13.38	13.37	*	-	
	NT2RP1000124	25.62	22.22	19.79	7.84	2.34	7.4	4.52	4.07	4.19	**	**	-
	NT2RP1000125	10.72	8.67	12.07	7.14	2.95	7.79	4.48	7.44	4.25	*	-	
30	NT2RP1000129	53.88	53.28	57.25	42.69	30.82	50.19	47.48	64.98	53.17			
	NT2RP1000130	19.47	14.75	28.76	11.14	15.19	12.69	8.3	10.06	14.98			
	NT2RP1000154	3.93	3.52	5.78	5.04	1.58	2.69	2	2.85	2.74			
	NT2RP1000163	9.61	17.58	16	11.58	5.58	5.03	6.39	4.65	5.07	*	-	
	NT2RP1000170	4.53	4.62	7.7	6.31	2.3	2.01	2.67	3.54	2.2			
	NT2RP1000174	9.99	10.63	9.3	6.41	2.75	3.81	5.44	4.09	3.96	**	**	-
35	NT2RP1000181	14.26	14.61	16.73	10.84	15.44	12.79	10.24	5.66	5.53	**	-	
	NT2RP1000191	12.96	10.86	7.92	16.4	11.07	15.31	6.1	13.72	9.91			
	NT2RP1000202	24.16	14.94	24.74	18.17	11.59	9.79	7.42	9.13	15.3			
	NT2RP1000239	9.53	5.6	7.62	9.29	2.89	11.94	8.48	12.01	11.59			
	NT2RP1000243	6.22	4.43	4.68	7.85	5.29	6.41	2.34	3.31	5.03			
40	NT2RP1000255	12.37	12.15	15.41	16.34	7.48	13.06	9.35	10.82	12.98			
	NT2RP1000259	10.81	8.35	10.69	9.6	2.44	9.12	13.53	11.26	13.39			
	NT2RP1000261	8.39	2.66	5.85	15.75	5.57	6.12	7.38	4.73	4.58			
	NT2RP1000269	2.25	3.12	1.21	5.48	2.06	2.18	4.74	1.71	2.26			
	NT2RP1000271	20.23	11.57	26.77	18.9	8.83	20.16	9.94	14.85	10.84			
	NT2RP1000272	2.12	2.3	9.68	5.22	1.59	2.18	2.89	2.48	2.25			
	NT2RP1000279	10.54	8.91	14.66	10.51	4.61	8.63	10.77	11.05	13.98			
45	NT2RP1000290	6.06	4.1	11.1	13.63	4.43	7.63	6.81	6.19	8.17			
	NT2RP1000293	3.83	4.19	7.55	5.54	1.62	3.86	2.95	1.13	3.16			
	NT2RP1000331	4.37	2.83	13.34	5.34	2.19	3.45	2.73	6.07	2.66			
	NT2RP1000333	10.16	8.8	16.01	10.64	5.56	6.94	8.71	5.87	8.68			
	NT2RP1000336	18.67	16.33	24.52	12.77	10.82	14.23	17.03	16.82	19.7			
	NT2RP1000347	3.46	4.07	7.92	6.45	3	4.58	4.14	3.03	3.73			
50	NT2RP1000348	34.17	39.38	47.03	19.99	17.54	15.37	14.54	7.37	12.73	**	**	-
	NT2RP1000349	3.22	4.33	6.7	6.49	4.16	3.15	4.9	4.23	3.34			
	NT2RP1000353	180.66	121.66	192.83	151.27	98.19	147.88	118.94	165.86	159.59			
	NT2RP1000356	8.01	8.29	12.26	8.92	4.2	7.42	6.21	5.29	12.39			
	NT2RP1000357	38.01	31.52	38.61	32.16	21.31	27.89	24.36	33.21	30.56			
	NT2RP1000358	9.65	6.55	14.28	10.15	5.03	7.68	4.14	4.11	2.37	*	-	
55	NT2RP1000360	11.08	7.25	16.85	18.78	9.48	8.41	8.09	9.21	9.08			
	NT2RP1000363	37.26	30.39	52.28	41.73	39.62	39.87	33.79	24.41	33.64			
	NT2RP1000376	6.26	6.27	9.53	5.76	4.97	3.76	4.87	4.58	3.63			

Table 419

	NT2RP1000386	37.77	48.73	51.62	24.07	21.15	29.99	24.61	14.84	15.66	*	**	-	-
	NT2RP1000407	20.7	11.19	17.51	22.94	11.29	15.13	8.7	15.9	29.09				
5	NT2RP1000409	24.93	20.8	32.63	23.46	10.36	22.79	11.36	15.76	11.35	*		-	
	NT2RP1000413	24.89	20.12	32.27	23.23	14.81	20.34	6.71	17.88	15.72				
	NT2RP1000416	9.92	9.55	19.32	9.98	6.1	6.11	5.35	8.54	6.35				
	NT2RP1000418	5.47	5.48	8.66	6.04	3.54	3.99	4.07	4.75	2.23				
	NT2RP1000420	22.79	21.95	33.37	16.39	16.84	13.03	9.29	9.88	11.08	*		-	
10	NT2RP1000434	13.91	15.33	17.37	9.5	9.94	9.87	16.13	15.05	16.89	**		-	
	NT2RP1000439	25.29	35.1	29.04	26.55	26.88	19.87	29.22	23.74	23.38				
	NT2RP1000443	20.2	15.54	27.59	12.04	8.66	7.66	5.79	6.64	10.23	*	*	-	-
	NT2RP1000447	8.08	15.72	18.03	9.49	4.04	7.9	4.98	7.69	18.07				
	NT2RP1000448	3.96	4.08	14.01	5.34	1.34	3.27	1.83	3.09	2.48				
	NT2RP1000451	4.39	7.13	7.39	6.28	2.08	2.05	2.16	2.95	1.76	*		-	
15	NT2RP1000458	7.7	7.09	11.38	7.06	4.06	2.49	4.41	2.72	2.94	*		-	
	NT2RP1000465	3.88	6.63	8.77	6.04	2.34	3	3.32	3.69	3.78				
	NT2RP1000468	10.59	11.91	14.42	9.41	9.31	7.51	8.52	6	7.58	*	*	-	-
	NT2RP1000470	5.79	2.68	10.41	5.27	1.59	4.02	1.42	2.51	2.5				
	NT2RP1000477	92.32	107.32	97.76	75.25	82.97	57.94	30.6	83.57	85.18	*		-	
	NT2RP1000478	15.37	19.72	31.56	11.53	8.67	8.82	5.74	7.51	6.16	*		-	
20	NT2RP1000481	26.31	30.78	29.03	24.24	26.58	11.39	8.04	10.78	12.11	**		-	
	NT2RP1000493	20.43	14.94	23.34	16.46	8.49	8.21	13.43	15.08	18.68				
	NT2RP1000513	46.32	35.58	52.07	60.82	43.2	48.5	36.73	37.16	31.64				
	NT2RP1000522	31.35	42.08	42.76	21.13	28.37	20.27	18.09	8.09	12.01	*	**	-	-
	NT2RP1000533	3.26	4.01	2.16	4.33	1.36	1.15	1.34	1	0.91	*	*	-	-
	NT2RP1000544	15.77	9.6	19.95	8.16	5.29	4.62	4.57	9.59	8.27	*		-	
25	NT2RP1000547	6.82	3.97	11.11	7.34	2.91	3.12	1.8	4.52	2.98				
	NT2RP1000551	7.57	6.25	20.26	6.79	4.51	3.96	3.69	5.06	3.29				
	NT2RP1000567	7.5	7.79	12.24	11.47	5.44	5.98	2.72	3.24	2.13	*		-	
	NT2RP1000574	10.39	7.63	14.91	6.66	4.35	2.94	2.41	2.6	3.1	*		-	
	NT2RP1000577	6.72	6.64	7.37	6.99	2.31	2.08	2	3.14	1.89	**		-	
	NT2RP1000579	6.59	4.72	10.08	5.29	2.62	2.74	2.3	1.65	2.85	*		-	
30	NT2RP1000581	11.66	12.4	16.41	11.21	8.47	7.93	11.76	7.04	4.88				
	NT2RP1000593	11.3	18.39	27.51	6.2	5.55	5.03	1.75	7.5	4.02	*	*	-	-
	NT2RP1000604	24.51	26.11	37.01	27.05	13.43	25.97	13.69	26.68	23.37				
	NT2RP1000609	11.66	13.43	21.36	13.95	9.13	6.99	3.92	12.37	8.18				
	NT2RP1000613	17.95	20.62	29.59	15.28	14.93	12.95	12.7	12.66	9.93	*		-	
	NT2RP1000622	5.38	3.34	9.13	5.39	2.07	1.13	2.51	2.21	0.46				
35	NT2RP1000627	4.69	3.23	5.07	4.57	2.03	1.44	1.45	1.18	1.66	**		-	
	NT2RP1000629	8.08	7.69	11.36	7.12	3.71	2.97	5.95	2.89	3.59	*		-	
	NT2RP1000630	7.73	9.3	8.35	7.9	4.49	4.92	4.54	3.4	2.81	**		-	
	NT2RP1000639	15.2	13.58	16.62	7.62	5.84	8.02	4.83	7.17	5.87	**	**	-	-
	NT2RP1000640	7.36	9.59	17.46	9.53	6.74	8.49	5.28	6.04	7.68				
	NT2RP1000646	4.24	5.51	12.04	6.49	2.96	3.77	4.79	5.79	2.35				
40	NT2RP1000659	23.32	18.8	20.24	8.66	11.69	4.88	4.8	5.33	5.99	**	**	-	-
	NT2RP1000674	5.93	7.17	11.83	6.23	3.45	3.46	1.76	2.58	3.57	*		-	
	NT2RP1000677	14.6	24.32	25.71	10.51	12.87	7.3	5.18	10.1	7.28	*	*	-	-
	NT2RP1000679	49.27	69.62	36.95	29.7	31.01	14.48	34.6	17.18	10.04				
	NT2RP1000688	8.01	6.65	7.8	7.2	2.8	2.42	6.02	2.46	2.38	*		-	
	NT2RP1000689	32.73	30.66	30.93	19.81	8.55	17.9	17.63	24.88	21.39	*	**	-	-
45	NT2RP1000695	17.35	14.65	15.87	10.45	3.47	5.36	2.82	6.77	7.19	*	**	-	-
	NT2RP1000701	7.19	4.67	10.84	7.55	5.43	2.64	2.6	6.76	2.45				
	NT2RP1000702	7.2	10.25	10.38	5.65	2.25	1.64	3.18	3.24	2.79	*	**	-	-
	NT2RP1000713	7.21	6.46	7.91	6.66	2.57	3.12	4.23	3.89	1.7	*		-	
	NT2RP1000721	15.01	8.63	33.56	6.6	3.3	4.77	2.95	3.62	2.32				
	NT2RP1000730	34.22	37.43	42.87	27.42	15.22	17.38	23.72	15.85	27.4	*	*	-	-
50	NT2RP1000733	9.95	10.41	8.91	8.92	3.88	5.5	7.94	2.92	5.71	*		-	
	NT2RP1000738	1.62	1.49	4.67	5.56	1.13	3.01	1.45	2.92	1.28				
	NT2RP1000739	19.87	17.5	27.32	13.76	6.59	15.22	15.07	28.31	27.46				
	NT2RP1000740	10.94	13.28	13.49	8.2	7.61	6.64	6.43	11.92	8.57	**		-	
	NT2RP1000746	3.82	5.92	7.73	5.64	4.22	2.64	2.76	3.96	2.29				
	NT2RP1000750	12.79	9.22	13.66	7.67	4.28	4.14	7.19	4.29	4.16	*	*	-	-
55	NT2RP1000751	10.42	10.46	12.4	8.57	5.65	4.98	4.2	5.02	5.07	*	**	-	-
	NT2RP1000767	10.46	7.93	10.97	6.93	2.33	2.54	1.45	2.21	3.81	*	**	-	-
	NT2RP1000769	4.03	4.96	3.53	5.29	3.09	2.58	3.04	5.45	2.56				



Table 420

	NT2RP1000780	19.06	11.29	17.88	11.55	12.19	16.36	7.6	12.92	8.96			
	NT2RP1000782	3.8	1.98	4.82	5.26	2.11	4.2	3.73	3.14	3.38			
5	NT2RP1000796	23.21	12.88	16.72	13.54	7.34	8.03	3.16	8.05	3.72	*	-	
	NT2RP1000797	8.11	7.21	12.88	6.28	1.88	5.78	3.95	3.02	3.35	*	-	
	NT2RP1000800	6.36	7.42	8.45	6.35	6.28	4.56	5.14	4.53	6.09	*	-	
	NT2RP1000825	6.14	10.58	8.77	8.58	2.44	5.18	5.33	5.66	4.12			
	NT2RP1000833	6.32	4.62	5.45	7.5	3.18	3.17	4.57	14.3	3			
10	NT2RP1000834	12.66	13.91	14.59	8.48	3.38	6.31	7.69	5.15	4.86	**	**	-
	NT2RP1000836	6.87	3.86	10.29	7.94	2.62	4.87	5.98	4.8	8.86			
	NT2RP1000837	4.76	2.83	13.29	5.43	1.86	3.86	3.47	3.54	3.43			
	NT2RP1000846	14.34	10.47	22.36	10.56	7.41	9.61	13.44	9.9	11.55			
	NT2RP1000847	17.63	21.93	45.89	20.33	17.15	15.75	21.4	13.87	15.38			
	NT2RP1000851	3.61	3.71	7.21	5	2.22	2.83	3.04	2.47	2.36			
15	NT2RP1000856	15.4	23.9	24.75	12.89	7.5	8.85	6.97	4.98	5.2	*	**	-
	NT2RP1000860	5.61	4.82	11.39	9.47	4.26	7.06	6.83	5.9	5.93			
	NT2RP1000902	10.67	7.93	13.65	15.09	8.49	17.09	4.79	9.4	9.51			
	NT2RP1000903	14.49	11.64	18.42	14.24	5.67	14.38	12.23	14.45	21.38			
	NT2RP1000905	11.82	8.69	16.54	6.96	4.86	6.4	5.28	5.14	5.21	*	-	
	NT2RP1000915	63.69	60.39	85.78	55.83	55.49	63.74	77.2	80.56	84.89			
20	NT2RP1000916	81.28	82.59	69.7	73.31	86.67	61.79	53.76	46.45	55.88	**	-	
	NT2RP1000921	71.86	52.08	72.49	27.75	31.76	38.72	21.98	23.9	25.92	*	**	-
	NT2RP1000943	6.66	5.16	12.72	6.58	6.6	3.97	5.26	4.45	3.75			
	NT2RP1000944	36.56	43.79	53.16	29.61	24.97	30.98	38.1	30.4	32.9	*	-	
	NT2RP1000947	229.13	162.3	242.56	211.36	169.75	208.5	187.13	230.69	193.69			
	NT2RP1000954	8.73	6.8	11.31	9.14	2.72	5.18	2.45	4.94	9.97			
25	NT2RP1000958	12.83	9.08	19.99	13.3	9.58	12.08	6.34	10.95	18.7			
	NT2RP1000959	51.88	27.73	29.26	17.4	13.14	15.25	9.23	12.74	9.9	*	-	
	NT2RP1000966	30.03	20.71	21.11	23.97	20.83	19.34	9.71	14.32	8.82	*	-	
	NT2RP1000974	16.61	13.83	23.36	13.15	11.64	14.93	7.2	7.22	7.83	*	-	
	NT2RP1000980	85.21	82.27	107.69	76.1	98.09	99.97	80	57.54	67.02			
	NT2RP1000981	14.84	15.8	18.22	12.59	10.09	13.46	23.72	16.48	19.72	*	-	
30	NT2RP1000988	21.09	10.38	16.08	11.96	7.25	9.77	8.85	10.68	7.42			
	NT2RP1001002	23.42	12.11	26.95	15.71	9.49	11.37	4.76	9.9	15.94			
	NT2RP1001004	3.32	4.31	12.34	5.67	1.55	2.59	2.12	2.77	2.28			
	NT2RP1001007	5.36	4.39	9.57	6.91	2.92	2.64	2.01	3.93	1.56			
	NT2RP1001011	5.98	6.54	6.16	6.28	2.04	2.66	2.36	4.56	2.02	*	-	
	NT2RP1001013	158.04	170.77	232.56	168.44	147.11	154.85	176.26	171.79	185.19			
35	NT2RP1001014	13.02	16.54	16.26	8.7	8	7.08	6.95	5.62	4.04	**	**	-
	NT2RP1001020	12.63	15.72	12.22	15.74	11.78	16.3	13.8	9.3	14.27			
	NT2RP1001023	16.05	14.39	18.27	13.53	16.55	17.02	5.93	11.56	12.91			
	NT2RP1001027	5.55	8.55	17.95	9.25	6.73	6.98	2.42	5.11	5.43			
	NT2RP1001031	5.67	4.8	13.77	5.12	2.4	2.34	1.77	3.34	2.2			
	NT2RP1001033	7.93	6.3	11.72	6.43	4.31	2.18	2.83	5.21	2.62	*	-	
40	NT2RP1001042	63.59	58.82	65.69	59.83	59.66	45.94	71.71	83.48	74.44	*	+	
	NT2RP1001045	9.83	10.21	13.29	8.26	4.99	5.95	3.06	4.58	3.85	*	**	-
	NT2RP1001073	12.41	18.41	17.37	9.19	7.47	7.07	4.73	4.66	5.19	*	**	-
	NT2RP1001079	38.47	46.51	52.14	22.17	29.03	25.48	25.23	15.77	15.85	*	**	-
	NT2RP1001080	21.61	6.66	17.31	12.32	7.25	12.68	6.59	12.92	8.31			
	NT2RP1001113	57.87	45.81	82.08	49.33	42.8	51.52	16.27	50.38	44.76			
45	NT2RP1001159	7.51	4.75	14.77	8.2	4.64	7.14	4.3	5.24	3.99			
	NT2RP1001173	4.39	5.23	11.13	7.48	3.15	1.42	1.19	2.31	1.17			
	NT2RP1001176	52.66	45.96	57.66	32.33	25.13	21.71	19.56	17.05	21.12	**	**	-
	NT2RP1001177	10.79	9.96	12.22	5.4	2.87	3.22	4.03	4.39	5.3	**	**	-
	NT2RP1001185	14.18	11.86	11.53	9.31	7.59	5.91	7.44	8.55	7.87	*	**	-
	NT2RP1001199	13.52	13.24	12.28	9.53	6.55	5.34	4.8	3.41	3.43	*	**	-
50	NT2RP1001205	93.58	72.48	94.49	51.42	53.78	86.93	52.32	75.19	84.87			
	NT2RP1001215	17.01	15.57	25.94	10.31	11.47	12.47	9.75	16.75	14.31			
	NT2RP1001225	11.8	18.2	17.52	11.07	6.07	5.97	4.13	11.34	3.6	*	*	-
	NT2RP1001245	6.59	5.31	9.93	6.03	2.96	4.57	2.73	3.24	2.91	*	-	
	NT2RP1001247	6.32	3.32	10.27	4.35	3.87	3.01	3.42	3.7	1.09			
	NT2RP1001248	15.25	12.77	20.45	15.52	14.1	11.98	13.33	13.26	15.08			
55	NT2RP1001253	84.68	116.5	77.6	46.18	37.13	24.55	27.4	9.2	25.65	*	**	-
	NT2RP1001286	5.14	8.32	6.96	7.42	3.69	3.62	3.74	2.33	2.9	*	-	
	NT2RP1001294	57.97	32.23	60.31	62.38	43.54	78.24	53.21	40.65	43.49			

Table 421

	NT2RP1001302	13.32	15.35	23.89	11.51	7.14	10.86	5.3	9.24	8.54	*	-
5	NT2RP1001310	78.58	77.83	107.95	40.93	36.67	35.03	13.95	16.52	15.88	**	**
	NT2RP1001311	12.5	10.19	20.17	13.97	8.87	11.71	8.61	11.48	9.2		
	NT2RP1001313	47.33	35.38	51.8	18.55	17.75	13.75	4.5	6.14	3.62	**	**
	NT2RP1001324	13.11	11.52	14.26	8.91	7.65	4.65	7	7.07	7.14	*	**
	NT2RP1001349	8.69	8.34	8.01	6.09	3.96	4.38	3.75	1.87	3.49	**	**
	NT2RP1001361	9.54	13.7	11.81	11.62	6.33	6.68	6.92	4.67	4.5	*	-
10	NT2RP1001379	13.14	11.82	15.33	13.1	6.47	9.99	7.99	14.61	8.34		
	NT2RP1001385	24.66	22.66	28.03	8.27	7.17	9.45	13.37	13.91	22.49	**	-
	NT2RP1001395	5.65	15.28	10.96	10.51	4.01	1.7	3.74	3.38	2.71		
	NT2RP1001410	13.37	15.22	15.93	8.65	10.09	5.26	5.57	5.86	7.15	*	**
	NT2RP1001424	28.73	25.67	34.05	32.06	24.11	29.55	22.85	15.99	24.49		
	NT2RP1001432	9.64	7.96	12.22	8.86	4.28	6.46	5.04	7.62	6.96		
15	NT2RP1001449	19.34	21.85	20.51	10.44	6.36	4.06	9.88	5.66	6.23	**	**
	NT2RP1001457	23.3	38.81	37.3	24.2	13.72	10.77	10.68	7.09	13.11	*	-
	NT2RP1001459	13.65	11.76	16.02	12.39	4.68	8.62	6.06	9.05	6.34	*	-
	NT2RP1001466	8.39	4.23	8.84	7.44	4.36	4.01	3.12	6.63	4.14		
	NT2RP1001475	11.89	17.85	12.86	11.05	10.38	6.52	5.05	12.24	6.54		
	NT2RP1001482	15.19	20.93	20.15	19.85	11.71	18.03	11.8	14.09	12.75	*	-
20	NT2RP1001494	3.95	5.63	10.18	5.63	2.65	3.16	2.73	3.52	2.73		
	NT2RP1001500	9.08	4.79	11.52	5.37	1.85	1.77	2.31	4.4	3.24		
	NT2RP1001517	18.13	18.45	18.1	8.4	4.89	3.69	7.15	5.46	6.44	**	**
	NT2RP1001540	28.09	31.99	28.56	25.07	15.6	22.78	25.04	22.39	21.45	*	-
	NT2RP1001543	20.19	16.33	24.14	16.6	10.69	13.4	7.07	16.07	9.64		
	NT2RP1001546	12.99	15.98	15.41	9.88	3.03	7.01	6.04	9.72	7.53	*	**
25	NT2RP1001550	8.32	14.7	14.31	7.95	15.82	5.57	6.4	9.76	9.43		
	NT2RP1001553	5.3	7.23	13.14	7.37	4.11	4.11	3.68	3.77	3.88		
	NT2RP1001555	54.76	52.6	55.46	31.87	21.44	34.31	43.17	41.32	32.44	**	*
	NT2RP1001563	39.08	33.85	48.64	38.88	21.62	23.18	31.1	28.26	33.8		
	NT2RP1001569	3.96	1.69	1.05	5.34	1.73	1.64	1.66	1.23	2		
30	NT2RP1001584	172.68	220.01	198.04	20.64	11.47	19.54	81.72	38.4	33.43	**	**
	NT2RP1001599	4.12	3.82	5.18	7.25	3.83	4.97	3.61	3.84	3.39		
	NT2RP1001616	4.03	1.77	2.09	6.09	1.64	4	2.04	2.76	1.59		
	NT2RP1001654	14.62	9.64	12.33	11.97	7.7	10.52	5.54	7.93	4.12	*	-
	NT2RP1001665	5.76	6.54	8.08	8.07	4.13	4.72	3.98	9.32	5.29		
	NT2RP1001679	8.69	7.12	7.86	9.21	3.08	4.08	4.04	6.22	5.1	*	-
35	NT2RP1001681	18.99	18.82	24.49	14.39	5.58	9.22	11.12	13.68	12.99	*	*
	NT2RP1001694	6.52	3.33	5.96	7.17	2.61	3.23	4.87	4.47	3.87		
	NT2RP2000001	6.24	4.74	8.49	6.13	5.97	4.89	6.42	5.79	3.58		
	NT2RP2000006	9.03	5.67	13.4	11.28	7.14	5.76	7.62	8.34	6.39		
	NT2RP2000007	10.8	6.31	17.13	11.11	4.89	9.86	6.74	8.3	8.67		
	NT2RP2000008	5.65	3.68	9.46	7.12	2.84	3.88	3.74	5.6	5.37		
	NT2RP2000010	6.84	5.53	11.05	6.98	2.63	4.35	3.2	3.54	2.21	*	-
40	NT2RP2000011	9.36	13.46	17.26	10.79	6.33	9.28	5.31	3.23	5.5	*	-
	NT2RP2000027	3.47	3.05	7.32	6.1	1.45	4.19	3.16	3	5.68		
	NT2RP2000028	4.74	6.32	6.74	8.06	2.13	4.67	3.21	1.66	4.03	*	-
	NT2RP2000032	3.24	7.28	8.03	10.28	5.5	7.28	3.26	3.13	4.05		
	NT2RP2000040	15.29	8.48	28.46	11.5	6.66	9.38	4.88	6.35	7.25		
	NT2RP2000042	21.14	15.46	35.04	11.42	8.01	11.22	12.48	11.99	17.82		
45	NT2RP2000045	5.83	3.94	13.32	7.43	3.18	3.46	3.62	5.2	3.95		
	NT2RP2000051	13.61	9.89	23.1	13.04	8.32	9.72	10.33	13.1	11.12		
	NT2RP2000054	16.51	12.89	19.57	11.63	9.66	11.02	9.64	7.65	7.91	*	-
	NT2RP2000056	6.15	6.7	14.22	6.37	4.1	4.09	7.75	7.98	8.74		
	NT2RP2000057	7.7	5.49	9.31	7.63	5.41	5.64	12.9	3.34	4		
	NT2RP2000067	7.64	15.12	15.54	18.12	16.74	10.35	9.45	6.54	9.35		
50	NT2RP2000070	522.83	440.99	557.3	464.06	449.31	610.82	418.05	662.99	650.93		
	NT2RP2000076	6.99	4.98	10.04	7.01	1.06	1.43	1.54	3.61	5.67		
	NT2RP2000077	14.55	10.4	23.49	9.32	7.18	6.26	8.55	8.84	8.57		
	NT2RP2000079	9.19	8.49	12.44	8.77	5.26	7.56	6.72	6.46	6.39	*	-
	NT2RP2000088	17.05	20.32	26.56	22.32	20.65	23.39	19.38	14.35	14.55		
	NT2RP2000091	33.24	19.21	39.37	24.16	20.9	17.89	11.58	9.95	7.77	*	-
55	NT2RP2000092	0.22	2.2	2.32	4.37	1.08	1	2.25	1.85	1.49		
	NT2RP2000097	10.19	11.77	12.54	11.39	5.79	8.17	7.35	3.3	4.01	**	-
	NT2RP2000098	14.34	13.24	18.96	13.26	6.07	9.3	5.46	9.38	18.63		

Table 422

	NT2RP2000108	10.87	8.33	17.31	10.58	6.71	6.74	4.11	5.62	13.35			
	NT2RP2000114	14.61	10.83	24.65	15.49	7.8	10.66	10.74	13.91	10.18			
5	NT2RP2000116	12.92	13.17	18.63	12.07	8.1	10.87	4.57	5.57	3.24	**	**	-
	NT2RP2000119	50.32	47.2	56.58	31.02	20.71	31.82	30.15	29.31	28.57	**	**	-
	NT2RP2000120	7.9	9.18	10.99	6.62	6.21	6.5	4.81	5.84	4.99	*	*	-
	NT2RP2000126	27.18	24.32	32.55	18.42	11.34	17.52	24.37	18.13	19.51	*		-
	NT2RP2000133	6.31	5.61	8.16	7.63	3.91	7.78	7.66	10.7	6.35			
10	NT2RP2000147	12.98	10.72	23.8	11.64	4.41	11.41	3.62	6.37	10.62			
	NT2RP2000153	4.49	6.28	13.18	7.15	3.26	3.2	2.66	3.8	4.92			
	NT2RP2000156	7.61	6.37	12.56	6.43	4.23	4.03	2.05	6.21	1.59			
	NT2RP2000157	64.87	55.86	69.1	57.96	47.99	49.02	51.12	61.28	54.87			
	NT2RP2000161	8.86	7.44	9.1	8.5	4.93	4.27	4.28	4.21	2.7	**		-
	NT2RP2000168	8.64	8.81	11.56	8.06	4.98	11.13	4.05	3.85	9.74			
15	NT2RP2000173	5.87	12.11	13.07	7.31	10.56	7.74	13.29	16.36	4.1			
	NT2RP2000175	6.28	5.9	5.57	9.33	4.37	3.63	5.8	5.65	4.1			
	NT2RP2000178	7.4	9.25	18.07	7.99	4.34	5.36	2.6	5.71	4.5			
	NT2RP2000183	5.74	7.89	15.69	7.74	4.42	5.84	3.67	6.86	4.04			
	NT2RP2000195	16.12	12.54	17.86	16.63	13.32	13.8	5.12	8.05	4.54	**		-
	NT2RP2000204	22.18	23.46	35.46	16.84	14.7	7.3	7.36	8.83	4.75	*		-
20	NT2RP2000205	306.16	263.17	279.79	153.75	186.84	122.03	44.13	69.43	57.15	**	**	-
	NT2RP2000208	5.24	2.8	6.75	5.38	2.18	0.7	2.69	2.06	2.36			
	NT2RP2000224	24.97	24.03	27.21	17.41	19.54	13.73	10.21	10.44	6.58	*	**	-
	NT2RP2000230	26.52	31.48	20.02	29.78	28.26	14.04	27.93	14.94	32.18			
	NT2RP2000231	102.91	95.51	132.32	51.89	45.81	56.22	28.1	59.69	105.21	**		-
	NT2RP2000232	18.39	14.23	28.59	15.4	9.71	12.46	6.13	9.73	7.72	*		-
25	NT2RP2000233	7.64	7.96	15.89	7.58	4.07	3.39	2.14	3	2.26	*		-
	NT2RP2000239	66.01	139	172.9	85.94	84.53	44.49	55.89	55.75	25.78			
	NT2RP2000240	5.47	3.94	10.61	4.6	1.25	2.17	1.78	2.32	0.43			
	NT2RP2000248	6.07	5.52	8.36	6.23	4.28	2.64	2.65	2.47	2.64	**		-
	NT2RP2000256	16.57	14.62	18.18	13.37	8.16	8.91	7.89	5.94	4.14	*	**	-
	NT2RP2000257	39.73	47.22	36.2	40.72	25.44	29.27	36.28	29.33	25.56			
30	NT2RP2000258	13.09	11.66	21.23	12.78	8.27	8.08	5.57	13.01	9.17			
	NT2RP2000261	8.27	7.35	17.74	7.68	2.93	4.17	3.42	5.31	3.64			
	NT2RP2000270	3.96	6.69	13.81	17.92	6.26	3.85	3.35	9.95	4.71			
	NT2RP2000274	91.36	80.94	71.7	59.79	55.47	43.9	66.54	63.63	61.61	*	*	-
	NT2RP2000277	4.35	3.88	5.68	6.38	1.67	1.79	1.78	1.55	2.23	**		-
	NT2RP2000279	7.44	6.18	9.49	6.39	2.22	2.73	3.81	2.76	3.21	*		-
35	NT2RP2000283	5.12	8.14	7.43	6.14	1.91	2.31	3.36	2.12	4.13	*		-
	NT2RP2000288	10.29	7.99	9.75	9.32	5.86	5.55	9.02	7.12	9.38			
	NT2RP2000289	21.4	17.79	32.55	15.37	7.32	16.77	22.06	23.42	27.43			
	NT2RP2000297	4.51	6.32	10.63	6.94	2.23	3.64	3.53	4.19	2.55			
	NT2RP2000298	8.05	8.79	13.64	5.87	3.8	2.92	2.96	3.04	1.11	*	*	-
	NT2RP2000310	80.52	91.37	87.72	32.16	27.21	29.67	20.91	14.48	20.59	**	**	-
40	NT2RP2000327	9.08	9.43	13.33	5.88	3.81	4.9	2.31	2.04	2.13	*	**	-
	NT2RP2000328	21.82	17.34	15.94	8.37	8.84	6.89	5.86	4.83	2.63	**	**	-
	NT2RP2000329	17.76	16.87	20.08	10.58	7.07	6.38	10.73	6.62	8.14	**	**	-
	NT2RP2000333	8.83	7.98	9.31	8.74	1.76	4.67	8.04	7.67	6.48			
	NT2RP2000337	26.86	26.84	31.77	17.74	6.47	12.94	6.6	13.35	15.87	*	**	-
	NT2RP2000346	6.79	9.29	9.75	14.24	7.42	4.48	6.69	17.82	10.4			
45	NT2RP2000357	14.11	13.18	22.49	5.83	2.27	3.95	3.56	4.39	2.66	*	*	-
	NT2RP2000358	9.23	5.13	8.16	5.34	2.02	3.61	4.07	3.18	2.94	*		-
	NT2RP2000366	5.06	4.61	6.09	5.12	1.19	2.67	2.27	2.31	1.55	**		-
	NT2RP2000369	29.84	26.23	39.9	17.03	12.11	15.49	15.78	7.96	15.06	*	*	-
	NT2RP2000376	26.15	35.86	51.75	24.31	15.42	18.34	35.37	27.75	35.03			
	NT2RP2000394	11.62	6.66	9.45	10.5	5.28	8.79	9.06	9.09	12.53			
50	NT2RP2000396	2.03	7.18	10.2	4.43	3.16	1.53	2.05	5.24	2.77			
	NT2RP2000412	13.13	15.96	18.35	14.6	6.73	8.07	6.73	16.17	12.59			
	NT2RP2000414	19.9	19.23	18.62	8.95	6.33	5.66	6.29	8.15	6.52	**	**	-
	NT2RP2000420	5.15	7.34	11.45	10.83	6.03	5.33	5.71	4.93	7.76			
	NT2RP2000422	10.72	8.26	11.6	8.9	4.28	5.31	4.96	4.79	6.17	*		-
	NT2RP2000426	7.55	6.99	6.8	4.75	1.02	1.72	2.91	2.26	1.94	*	**	-
55	NT2RP2000428	8.74	4.22	5.73	4.39	1.17	2.36	8.21	2.73	3.16			
	NT2RP2000438	12.17	11.38	11.77	10.69	3.56	5.65	4.51	2.36	2.93	**		-
	NT2RP2000447	12.75	6.94	10.08	6.36	4.33	7.41	3.21	7.55	5.61			

Table 423

	NT2RP2000448	25.71	13.78	32.06	17.1	19.22	17.26	5.88	10.24	7.42	*	-
5	NT2RP2000459	9.24	9.95	9.52	9.52	4.14	4.36	2.59	6.53	3.6	*	-
	NT2RP2000479	6.63	5.55	7.74	7.89	3.36	5.52	5.8	5.59	6.42		
	NT2RP2000498	11.27	6.84	9.95	5.98	2.48	3.08	4.73	2.88	2.16	*	*
	NT2RP2000503	14.72	13.18	15.3	32.52	21.1	19.93	18.56	11.89	14.4		
	NT2RP2000510	7.33	5.8	8.13	5.52	2.28	3.46	4.2	5.04	2.87	*	*
	NT2RP2000514	4.57	2.69	2.25	7.44	1.96	3.28	5.71	4	3.87		
10	NT2RP2000516	6.54	4.62	8.39	7.51	4.34	6.37	3.47	4.35	4.95		
	NT2RP2000523	4.11	2.38	11.01	7.29	1.39	3.22	3.15	2.27	3.38		
	NT2RP2000533	2.68	1.37	7.63	4.63	1.22	2.09	0.79	2.38	0.48		
	NT2RP2000540	6.16	5.88	8.08	5.48	4.38	3.8	3.01	4.98	1.52	*	-
	NT2RP2000547	7.42	7.44	10.91	6.02	3.13	4.89	2.98	4.52	3.39	*	-
	NT2RP2000557	49.31	60.55	82.94	43.46	53.17	74.9	83.43	53.58	63.67		
15	NT2RP2000558	18.68	19.95	27.42	20.69	14.13	19.17	24.64	17.82	18.81		
	NT2RP2000564	0.43	0.11	2.04	5.89	0.93	1.24	2.05	1.59	0.53		
	NT2RP2000565	13.78	7.23	14.74	12.39	9.94	11.42	3.9	7.3	8.83		
	NT2RP2000583	10.87	6.32	13.24	7.55	3.8	5.68	4.41	5.83	9.68		
	NT2RP2000591	7.05	5.42	12.75	6.46	3.08	3.75	3.89	6.69	2.85		
	NT2RP2000599	45.38	33.04	53.33	45.68	38.74	39.04	49.46	50.96	42.92		
20	NT2RP2000601	5.8	2.35	8.26	6.01	2.72	4.74	3.53	6.5	4.71		
	NT2RP2000603	10.6	10.97	14.76	12.57	11.91	10.27	11.35	11.32	10.57		
	NT2RP2000610	16.79	27.41	21.69	12.86	12.08	9.62	7.92	6.77	7.19	*	**
	NT2RP2000614	22.5	27.77	21.5	15.84	12.38	13.2	11.46	7.34	10.15	*	**
	NT2RP2000616	15.9	10.73	17.88	14.04	10.65	8.26	8.53	13.65	30.31		
	NT2RP2000617	7	4.89	10.44	5.79	2.49	3.27	2.33	3.91	6.08		
25	NT2RP2000623	30.93	27.18	42.39	23.25	19.11	22.34	22.03	24.06	17.67		
	NT2RP2000634	5.41	5.13	8.98	7.02	5.17	5.22	4.91	6.31	5.96		
	NT2RP2000636	6.22	7.05	7.96	5.06	2.33	3.65	3.42	4.64	2.62	*	*
	NT2RP2000638	5.4	5.87	8.77	7.49	5.36	5.46	5.01	4.21	4.57		
	NT2RP2000644	6.06	11.57	13.6	11.21	5.35	7.7	5.1	5.24	4.14		
	NT2RP2000649	69.57	64.76	72	79.36	45.65	56.22	93.91	57.37	68.85		
30	NT2RP2000652	14.9	10.94	49.84	10.88	5.91	11.87	6.2	5.26	32.14		
	NT2RP2000656	12.57	7.15	13.54	6.29	4.4	6.3	1.69	9.03	14.78		
	NT2RP2000658	5.45	4.52	10.98	5.11	2.13	3.91	1.81	2.12	1.71		
	NT2RP2000663	4.6	4.28	7.43	5.58	2.25	5.97	4.47	2.44	1.11		
	NT2RP2000664	10.9	7.61	12.36	9.42	3.88	8.64	13.44	10.25	9.81		
	NT2RP2000668	33.38	33.11	48.17	36.56	39	37.32	34.56	25.63	30.2		
35	NT2RP2000678	6.12	9.03	9.25	9.6	7.57	6.65	6.86	6.02	5.34		
	NT2RP2000694	16.87	11.51	13.29	13.35	8.47	12.93	22.9	14.8	18.71		
	NT2RP2000704	2.84	3.9	14.85	6.19	2.87	7.29	2.98	6.45	4.78		
	NT2RP2000710	8.84	8.7	19.22	7.25	3.74	6.4	5.24	6.81	6.9		
	NT2RP2000712	5.84	5.25	16.26	7.12	3.27	5.34	2.82	4.15	2.23		
	NT2RP2000715	23.49	31.67	27.44	16.78	13.7	10.05	7.2	11.02	9.66	*	**
40	NT2RP2000720	14.6	11.95	17.99	9.67	7.04	6.8	9.67	8.11	6.87	*	*
	NT2RP2000731	130.46	114.16	171.06	139.58	136.44	144.08	91.22	91.1	91.43	*	*
	NT2RP2000739	10.56	11	13.93	9.61	7.28	5.99	9.06	6.03	5.15	*	*
	NT2RP2000748	12.42	9.17	9.8	13.86	6.05	5.01	6.86	4.28	5.36	*	*
	NT2RP2000749	11.23	7.84	14.76	7.12	4.44	6.62	1.43	4.83	4.58	*	*
	NT2RP2000758	18.71	12.4	22.27	12.06	7.43	9.25	3.34	5.27	4.96	*	*
45	NT2RP2000764	8.83	9.65	15.17	9.68	4.51	6.36	4.78	3.89	4.68	*	*
	NT2RP2000766	39.21	45.57	54.49	39.05	26.43	20.35	16.67	26.46	19.71	**	**
	NT2RP2000777	37.43	31.1	43.71	20.28	16.78	21.16	3.56	8.61	6.24	**	**
	NT2RP2000786	10.79	9.6	16.45	9.08	5.82	3.61	8.49	11.1	8.19		
	NT2RP2000793	8.96	7.43	14.72	5.59	4.46	3.27	3.41	3.35	2.39	*	*
	NT2RP2000796	13.41	11.17	11.19	12.52	8.7	5.88	4.89	4.55	5.82	**	*
50	NT2RP2000809	9.51	8.66	16.69	9.15	5.7	10.07	8.67	9.07	9.06		
	NT2RP2000812	10.78	5.64	19.76	9.49	6.33	7.02	9.58	10.65	9.48		
	NT2RP2000814	2.73	2.98	11.46	6.79	1.46	2.03	1.53	1.11	1.73		
	NT2RP2000816	5.26	5.27	12.58	5.83	4.32	3.54	2.61	2.6	1.81		
	NT2RP2000818	64.67	52.94	68.69	38.83	38.29	31.92	36.98	34.96	36.14	**	**
	NT2RP2000819	10.64	9.84	11.3	8.11	4.61	3.58	6.06	2.23	3.74	*	**
55	NT2RP2000841	19.27	13.42	17.68	15.7	9.96	11	12.88	9.6	13.79		
	NT2RP2000842	7.9	5.25	9.24	8.2	4.88	2.43	6.17	3.9	4.72		
	NT2RP2000845	1.64	3.58	10.06	6.26	3.24	5.16	2.58	3.32	3.23		

Table 424

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NT2RP2000863	9.23	2.37	9.61	12.6	5.57	10.29	2.95	6.5	2.03				
NT2RP2000880	6.89	4.15	10.09	8.75	3.65	3.61	3.32	7.64	2.92				
NT2RP2000892	6.48	7.22	10.47	6.68	3.59	2.44	2.63	2.13	2.32	**		-	
NT2RP2000894	6.84	8.43	12.75	7.7	5.61	3.86	6.32	3.41	5.03				
NT2RP2000903	14.72	12.47	10.22	6.37	7.06	6.25	6.3	4.12	3.45	*	**	-	-
NT2RP2000906	7.83	5.78	8.49	5.67	3.5	4.08	5.51	1.9	1.89	*	*	-	-
NT2RP2000910	7.08	7.41	7.6	9.95	3.31	4.88	6.74	6.36	7.22				
NT2RP2000931	17.23	16.66	19.14	9.83	11.03	7.29	5.66	13.37	8.87	**	*	-	-
NT2RP2000932	4.85	5.4	12.51	5.58	2.98	2.75	2.51	3.48	1.84				
NT2RP2000938	32.12	38.62	41.75	20.34	22.26	19.86	28.05	24.64	29.99	**	*	-	-
NT2RP2000943	6.65	4.28	8.98	6.63	2.06	1.49	2.39	2.3	2.44		*	-	-
NT2RP2000957	8.82	7.9	11.5	5.58	3.81	3.6	2.18	2.83	1.56	*	**	-	-
NT2RP2000958	5.64	6.03	15.9	6.17	2.43	2.74	1.92	2.26	3.56				
NT2RP2000959	11.75	9.04	10.68	6.59	3.84	2.64	4.69	3.69	5.66	*	**	-	-
NT2RP2000965	4.05	2.66	2.8	5.91	0.94	1.41	2.34	1.56	2.95				
NT2RP2000970	58.85	65.2	74.74	64.15	40.74	92.64	72.54	97.39	89.84				
NT2RP2000973	5.19	3.92	9.39	8.06	5.68	3.54	3.01	9.76	7.5				
NT2RP2000985	3.85	2.51	4.33	4.79	3.19	4.55	1.82	2.45	2.12				
NT2RP2000987	39.38	36.27	32.68	33.06	40.49	26.38	33.61	26.04	27.01				
NT2RP2000997	9.33	8.58	9.52	9.72	3.47	7.24	9.63	9.44	11.63				
NT2RP2001024	12.74	7.92	18.67	6.22	2.48	2.6	4.96	3.99	3.75	*	*	-	-
NT2RP2001028	38.71	37.69	41.88	33.98	15.8	30.64	34.47	25.69	33.62				
NT2RP2001036	10.56	11.08	9.13	9.7	2.35	6.59	6.06	3.75	3.17	**		-	
NT2RP2001039	29.77	24.74	30.19	17.85	11.75	29.98	20.42	28.95	23.24				
NT2RP2001044	111.16	103.9	116.83	65.77	42.98	31.59	30.2	74.24	42.92	**	*	-	-
NT2RP2001056	16.47	11.38	12.03	9.34	5.04	8.68	12.51	8.41	8.95				
NT2RP2001065	12.87	18.54	21.09	9.6	6.83	8.58	6.23	6.54	8.28	*	*	-	-
NT2RP2001067	18.27	13.06	19.79	9.25	5.26	3.58	5.5	6.23	8.66	*	*	-	-
NT2RP2001070	4.55	6.03	7.25	6.14	2.9	2.2	3.37	2.83	1.95		*	-	-
NT2RP2001081	11.96	15.94	13.97	8.19	3.81	5.26	5.58	4.15	6.83	**	**	-	-
NT2RP2001087	65.9	61.9	76.08	39.7	16.73	50.09	38.08	21.24	22.36	*	**	-	-
NT2RP2001094	12.2	8.99	11.02	14.61	10.72	9.52	11.02	11.03	11.05				
NT2RP2001119	4.16	4.58	7.07	10.85	1.99	7.07	4.12	3.63	2.63				
NT2RP2001127	11.36	13.12	3.9	16.08	4.14	7.73	5.38	7.85	3.42				
NT2RP2001133	5.67	4.14	5.86	10.97	6.13	8.56	8.68	4.41	3.17				
NT2RP2001137	49.8	41.1	45.81	39.26	21.06	24.92	25.21	45.63	17.6	*		-	
NT2RP2001142	5.27	5.53	5.06	5.3	2.26	3.98	2.41	3.56	3.78		*	-	
NT2RP2001149	6.92	5.61	5.45	13.36	3.82	6.27	6.19	4.78	4.91				
NT2RP2001168	6.12	7.49	5.66	8.34	5.85	5.09	5.44	4.63	5.1				
NT2RP2001173	4.74	3.23	8.28	7.11	2.4	3.67	4.61	6.54	6.37				
NT2RP2001174	44.63	21.39	37.72	44.99	18.88	46.31	52.67	53.94	56.67	*		+	
NT2RP2001184	7.2	4.99	10.33	8.93	4.09	3.96	4.88	4.86	5.6				
NT2RP2001196	188.27	171.63	278.21	277.29	156.05	217.9	310.45	339.15	334.54	*		+	
NT2RP2001200	5.84	6.42	11.03	6.08	6.9	5.52	4.06	2.49	4.45				
NT2RP2001218	12.41	10.49	14.66	10.34	6.96	7.23	9.11	8.8	8.23	*		-	
NT2RP2001223	10.09	12.26	12.04	13.71	9	9.77	10.94	7.86	9.72				
NT2RP2001226	295.34	151.71	253.15	264.52	155.79	205.35	225.76	302.68	279.91				
NT2RP2001227	9.29	9.83	15.24	10.83	5.91	8.02	6.71	6.54	8.43				
NT2RP2001232	6.25	9.05	13.72	6.11	9.52	4.37	3.08	5.35	5.73				
NT2RP2001233	17.2	11.64	26.2	12.06	8.02	7.48	8.66	8.69	6.62				
NT2RP2001245	42.01	30.76	56.72	22.72	58.34	32.96	29.15	30.96	32.88				
NT2RP2001246	5.12	5.92	8.66	6.91	4.33	3.68	3.64	7.01	3.2				
NT2RP2001268	76.86	63.92	101.42	88.4	109.5	90.32	72.85	73.19	77.59				
NT2RP2001270	10.64	12.74	14.24	12.74	10.24	11.95	10.68	9.82	10.94				
NT2RP2001276	23.31	16.76	30.97	21.15	16.68	10.08	14.57	16.7	14.66				
NT2RP2001277	24.91	10.73	18.18	16.47	6.03	6.24	22.15	25.09	49.12				
NT2RP2001290	8.95	7.82	10.48	8.48	7.41	5.73	5.82	9.63	10.81				
NT2RP2001295	14.82	7.48	15.13	8.28	5.62	4.48	5.33	6.4	4.82				
NT2RP2001297	8.15	6.67	10.81	9.36	7.32	4.92	4.17	4.98	6				
NT2RP2001301	47.34	44.45	63.71	42.51	36.25	33.89	33.81	29.8	26.52	*		-	
NT2RP2001312	8.43	10.98	14.02	7.43	5.35	5.08	6.81	4.46	4.32	*	*	-	-
NT2RP2001327	20.88	28.57	34.54	16.53	15.03	15.84	11.1	20.64	9.65	*		-	
NT2RP2001328	10.32	3.77	9.25	9.2	3.81	6.74	4.44	5.56	7.15				
NT2RP2001341	3499.3	2809.3	4099.1	1364.9	1644.2	898.17	1201.7	2570.4	2392	**		-	

Table 425

	NT2RP2001347	539.84	514.01	628.74	565.74	422.96	416.2	495.32	585.14	429.89				
5	NT2RP2001366	38.71	33.77	43.04	29.42	28.24	19.52	18.19	26.65	21.17	*	*	-	-
	NT2RP2001378	8.65	6.18	12.14	10.82	6.77	5.51	3.49	4.36	4.96				
	NT2RP2001381	20.33	22.01	25.11	15	9.62	10.21	6.87	12.31	12.9	**	**	-	-
	NT2RP2001388	23.09	21.55	19.16	14.87	11.09	13.2	20	18.4	14.87	**		-	-
	NT2RP2001391	19.47	21.48	20.82	19.07	15.36	11.27	15.83	12.93	10.03		*	-	-
	NT2RP2001392	6.22	2.39	9.23	6.23	2.48	4.35	2.68	3.41	3.72				
10	NT2RP2001394	9	9.52	18.06	7.33	4.64	3.55	4.34	5.54	7.88				
	NT2RP2001397	5.52	4.95	15.76	7.71	3.52	1.79	2.61	4.45	3.74				
	NT2RP2001400	33.05	35.87	41.2	15.06	15.67	8.49	5.11	9.86	5.55	**	**	-	-
	NT2RP2001408	22.02	23.86	22.82	11.45	12.19	9.24	10.98	11.38	13.8	**	**	-	-
	NT2RP2001420	13.99	18.37	19.98	12.59	10.04	8.9	9.18	10.79	13.16	*	*	-	-
	NT2RP2001423	138.22	161.12	169.36	120.84	140.16	121.74	142.58	124.54	152.09				
15	NT2RP2001427	11.99	17.22	16.25	9.35	7.9	6.74	7.44	6.11	3.28	*	**	-	-
	NT2RP2001428	11.05	7.81	14.33	11.13	3.4	8	3.33	6.84	8.32				
	NT2RP2001436	28.98	21.86	34.92	22.78	25.35	19.1	15.23	27.9	27.44				
	NT2RP2001440	21.88	12.74	27.62	14.71	9.47	17.13	15.85	24.15	14.86				
	NT2RP2001445	9	10.8	19.43	10.91	10.54	6.62	8.66	8.73	7.21				
	NT2RP2001449	28.07	34.09	40.82	25.02	19.29	16.65	14.58	19.57	13.99	*	*	-	-
20	NT2RP2001450	20.8	28.19	27.38	18.17	18.42	8.85	15.67	22.32	18.66				
	NT2RP2001467	77.4	117.05	74.08	41.14	94.21	47.44	46.82	38.8	29.18		*	-	-
	NT2RP2001469	12.38	11.13	18.21	9.61	8.91	7.86	5.16	5.66	4.91	*		-	-
	NT2RP2001480	16.58	12.17	23.4	14.68	6.35	9.1	6.53	11.37	10.31				
	NT2RP2001495	5.39	5.05	10.71	5.62	3.39	3.05	2.02	2.99	3.13				
	NT2RP2001499	31.27	46.77	45.33	29.35	33.83	17.6	16.09	21.38	15.2		*	-	-
25	NT2RP2001506	7.58	7.79	10.57	9.25	7.24	4.11	3.34	2.96	2.75		**	-	-
	NT2RP2001508	10.21	8.66	19.01	9.32	5.78	3.48	10.19	10.43	10.1				
	NT2RP2001511	18.18	10.36	14.04	8.06	6.96	5.65	4.43	6.31	7.52	*	*	-	-
	NT2RP2001514	8.2	7.15	8.01	6.7	3.51	2.31	2.13	3.46	3.84	**		-	-
	NT2RP2001520	8.17	6.6	9.18	8.28	6.18	3.08	5.09	4.32	4.95	*	*	-	-
30	NT2RP2001526	15.63	17.52	16.82	11.75	3.98	10.59	5.68	10.57	11.64	*	*	-	-
	NT2RP2001529	18.96	9.11	22.28	13.03	8.09	10.02	6.2	8.22	8.57				
	NT2RP2001536	14.16	10.36	18.6	12.98	11.79	8.28	7.74	11.37	11.72				
	NT2RP2001538	8.11	6.47	12.78	7.67	5.34	3.77	4	4.36	2.56		*	-	-
	NT2RP2001547	9.99	10.57	12.92	9.74	7.58	3.49	4.05	3.74	4.33		**	-	-
	NT2RP2001560	11.5	10.74	9.02	6.82	5.56	7.18	6.87	5.66	4.21	*	*	-	-
	NT2RP2001562	17.39	15.7	17.62	10.84	8.02	7.21	8.92	9.2	10.24	**	**	-	-
35	NT2RP2001566	14.26	13.81	10.49	11.53	7.07	4.68	7.24	4.21	4.54		**	-	-
	NT2RP2001569	25.02	15.42	32.18	22.03	11.09	26.81	24.28	25.39	21.94				
	NT2RP2001576	129.89	178.91	114.02	47.3	49.96	55.77	33.67	55.78	72.18	*	*	-	-
	NT2RP2001581	20.4	22.7	22.23	13.8	17.88	10.54	10.57	16.71	15	*	*	-	-
	NT2RP2001597	17.49	9.3	13	11.25	8.35	11.5	4.54	4.57	3.83		*	-	-
40	NT2RP2001601	376.46	416.73	382.11	192.76	196.04	131.77	252.12	219.45	367.42	**		-	-
	NT2RP2001613	6.29	5.75	7.26	4.54	4.25	3.06	3.72	3.99	3.96	*	**	-	-
	NT2RP2001628	20.46	20.27	25.19	14.18	13.5	11.94	11.98	13.91	12.32	**	**	-	-
	NT2RP2001634	4.72	7.04	6	7.61	3.83	2.93	4.15	1.66	3.09		*	-	-
	NT2RP2001635	20.18	16.77	22.18	15.58	7.6	10.65	10.91	15.44	14.53	*	*	-	-
	NT2RP2001660	27.92	47.45	35.98	27.8	15.26	22.85	16.57	20.69	20.06		*	-	-
	NT2RP2001662	141.98	137.52	151.45	151.4	116.43	136.78	154.6	188.28	148.8				
45	NT2RP2001663	102.28	119.36	140.87	48.03	51.07	39.15	80.45	80.81	83.65	**	*	-	-
	NT2RP2001672	6.83	9.61	11.14	6.86	4.73	5.02	7.16	6.7	5.29				
	NT2RP2001675	7.51	11.75	9.95	6.41	3.17	2.8	4.39	4.7	4.26	*	*	-	-
	NT2RP2001677	18.83	22.14	19.19	10.64	6.34	6.91	9.72	6.83	7.68	**	**	-	-
	NT2RP2001678	10.06	8.87	8.92	7.97	6.41	4.67	9.59	5.34	9.32	*		-	-
	NT2RP2001683	98.93	103.45	119.49	195.62	102.44	134.62	102.34	95.16	65.68				
50	NT2RP2001699	36.15	36.2	44.96	18.8	7.95	13.41	6.7	9.44	13.11	**	**	-	-
	NT2RP2001707	6.77	3.9	7.75	5.48	4.72	5.02	3.35	4.21	3.45				
	NT2RP2001720	8.16	6.41	9.93	7.22	8.68	5.49	4.59	6.11	5.89				
	NT2RP2001721	33.41	34.55	34.5	25.33	18.3	17.93	32.85	38.18	33.9	**		-	-
	NT2RP2001740	64.22	76.89	65.2	34.74	42.49	31.73	26.06	24.24	41.05	**	**	-	-
	NT2RP2001748	6.3	15.07	7.65	6.61	1.99	2.37	4.7	3.94	2.45				
55	NT2RP2001755	8.56	8.68	5.59	6.1	3.13	5.08	4.74	3.64	4.01		*	-	-
	NT2RP2001762	4.42	4.43	4.61	6.06	1.37	4.5	3.19	3.5	2.83	**		-	-
	NT2RP2001768	7.43	5.23	6.6	7.86	2.49	4.84	3.03	5.68	3.45				

Table 426

	NT2RP2001769	74.25	64.35	76.05	49.19	51.48	48.88	16.14	29.26	21.95	**	**	-	-
	NT2RP2001784	6.1	6.64	9.79	6.92	5.74	5.64	4.78	4.07	4.19				
5	NT2RP2001805	18.64	23.08	23.59	18.75	15.28	15.88	12.77	15.01	19.71				
	NT2RP2001813	12.2	15.41	15.49	8.88	4.21	6.14	9.29	6.92	9.66	*	*	-	-
	NT2RP2001817	50.4	58.09	53.81	41.79	32.65	39.63	54.02	42.75	56.58	*		-	
	NT2RP2001818	7.27	4.11	3.7	5.91	1.54	5.16	5.71	4.24	6.18				
	NT2RP2001837	24.91	17.75	31.06	23.35	23.21	19.49	21.43	23.69	22.4				
10	NT2RP2001839	16.58	14.52	27.11	17.12	15.87	19.03	13.8	13.73	15.93				
	NT2RP2001861	19.37	18.6	26.95	11.83	7.45	7.51	9.29	9.04	10.22	*	*	-	-
	NT2RP2001869	8.35	8.88	14.85	9.01	6.82	4.27	3.19	6.52	4.2				
	NT2RP2001876	52.07	48.1	60.43	41.56	38.63	33.22	53.55	54.23	52.55	*		-	
	NT2RP2001878	10.64	8.11	16.99	8.71	6.81	6.18	8.15	6.26	6.36				
	NT2RP2001881	11.51	12.01	17.12	11.39	8.77	9.36	10.8	14.93	9.65				
15	NT2RP2001883	15.67	6.93	15.2	18.32	7.55	11.74	13.41	14.76	12.05				
	NT2RP2001884	1443.8	767.12	607.01	701.8	356.77	733.69	199.74	492.38	1929.8				
	NT2RP2001885	86.63	81.18	119.19	86.34	68.67	72.27	80.49	93.38	87.15				
	NT2RP2001898	13.46	6.9	14.73	6.96	6.72	3.84	5.67	4.43	5				
	NT2RP2001900	20.73	14.58	24.69	18.79	8.43	10.74	17.28	16.1	17.71				
	NT2RP2001903	11.05	14.47	16.38	12.77	7.63	7.86	11	14.28	12.43				
20	NT2RP2001907	9.79	12.89	12.82	8.11	6.3	4.57	8.52	7.33	7.63	*	*	-	-
	NT2RP2001915	17.49	19.44	20.82	11.45	7.41	6.04	7.94	7.59	6.62	**	**	-	-
	NT2RP2001921	13.67	9.05	20.66	11.35	6.61	9.21	6.21	10.48	17.99				
	NT2RP2001926	34.47	22.9	35.27	22.68	13.7	11.83	10.15	26.13	26.9	*		-	
	NT2RP2001933	36.39	16.3	35.12	23.35	20.81	17.87	10.85	17.5	22.37				
	NT2RP2001936	11.42	9.59	15.71	9.32	7.07	4.58	8.12	12.42	62.46				
25	NT2RP2001943	14.71	11.45	18.53	11.8	23.77	7.53	6.86	10.79	7.88				
	NT2RP2001946	20.64	20.42	25.84	8.64	12.56	9.33	5.24	6.37	7.54	**	**	-	-
	NT2RP2001947	6.28	10.5	8.57	7.88	5.98	1.91	4.36	3.2	4.16		*	-	
	NT2RP2001956	21.67	10.17	24.79	16.61	12.12	14.12	16.82	19.29	13.33				
	NT2RP2001969	201.65	149.79	301.42	176.35	143.62	157.42	143.79	183.78	182.57				
	NT2RP2001976	4.33	7.95	17.7	7.78	4.49	4.49	2.81	5.46	10.35				
30	NT2RP2001978	14.35	12.6	20.91	12.02	5.57	5.03	3.1	3.56	4.91		**	-	-
	NT2RP2001985	13.77	15.22	14.24	9.55	5.93	6.64	4.89	6.51	5.47	**	**	-	-
	NT2RP2001991	37.12	36.77	50.48	37.16	44.84	28.4	28.39	20.28	24.2		*	-	
	NT2RP2001997	13.99	12.07	14.92	11.27	12.08	8.47	13.49	12.5	12.19				
	NT2RP2002015	3.95	7.2	5.18	7.51	4.61	2.96	3.72	6.25	2.61				
	NT2RP2002017	14.92	13.42	18.23	7.3	5.04	8.42	3.4	6.85	8.43	**	*	-	-
35	NT2RP2002025	39.84	48.8	68.43	33.02	35.2	30.44	23.31	31.13	31.97				
	NT2RP2002030	28.92	28.65	40.93	26.27	23.9	23.74	29.55	36.7	30.22				
	NT2RP2002032	41.77	39.39	41.34	31.44	32.7	25.79	15.28	25.82	17.93	**	**	-	-
	NT2RP2002033	7.84	6.18	11.1	7.44	5.25	3.93	2.63	4.43	2.72		*	-	-
	NT2RP2002041	63.15	38.11	58.94	48.43	54.38	37.99	33.68	26.24	30.79		*	-	-
	NT2RP2002046	19.79	18.39	22.62	13.61	15.41	9.7	20.12	17.67	17.54	*		-	-
40	NT2RP2002047	15.96	12.18	14.55	9.42	12.66	9.04	9.26	8.52	3.77		*	-	-
	NT2RP2002050	6.47	7.96	8.94	7.07	2.69	4.33	1.22	3.6	2.62	**		-	-
	NT2RP2002052	16.16	10.25	17.67	10.56	6.94	8.28	6.44	8.83	9.43				
	NT2RP2002058	10.7	8.12	13.82	9.12	8.72	4.7	3.71	8.14	3.23				
	NT2RP2002060	7.22	6.32	13.21	7.18	3.78	3.46	2.87	4.32	2.16				
	NT2RP2002063	27.7	19.33	28	16.06	12.42	6.01	14.89	17.06	15.58	*	*	-	-
45	NT2RP2002066	14.12	10.25	16.69	11.69	8.3	5.49	7.86	7.37	6.79		*	-	-
	NT2RP2002070	47.82	69.53	26.7	25.88	50.9	22.08	11.62	12.95	13.2		*	-	-
	NT2RP2002076	50.79	54.44	56.91	34.7	35.7	26.78	21.75	13.06	12.15	**	**	-	-
	NT2RP2002078	3.82	6.23	12.24	6.03	3.97	4.06	0.81	5.31	3.09				
	NT2RP2002079	13.68	8.15	17.98	8.69	6.98	8.2	5.55	8.29	6.41				
	NT2RP2002099	11.59	12.19	18.2	8.81	6.98	5.14	5.57	8.29	5.75	*	*	-	-
50	NT2RP2002105	15.09	12.54	15.38	10.34	7.26	6.01	5.5	9.12	6.68	*	**	-	-
	NT2RP2002115	15.39	14.23	22.91	11.04	12.24	9.95	11	13.28	11.06				
	NT2RP2002124	59.86	56.27	77.47	56.59	47.35	36.88	55.21	47.08	46.87				
	NT2RP2002137	8.42	8.75	8.28	6.56	6.55	3.48	2.47	3.09	3.68	*	**	-	-
	NT2RP2002139	93.62	131.25	91.96	52.77	52.45	52.95	81.88	52.45	48.22	*		-	-
	NT2RP2002154	6.04	5.02	12.4	5.24	1.47	5.98	2.02	3.26	3.03				
55	NT2RP2002155	16.04	17.28	22.84	17	10.94	11.7	12.12	14.76	13.07				
	NT2RP2002172	26.05	32.14	34.35	17.74	14.37	15.16	12.78	22.56	16.28	**	*	-	-
	NT2RP2002185	13.73	14.4	21.2	14.18	14.86	10.72	12.32	12.52	11.2				

Table 427

	NT2RP2002188	222.52	243.75	126.54	151.89	124.73	74.73	64.57	82.95	98.67	*	-
	NT2RP2002192	66.59	140.59	123.86	61.74	74.83	59.86	111.82	74.79	70.77		
5	NT2RP2002193	9.92	9.38	5.54	5.64	8.2	3.35	4.38	2.62	2.3	*	-
	NT2RP2002208	24.07	21.97	26.87	14.79	10.85	11.7	14.39	13.9	16.1	**	**
	NT2RP2002219	67.68	67.68	54.54	42.26	45.01	39.83	12.23	52.49	39.63	*	-
	NT2RP2002231	7.62	8.91	9.95	5.33	3.41	3.41	3.43	5.73	5.85	**	*
	NT2RP2002232	82.24	77.63	81.5	78.38	94.62	65.26	53.25	57.27	56.31	**	-
10	NT2RP2002235	28.16	33.42	30.04	28.68	25.16	22.07	20.58	21.22	23.01	**	-
	NT2RP2002239	46.02	63.63	67.29	21.58	16.63	25.15	34.54	22.68	19.45	**	*
	NT2RP2002252	7.05	9.07	9.23	8.29	3.79	3.9	4.57	3.45	2.91	**	-
	NT2RP2002256	27.97	26.83	27.09	15.84	11.06	11.47	26.86	22.34	28.47	**	-
	NT2RP2002257	7.18	9.4	7.52	6.89	3.78	4.59	5.56	4.76	6.16	*	-
	NT2RP2002259	18.53	13.43	11.26	24.93	14.6	14.24	10.77	18.34	15.94		
15	NT2RP2002264	26.23	33.28	22.8	12.91	13.58	12.04	9.7	17.76	13.48	**	*
	NT2RP2002267	32.17	30.65	32.28	23.04	23.01	26.57	18.83	21.9	22.12	**	**
	NT2RP2002270	24.56	42.02	39.93	12.58	23.51	8.23	20.01	17.31	11.5	*	*
	NT2RP2002281	77.89	96.13	97.81	150.54	78.9	96.99	77.36	60.86	55.61	*	-
	NT2RP2002288	21.39	25.5	23.86	18.7	13.7	14.18	19.97	22.13	17.3	*	-
	NT2RP2002292	54.6	51.47	64.64	33.71	24.08	25.61	33.57	27.11	23.57	**	**
20	NT2RP2002299	38.27	50.42	61.77	19.48	10.3	12.83	10.02	9.38	6.36	**	**
	NT2RP2002304	11.94	6.17	8.22	10.44	3.85	9.51	5.62	11.16	9.83		
	NT2RP2002312	27.46	21.25	33.99	24.99	23.29	27.25	22.52	32.61	25.31		
	NT2RP2002316	51.29	40.93	55.81	26.92	27.74	16.77	8.08	18.25	13.09	*	**
	NT2RP2002325	14.79	13.26	29.38	13.29	7.49	7.83	6.29	6.54	6.53		
	NT2RP2002333	37.71	73.03	60.93	25.88	22.98	32.97	22.31	24.03	28.79	*	*
25	NT2RP2002371	18.55	14.9	20.81	15.66	7.83	11.84	19.13	18.46	18.7		
	NT2RP2002373	7.7	6.37	4.6	6.91	3.79	4.83	4.84	5.13	5.14		
	NT2RP2002381	9.55	13.3	13.26	6.59	3.77	3.7	6.54	4.52	6.36	**	*
	NT2RP2002385	0.45	2.78	2.19	4.9	1.81	3.5	0.24	0.66	1.05		
	NT2RP2002394	32.72	28.71	26.62	28.1	25	26.16	15.67	15.8	20.33	**	-
	NT2RP2002408	6.97	5.52	5.11	6.31	2.85	4.31	2.1	5.36	5.24		
30	NT2RP2002409	7.43	7.51	7.75	10.28	4.99	7.17	4.61	5.21	4.74	**	-
	NT2RP2002424	13.74	18.21	4.21	14.47	4.22	10.67	7.29	17.72	5.01		
	NT2RP2002426	31.08	22.01	26.45	29.33	10.8	28.89	38.27	34.35	51.45		
	NT2RP2002429	5.25	5.45	6.58	6.82	3.95	4.26	5.54	2.96	5.77		
	NT2RP2002437	5.68	8.15	5.2	8.99	3.78	4.37	5.91	5.66	5.8		
	NT2RP2002439	23.83	11.85	28.63	30	21.32	18.74	18.69	27.87	21.85		
35	NT2RP2002442	4.21	2.48	10.06	7.13	2.17	3.83	3.89	4.18	3.7		
	NT2RP2002457	5.91	3.86	9.43	6.08	1.82	4.35	4.32	3.38	4.15		
	NT2RP2002464	14.04	9.04	19.39	8.26	2.91	3.02	6.2	7.3	8.31		
	NT2RP2002475	18.47	16.05	30.87	26.73	13.63	23.54	27.01	26.72	27.62		
	NT2RP2002479	4.38	4.25	7.68	9.08	3.28	4.87	3.36	7.1	3.51		
	NT2RP2002487	8.46	11.73	16.26	11.78	4.98	7.15	5.71	5.33	8.37		
40	NT2RP2002498	12.42	14.56	14.54	14.3	15.74	13.48	11.49	11.5	14.04		
	NT2RP2002503	38.54	26.71	38.28	36.97	26.13	31.51	31.04	37.76	40.27		
	NT2RP2002504	10.58	11.45	20.66	9.47	10.7	9.29	7	7.64	9.65		
	NT2RP2002510	35.82	27.78	43.7	25.78	25.92	21.7	29.92	29.43	28.5		
	NT2RP2002520	21.45	19.39	27.79	16.61	13.24	8.38	14.06	12.04	8.59	*	*
	NT2RP2002527	36.1	23.32	35.4	20.76	25.32	20.27	27.42	26.23	15.63		
45	NT2RP2002533	13.17	14.75	23.11	11.93	9.58	7.87	8.62	7.96	9		
	NT2RP2002537	13.08	12.39	14.79	10.65	13.69	8	8.5	6.59	7.09	**	-
	NT2RP2002542	68.44	80.08	72.33	74.6	46.95	45.75	49.02	39.47	37.92	**	-
	NT2RP2002546	14.88	18.96	17.6	15.64	9.66	8.83	6.06	11.83	13.87		
	NT2RP2002549	14.96	11.64	16.89	10.43	8.76	6.03	5.02	9.52	9.5	*	*
	NT2RP2002564	39.56	26.21	34.95	20.11	17.81	17.77	18.21	24.98	19.23	*	*
50	NT2RP2002591	42.59	28.9	37.43	32.97	30.53	25.24	25	30.71	25.2		
	NT2RP2002595	5.68	8	12.85	9.34	7.39	5.51	5.35	4.75	4.31		
	NT2RP2002602	54.53	55.87	75.68	59.64	57.23	46.71	59.72	54.59	54.85		
	NT2RP2002606	12.52	13.19	14.5	13.95	17.61	9.8	13.98	12.61	14.58		
	NT2RP2002609	11.6	17.33	13.31	20.12	19.43	14.55	10.05	12.64	13.06		
	NT2RP2002618	14	10.22	19.04	13.28	7.51	9.59	7.56	12.06	11.33		
55	NT2RP2002621	11.85	9.77	15.54	8.04	5.31	5.01	3.35	5.97	7.64	*	*
	NT2RP2002643	11.04	8.19	16.62	9.29	6.05	6.59	3.63	6.53	4.9		
	NT2RP2002672	6.88	6.19	9.33	7.99	5.59	4.36	3.64	6.54	3.29		



Table 428

	NT2RP2002673	103.76	111.24	114.16	70.07	45.09	85.59	92.44	85.88	91.14	*	**	-	-
	NT2RP2002674	28.24	27.69	34.14	21.06	20.78	16.49	24.37	22.8	22.81	*	*	-	-
5	NT2RP2002686	20.76	27.04	31.72	23.26	22.04	15.33	8.73	8.68	8.13		**	-	-
	NT2RP2002688	13.92	12.24	10	14.56	10.69	8.28	14.43	8.67	10.91			-	-
	NT2RP2002695	19.25	14.55	23.17	14.75	11.8	15.12	11.5	15.77	21.62			-	-
	NT2RP2002701	4.75	5.4	12.91	6.52	3.02	5.45	3.43	3.42	5.6			-	-
	NT2RP2002706	14.53	15.48	22.22	9.32	11.09	8.76	5.34	11.12	9.16	*	*	-	-
	NT2RP2002710	30.61	29.84	37.75	21.5	19.35	13.67	11.45	15.23	13.68	*	**	-	-
10	NT2RP2002721	7.29	6.84	7.35	5.81	4.84	2.96	3.61	3.96	1.62	*	**	-	-
	NT2RP2002727	6.54	9.38	10.59	7.9	7.44	4.24	4.08	5.05	3.6	*		-	-
	NT2RP2002734	48.13	41.34	40.09	29.15	43.09	31.56	39.87	34.2	33.11			-	-
	NT2RP2002736	9.71	9.47	8.91	9.58	7.4	9.48	7.64	7.21	5.83	*		-	-
	NT2RP2002740	19.4	13.22	23.87	11.87	7.31	11.43	6.19	11.24	13.39			-	-
	NT2RP2002741	23.72	17.52	33.51	16.7	12.26	14.24	12.67	22.55	22.7			-	-
15	NT2RP2002750	63.6	50.03	64.42	39.1	24.44	35.13	36.13	36.29	30.98	*	**	-	-
	NT2RP2002752	10.52	9.47	15.12	8.58	15.15	3.88	2.8	5.03	3.54	*		-	-
	NT2RP2002753	12.15	11.11	17.25	9.74	6.82	4.55	5.04	8.44	4.88	*		-	-
	NT2RP2002760	73.48	81.4	101.38	101.02	88.73	62.2	63.54	64.02	59.41			-	-
	NT2RP2002769	92.25	85.07	85.98	43.44	97.23	54.77	13.8	14.78	19.89	**		-	-
	NT2RP2002778	10.58	7.74	8.45	8.8	4.88	4.14	4.05	4.2	5.19	**		-	-
20	NT2RP2002791	21.96	17.69	24.67	15.97	10.79	19.44	8.98	15.96	17.2			-	-
	NT2RP2002800	57.56	44.66	67.26	27.41	29.24	35	38.77	66.85	61.35	*		-	-
	NT2RP2002805	10.55	19.25	27.64	13.98	23.59	9.88	7.4	10.07	7.75			-	-
	NT2RP2002811	13.01	13.43	18.61	12.19	7.67	8.64	7.15	10.12	7.7	*		-	-
	NT2RP2002824	16.63	12.33	20.93	15.22	10.57	11.14	9.08	9.37	7.94	*		-	-
25	NT2RP2002839	7.61	6.4	5.94	5.9	4.06	3.3	9.77	3.03	3.13			-	-
	NT2RP2002845	12.27	9.25	11.68	10.47	8.06	5	6.84	6.96	4.06	*		-	-
	NT2RP2002857	13.78	16.15	14.57	14.65	30.41	11.09	9.34	6.45	5.36	**		-	-
	NT2RP2002862	39.8	48.81	41.43	30.51	20.27	24.76	25.07	37.41	27.22	*	*	-	-
	NT2RP2002880	68.2	65.99	77.82	51.13	34.35	43.94	48.02	65.53	66.61	*		-	-
	NT2RP2002885	6.6	7.46	15.43	8.27	7.08	4.47	4.01	3.85	3.27			-	-
30	NT2RP2002891	7.27	7.43	13.2	9.04	9.22	4.71	4.88	7.24	5.8			-	-
	NT2RP2002907	27.84	27.28	39.25	27.93	20.22	19.34	24.71	20.15	30.92			-	-
	NT2RP2002925	8.14	12.06	8.92	6.22	5.24	3.39	2.57	2.53	2.32	*	**	-	-
	NT2RP2002927	11.04	11.53	9.75	8.5	11.71	5	4.88	3.47	4.87	**		-	-
	NT2RP2002928	14.93	19.65	15.07	19.82	17.04	17.08	11.05	6.88	7.13	*		-	-
	NT2RP2002929	34.38	37.86	32.48	20.14	17.6	22.45	18.17	27.25	31.67	**		-	-
35	NT2RP2002934	25.44	20.87	30.69	18.19	13.85	16.46	17.37	22.76	21.39	*		-	-
	NT2RP2002939	16.49	24.31	21.25	14.42	15.1	11.79	7.22	8.55	7.99	*	**	-	-
	NT2RP2002942	60.99	80.16	86.43	63.29	72.69	51.11	69.34	65.39	67.68			-	-
	NT2RP2002954	14.37	21.3	26.97	15.75	10.45	11.22	8.24	9.15	9.35	*		-	-
	NT2RP2002959	11.9	10.85	14.73	7.3	8.01	4.57	5.17	3.69	3.58	*	**	-	-
	NT2RP2002974	27.97	23.95	30.02	18.63	11.35	13.46	21.06	14.1	16.2	*	*	-	-
40	NT2RP2002976	33.37	27.08	30.74	41.03	19.52	40.87	48.18	35.03	46.65	*		-	+
	NT2RP2002979	34.44	28.83	35.03	24.79	13.64	25.53	28.21	33.42	38.67			-	-
	NT2RP2002980	56.79	52.53	62.74	67.66	61.62	49.88	36.91	45.4	40.52	*		-	-
	NT2RP2002986	8.8	8.37	8.86	6.06	9.31	3.85	4.83	5.06	6.03	**		-	-
	NT2RP2002987	103.6	100.12	86.59	73.66	56.64	94.83	99.25	107.73	109.15			-	-
	NT2RP2002988	13.55	24.45	23.43	8.39	5.16	5.67	6.67	7.13	6.64	*	*	-	-
45	NT2RP2002993	30.07	31.12	32.86	20.82	20.33	19.14	25.73	28.68	29.96	**		-	-
	NT2RP2003000	23.19	27.52	36.47	14.21	13.97	11.57	16.09	13.68	17.86	*	*	-	-
	NT2RP2003008	20.38	21.66	17.68	30.65	18.58	30.92	20.83	11.54	23.71			-	-
	NT2RP2003020	8.4	9.59	8.76	9.59	3.53	4.92	4.04	6.43	6.19	*		-	-
	NT2RP2003032	16.62	21.12	22.97	11.47	10.11	7.97	7.7	9.72	7.64	**	**	-	-
	NT2RP2003034	9.72	12.06	10.53	7.37	15.19	4.72	7.75	4.61	8.9			-	-
50	NT2RP2003042	7.27	6.68	12.91	7.34	5.07	3.54	6.69	5.74	4.38			-	-
	NT2RP2003050	41.14	39.77	34.47	22.7	14.89	22.18	30.79	33.73	32.33	**	*	-	-
	NT2RP2003060	13.62	10.73	6.38	6.73	19.61	3.28	5.01	3.28	4.49			-	-
	NT2RP2003073	11.88	8.02	5.9	7.53	3.76	4.73	2.61	3.98	5.14			-	-
	NT2RP2003099	15.8	18.78	12.88	19.36	10.86	16.96	13.15	11.19	10.41			-	-
	NT2RP2003108	16.99	10.19	16.94	12.41	6.81	13.81	6.41	10.09	7.95			-	-
55	NT2RP2003115	140.52	119.44	125.07	149.82	106.25	154.27	145.7	152.43	149.71	*		-	+
	NT2RP2003117	8.58	4.12	8.6	7.48	2.66	5.97	6.92	5.37	6.56			-	-
	NT2RP2003121	15.37	11.96	21.6	10.75	8.2	9.97	7.29	7.74	8.68	*		-	-

Table 429

	NT2RP2003125	148.62	154.21	165.76	136.93	87.76	119.3	202.39	170.18	181.03				
	NT2RP2003127	8.19	13.35	12.24	9.29	4.08	4.24	7.52	6.27	6.75				
5	NT2RP2003129	5.37	4.98	2.74	4.8	1.83	1.5	2.73	2.54	2.23				
	NT2RP2003137	9.57	8.81	8.47	10.46	3.57	7.13	10.02	8.73	11.39				
	NT2RP2003138	289.53	193.02	256.72	147.84	144.9	131.2	108.58	156.98	150.94	*	*	-	-
	NT2RP2003146	1.24	1.09	7.94	3.13	0.31	1.29	1.86	1.99	1.77				
	NT2RP2003148	8.05	4.25	16.47	5.03	5.56	4.21	3.03	3.24	3.73				
10	NT2RP2003150	10.24	5.66	13.18	8.31	3.11	3.88	5.08	3.43	3.42				
	NT2RP2003157	3.48	4.11	8.05	5.53	2.9	2.53	3.08	2.08	2.29				
	NT2RP2003158	154.65	121	143.84	65.15	86.73	95.34	71.82	47.48	71.44	*	**	-	-
	NT2RP2003161	7.49	10.19	13.16	11.02	5.25	6.57	6.09	5.72	4.72		*	-	-
	NT2RP2003164	3.55	3.69	5.64	7.04	3.38	4.04	7.46	5.26	5.34				
	NT2RP2003165	12.93	8.52	16.52	10.68	5.85	8.09	3.19	7.18	6.13				
15	NT2RP2003177	20.41	17.38	32.83	19.51	10.51	7.06	22.73	21.74	21.1				
	NT2RP2003179	13.75	8.83	17.7	6.83	5.73	5.2	6.82	13.09	8.84	*		-	-
	NT2RP2003194	60.36	55.91	80.01	51.34	60.6	65.85	42.59	38.48	56.22				
	NT2RP2003206	4.24	5.6	7.88	6.81	4.57	3.96	3.75	3.9	1.77				
	NT2RP2003210	9.9	9.36	13.05	7.55	5.04	4.08	4.47	4.65	4.08	*	**	-	-
	NT2RP2003227	13.08	17.16	19.16	9.3	7.87	5.3	8.38	6.37	6.65	*	**	-	-
20	NT2RP2003228	16.97	20.02	17.73	19.68	23.22	23.38	16.96	9.41	24.11				
	NT2RP2003230	8.37	4.38	11.24	9.26	4.24	4.38	5.34	6.55	20.33				
	NT2RP2003231	19.49	17.75	28.22	19.04	13.83	13.5	4.32	15.06	15.52				
	NT2RP2003237	7.53	6.29	14.94	7.53	4.21	4.44	2.72	5.12	9.5				
	NT2RP2003239	14.69	12.62	13.82	13.64	7.63	7.59	6.01	11.3	7.74		*	-	-
	NT2RP2003243	18.5	16.09	21.39	14.68	13.35	11.44	13.72	14.6	10.6	*	*	-	-
25	NT2RP2003265	4.16	3.24	4.88	3.11	1.7	1.76	2.29	2.88	1.56	*	*	-	-
	NT2RP2003267	60.51	57	71.61	43.05	41.52	45.26	62.57	46.27	55.1	*		-	-
	NT2RP2003272	18.93	12.31	21.16	15.62	7.25	9.68	9.71	5.82	7.07		*	-	-
	NT2RP2003277	51.75	42.05	60.1	30.74	24.84	22.69	27.09	34.52	27.77	*	*	-	-
	NT2RP2003280	28.6	31.79	33.98	27.16	26.4	22.37	7.26	22.23	17.9	*	*	-	-
	NT2RP2003286	5.27	5.54	11.77	5.48	3.75	3.02	2.08	4.89	2.65				
30	NT2RP2003293	449.62	544.88	531.61	480.84	613.42	591.27	492.68	295.17	642.99				
	NT2RP2003295	31.05	28.41	29.77	21.7	14.01	19.1	19.18	18.46	19.51	**	**	-	-
	NT2RP2003297	16.92	17.67	19.83	9.38	11.73	7.84	3.24	6.26	6.08	**	**	-	-
	NT2RP2003300	2.42	4.36	4.19	5.32	2.8	1.56	2.33	1.69	1.31				
	NT2RP2003302	4.27	4.34	3.48	7.02	4.29	2.92	3.56	4.67	4.2				
	NT2RP2003307	17.52	15.84	29.67	14.93	9.5	10.4	16.58	17.1	22.41				
35	NT2RP2003308	7.26	8.66	14.15	6.9	4.51	4.44	3.22	4.76	6.65				
	NT2RP2003311	29.64	20.85	41.04	22.79	16.59	15.7	26.2	28.58	26.19				
	NT2RP2003329	11.36	11.27	19.3	9.84	10.72	8.3	6.72	6.84	5.55		*	-	-
	NT2RP2003339	44.06	51.39	68.66	63.28	61.45	41.92	35.03	31.79	30.76		*	-	-
	NT2RP2003345	25.41	28.87	30.12	15.65	24.89	17.7	13.62	14.02	13.58	*	**	-	-
	NT2RP2003347	8.25	20.81	11.17	7.75	7.09	4.08	5.16	5.37	4.53				
40	NT2RP2003367	15.71	9.07	15.92	25.01	12.88	13.97	19.6	13.55	17.34				
	NT2RP2003369	28.62	21.24	26	8.89	11.95	10.09	4.71	10.13	9.11	**	**	-	-
	NT2RP2003383	14.02	11.63	23.31	10.33	7.37	5.29	4.94	12.01	8.63				
	NT2RP2003390	5.02	4.43	9.92	6.51	4.16	1.23	2.19	2.28	1.48				
	NT2RP2003391	7.9	10.18	14.85	7.86	4.63	3.15	3.6	3.53	4.66		*	-	-
	NT2RP2003393	17.88	10.78	13.47	5.99	12.67	3.97	3.38	3.45	4.48		**	-	-
45	NT2RP2003394	86	76.58	96.35	85.96	75.14	69.1	44.7	55.38	51.85		**	-	-
	NT2RP2003401	6.44	4.6	7.19	7.26	3.17	2.2	2.64	2.79	2.35		*	-	-
	NT2RP2003403	18.73	19.58	18.59	16.65	31.07	15.94	9.34	7.98	7.02		**	-	-
	NT2RP2003433	8.13	7.64	13.92	4.56	2.36	2.9	0.77	3.05	2.35	*	*	-	-
	NT2RP2003445	11.02	10.94	17.55	8.15	5.02	3.19	3.72	5.83	4.71	*	*	-	-
	NT2RP2003446	7.38	5.87	15.32	8.9	3.31	1.64	2.84	3.34	2.61				
50	NT2RP2003456	14.58	16.09	17.24	7.76	9.78	4.68	6.41	6.61	4.94	**	**	-	-
	NT2RP2003466	163.89	136.64	191.26	110.44	140.48	151.43	83.63	87.04	121.39		*	-	-
	NT2RP2003469	5.44	3.7	5.03	4.74	2.31	1.35	2.28	1.42	1.62		**	-	-
	NT2RP2003470	4.83	5.55	5.49	5.65	3.19	3.4	4.42	1.43	3				
	NT2RP2003471	12.29	11.22	13.81	11.17	23.08	8.88	5.31	3.9	2.98		**	-	-
	NT2RP2003480	133.45	297.88	151.87	131.22	166.23	117.7	104.84	202.75	202.47				
55	NT2RP2003495	2.81	3.4	10.31	5.19	1.55	2.41	0.68	1.49	0.7				
	NT2RP2003499	5.25	3.3	9.47	3.94	2.15	2.35	2.44	6.25	5.89				
	NT2RP2003505	1.66	1.94	6.72	4.41	2.46	0.11	0.21	3	0				

Table 430

	NT2RP2003506	18.91	15.11	21.41	10.64	13.4	7.04	4.15	4.83	3.94	*	**	-	-
	NT2RP2003511	12.05	3.9	4.64	8.42	8.48	3	2.22	2.49	1.23			-	-
5	NT2RP2003513	5.02	4.48	4.09	4.53	1.64	2.04	2.58	1.55	3.7	*		-	-
	NT2RP2003517	3.09	1.94	2.24	4.01	1.27	1.81	1.81	0.62	1.53			-	-
	NT2RP2003522	5.79	5.52	8.11	4.61	3.87	1.76	1.31	4.96	5.44			-	-
	NT2RP2003525	12.34	13.08	16.44	6.02	5.34	4.08	6.04	6.6	5.02	**	**	-	-
	NT2RP2003533	88.01	167.21	169.95	95.54	157.31	89.62	178.82	120.18	151.89			-	-
10	NT2RP2003541	3.67	3.34	5.25	3.35	1.69	1.26	1.11	0.78	0.47		**	-	-
	NT2RP2003543	6.02	7.31	6.9	4.81	3.89	1.42	3.96	1.71	3.06	*	**	-	-
	NT2RP2003545	16.66	28.91	37	10.57	5.83	7.38	9	7.02	10.57	*	*	-	-
	NT2RP2003559	24.73	30.59	37.42	18.05	13.28	13.04	17.81	5.8	6.39	*	*	-	-
	NT2RP2003564	4.21	3.5	2.84	5.11	2.21	2.76	1.47	1.11	1.54	**		-	-
	NT2RP2003565	5.56	6.05	9.75	8.3	2.97	4.12	3.13	4.62	3.34			-	-
15	NT2RP2003567	52.47	49.61	31.71	25.62	16.56	16.12	8.17	19.23	14.83	*	*	-	-
	NT2RP2003575	228.18	422	264.34	79.35	234.74	114.07	248.45	399.29	319.2			-	-
	NT2RP2003576	12.51	13.48	14.93	11.41	10.35	7.47	9.35	12.38	11.58	*		-	-
	NT2RP2003579	6.35	14.72	8.69	5.77	5	3.85	5.14	3.96	3.9			-	-
	NT2RP2003581	5.18	8.39	5.74	5.34	1.72	1.57	1.66	0.89	1.73	**		-	-
	NT2RP2003587	5.23	4.31	3.93	4.85	1.48	2.81	2.91	3.12	2.6	*		-	-
20	NT2RP2003590	10.26	7.56	7.31	8.22	4.4	10.25	8.81	5.02	6.24			-	-
	NT2RP2003593	30.36	26.83	29	16.89	17.04	17.86	10.43	21.71	15.35	**	*	-	-
	NT2RP2003596	9.32	8.79	11.25	13.55	9.73	9.49	8.79	14.74	9.47			-	-
	NT2RP2003599	23.27	13.17	35	8.05	27.81	6.94	3.86	4	10.53			-	-
	NT2RP2003600	19.86	30.4	31.86	22.5	9.14	19.7	15.99	13.53	9.08		*	-	-
	NT2RP2003604	5.88	9.89	7.47	5.4	1.89	1.85	3.39	3.16	2.76	*	*	-	-
25	NT2RP2003629	8.19	7.7	5.26	5.58	3.64	2.51	3.1	3.51	2.87	*		-	-
	NT2RP2003630	4.6	3.1	1.8	4.67	0.47	1.48	1.43	1.9	2.02			-	-
	NT2RP2003643	14.26	14.44	12.75	14.01	7.67	9.12	19.42	10.04	13.07			-	-
	NT2RP2003655	7.62	6.24	7.73	7.33	2.44	6.8	2.97	5.19	4.57	*		-	-
	NT2RP2003664	8.96	13.57	11.03	11.23	17.02	7.98	3.52	3.83	3.73	**		-	-
	NT2RP2003668	5.83	2.7	3.35	6.14	1.92	4.61	2.43	9.15	4.25			-	-
30	NT2RP2003687	2.45	2.75	3.32	4.63	0.64	2.77	0.71	2.3	0.91			-	-
	NT2RP2003691	2.86	0.41	1.55	4.29	1.06	2.07	1.69	2.35	1.51			-	-
	NT2RP2003702	7.99	4.44	8.03	9.77	1.89	6.56	5.26	5.52	3.42			-	-
	NT2RP2003704	6.11	9.87	8.33	7.33	6.55	3.79	6.43	2.95	5.24			-	-
	NT2RP2003706	7.36	9.13	9.09	6.95	3.88	3.8	6.16	3.16	4.56	*	*	-	-
	NT2RP2003713	10.55	5.71	14.4	8.75	4.92	4.56	5.34	3.61	4.08			-	-
35	NT2RP2003714	8.27	4.37	12.63	8.63	2.38	6.34	8.02	5.56	6.23			-	-
	NT2RP2003727	13.72	9.91	16.65	14.5	8.49	5.28	4.4	3.92	5.54	*		-	-
	NT2RP2003737	5.45	5.17	12.85	7.76	3.42	3.25	3.61	5.76	7.42			-	-
	NT2RP2003751	4.58	1.12	4.62	4.58	0.42	0.71	2.16	1.87	0.69			-	-
	NT2RP2003760	5.71	6.37	7.89	7.16	2.44	3.65	5.58	4.39	4.01			-	-
	NT2RP2003764	4.38	3.82	3.93	5.42	1.13	2.52	3.39	1.74	2.45	*		-	-
40	NT2RP2003769	20.81	10.06	18.85	16.88	9.37	7.83	5.73	10.32	7.17			-	-
	NT2RP2003770	46.73	23.49	36.27	27.58	17.68	15.16	13.53	17.82	25.92			-	-
	NT2RP2003777	15.17	10.4	15.63	9.4	5.35	5.3	5.51	8.22	8.17	*	*	-	-
	NT2RP2003781	85.09	53.2	80.23	44.9	32.89	44.6	88.34	75.84	75.38	*		-	-
	NT2RP2003785	11.62	18.04	20.61	13.78	15.2	6.96	6.32	9.84	5.9	*		-	-
	NT2RP2003793	16.4	16.91	28.84	17.84	16.4	19.5	8.6	5.86	10.58	*		-	-
45	NT2RP2003806	22.61	30.87	30.72	19.98	15.24	17.95	21.46	20.85	31.8	*		-	-
	NT2RP2003825	121.72	69.01	127.36	108.65	103.08	122.02	106.86	101.92	114.26			-	-
	NT2RP2003840	11.66	9.2	14.49	9.94	6.01	4.99	5.06	8.29	6.32	*		-	-
	NT2RP2003857	12.37	17.33	20.12	13.2	12.38	5.39	3.92	13.14	19.37			-	-
	NT2RP2003859	19.27	8.66	21.11	12.54	7.05	8.25	8.14	9.73	13.41			-	-
	NT2RP2003871	24.21	21.74	19.35	11.95	9.6	10.67	5.81	8.41	8.75	**	**	-	-
50	NT2RP2003876	10.53	11.98	18.66	19.02	25.1	11.05	7.68	10.36	8.8			-	-
	NT2RP2003878	8.32	9.1	10.32	8.36	3.76	3.6	4.02	3.95	3.32	**		-	-
	NT2RP2003885	6.08	8.46	6.77	5.72	4.33	2.2	4.11	3.32	4.21	*		-	-
	NT2RP2003898	16.47	22.78	20.73	12.55	8.77	11.94	7.99	8.27	7.33	*	**	-	-
	NT2RP2003902	21.99	10.54	20.36	16.69	8	10.58	8.28	15.68	15.89			-	-
	NT2RP2003912	35.16	73.65	32.26	21.86	23.82	12.49	13.87	18.46	19.33			-	-
55	NT2RP2003931	16.31	15.84	40.63	15.98	12.61	14.09	15.19	20.43	45.95			-	-
	NT2RP2003940	26.29	28.19	28.81	19.73	11.64	14	20.12	28.2	22.66	**		-	-
	NT2RP2003950	10.42	7.47	13.08	10.4	5.75	5.62	6.83	8.37	6.11			-	-

Table 431

	NT2RP2003952	8.61	6.4	10.47	5.99	3.42	3.14	3.11	4	4.05	*	*	-	-
	NT2RP2003968	14.45	22.39	24.81	11.6	25.12	6.38	6.57	9.01	14.39				
5	NT2RP2003976	33.5	36.02	32.11	28.15	26.29	22.25	25.49	23.11	18.45	*	**	-	-
	NT2RP2003981	10.38	7.73	15.47	7.98	3.66	7.9	3.93	9.3	6.45				
	NT2RP2003984	21.86	17.33	21.82	17.29	10	7.7	4.79	10.99	18.59				
	NT2RP2003986	29.04	20.99	42.5	17.22	10.08	14.95	20.31	27.16	19.47				
	NT2RP2003988	17.98	13.51	22.96	15.07	9.71	10.14	10.31	12.25	15.8				
10	NT2RP2004013	76.9	66.49	68.74	48.94	44.57	34.09	28.41	25.31	32.75	**	**	-	-
	NT2RP2004014	12.05	10.78	9.86	7.34	4.69	5.32	4.75	6.66	7.06	**	**	-	-
	NT2RP2004036	38.11	34.32	48.47	33.97	30.52	34.54	23.89	26.94	32.83				
	NT2RP2004041	15.68	9.6	13.65	12.24	6.88	6.29	9.46	7.39	4.47				
	NT2RP2004042	10.47	6.9	14.24	8.26	4.18	4.2	3.12	8.29	6.46				
	NT2RP2004049	50.08	29.35	58.86	54.03	47.21	47.08	23.48	30.4	35.04				
15	NT2RP2004060	14.43	11.83	19.24	13.07	7.66	8.82	6.25	9.01	6.7	*		-	-
	NT2RP2004066	9.22	7.65	15.12	7.14	3.11	3.37	2.62	3.51	3.15	*		-	-
	NT2RP2004069	13.07	11	19.34	9.29	5.59	3.82	4.85	6.14	4.78	*		-	-
	NT2RP2004076	7.23	8.97	8.94	6.15	5.2	2.62	3.55	3.66	4.01	*	**	-	-
	NT2RP2004080	16.76	19.32	21.22	10.81	7.94	4.93	7.71	6.49	6.54	**	**	-	-
	NT2RP2004081	12.13	9.06	12.95	7.67	4.89	5.2	4.76	5.29	3.41	*	**	-	-
20	NT2RP2004098	14.04	9.1	18.6	7.17	4.55	6.94	5.74	6.96	7.08				
	NT2RP2004108	15	13.48	22.62	10.06	6.21	6.99	5.4	7.73	10.17	*	*	-	-
	NT2RP2004124	8.21	9.75	17.19	8.66	5.64	4.42	4.13	6.1	2.63				
	NT2RP2004130	14.54	18.18	16.71	14.91	10.54	10.38	6.64	6.32	8.03	**		-	-
	NT2RP2004133	9.17	7.74	14.55	6.02	4.47	1.66	3.8	2.83	1.86	*		-	-
	NT2RP2004141	13.91	8.7	8.65	9.25	5.97	4.12	2.68	2.87	3.2	*		-	-
25	NT2RP2004142	20.24	20.66	23.15	12.58	8.99	0.11	7.76	8.1	8.83	*	**	-	-
	NT2RP2004152	12.94	17.34	28.22	13.04	12.79	7.85	8.66	8.13	4.02				
	NT2RP2004165	23.06	20.1	27.11	14.41	8.19	16.16	10.91	12.82	15.14	*	*	-	-
	NT2RP2004170	14.84	22.1	21.27	11.56	5.42	12.52	7.64	14.97	10.1	*		-	-
	NT2RP2004172	11.82	8.43	19.13	9.78	6.86	6.4	5.08	5.49	3.29				
	NT2RP2004176	16.04	24.68	27.17	14.08	13.85	12.56	15.42	21.18	13.53				
30	NT2RP2004179	11.06	11.88	18.99	6.12	3.68	3.62	3.12	4.46	3.04	*	*	-	-
	NT2RP2004187	10.62	14.3	17.05	10.83	6.49	6	6.3	3.3	5.65	*		-	-
	NT2RP2004190	11.44	13.08	11.65	11.65	16.98	5.99	14.27	4.91	8.09				
	NT2RP2004194	34.23	32.85	35.34	19.96	14.64	15.16	22.5	12.25	14.92	**	**	-	-
	NT2RP2004196	30.83	39.33	27.33	12.84	5.98	11.23	10.98	13.1	14.08	**	**	-	-
	NT2RP2004205	29.01	29.84	37.62	20.1	10.4	15.74	17.25	16.98	24.08	*	*	-	-
35	NT2RP2004207	8.99	13.88	16.49	8.05	7.02	4.72	8.6	7.78	25.16				
	NT2RP2004226	17.66	11.75	16.67	11.25	9.6	5.13	9.93	6.52	8.04	*		-	-
	NT2RP2004232	9.38	7.39	12.33	6.45	7.37	3.57	6.49	3.42	8.98				
	NT2RP2004239	9.12	12.33	10.22	7.52	5.19	3.55	2.71	5.07	3.29	*	**	-	-
	NT2RP2004240	34.67	45.84	33.56	20.39	18.64	6.67	14.35	6.97	4.81	*	**	-	-
	NT2RP2004242	15.64	15.83	16.65	14.76	9.29	9.76	10.22	6.01	6.98	**		-	-
40	NT2RP2004245	7.49	8.21	10.79	7.33	2.04	4.45	4.33	4.59	4.95	*		-	-
	NT2RP2004270	62.73	47.21	68.41	46.4	33.04	45.75	50.52	75.49	70.49				
	NT2RP2004300	12.51	8.53	13.1	8.54	9.07	5.04	6.79	9.38	7.79				
	NT2RP2004304	16.04	25.81	28.38	10.74	8.89	6.86	7.57	8.7	9.4	*	*	-	-
	NT2RP2004313	5.32	5.55	8.05	4.79	1.11	1.27	2.98	2.46	2.35	*		-	-
	NT2RP2004316	7.59	19.66	19.22	7.37	4.16	2.63	3.4	2.3	5.68	*		-	-
45	NT2RP2004321	11.35	10.01	12.72	6.18	1.74	2.16	3.62	2.37	4.34	**	**	-	-
	NT2RP2004336	6.56	6.01	5.01	7.15	3.83	3.55	3.86	1.85	3.64	*		-	-
	NT2RP2004339	86.87	54.65	64.97	50.21	27.02	70.75	73.53	111.22	98.32				
	NT2RP2004347	9.56	12.29	15.81	9.78	3.94	5.75	4.47	6.18	9.27				
	NT2RP2004364	17.82	15.18	19.5	11.98	7.62	12.3	9.63	15.21	13.78	*		-	-
	NT2RP2004365	16.43	16.15	23.6	8.67	8.61	4.88	6.23	5.81	4.59	*	**	-	-
50	NT2RP2004366	6.71	10.58	9.59	7.66	3.53	5.17	5.46	3.22	3.29	*		-	-
	NT2RP2004373	12.26	11.21	11.74	7.26	2.71	4.58	3.35	3.56	4.51	**	**	-	-
	NT2RP2004375	63.47	77.52	81.72	36.96	16.48	21.89	34.46	29.81	18.56	**	**	-	-
	NT2RP2004389	11.31	16.36	12.26	9.91	2.21	4.95	5.82	4.38	4.02	*	**	-	-
	NT2RP2004392	57.13	31.73	43.78	20.38	16.25	19.24	10.86	16.27	14.58	*	*	-	-
	NT2RP2004396	13.42	9.2	11.06	9.69	3.89	7.39	5.67	7.43	7.76	*		-	-
55	NT2RP2004399	25.77	19.74	26.11	15.91	12.56	15.11	9.21	12.21	10.01	*	**	-	-
	NT2RP2004400	10.29	9.25	9.33	9.9	4.17	8.44	7.31	8.61	9.43				
	NT2RP2004404	142.91	126.47	123.47	87.01	85.43	109.26	171.94	127.81	174.94	*		-	-

Table 432

	NT2RP2004410	39.53	65.74	46.52	39.11	16.74	16.36	21.28	23.23	25.45	*	-
	NT2RP2004412	14.74	10.36	20.72	26.06	1.96	8.17	8.89	4.91	6.36		
5	NT2RP2004414	8.26	7	7.21	7.75	3.36	2.32	8.71	6.3	5.47		
	NT2RP2004425	10.2	6.28	19.09	7.43	2.9	4.39	7.1	5.14	4.24		
	NT2RP2004447	7.9	4.2	15.6	7.23	1.76	4.51	4.43	8.04	6.17		
	NT2RP2004463	53.44	48.94	45.23	51.07	39.96	24.66	38.74	19.02	17.11	*	-
	NT2RP2004476	18.45	12.59	23.94	14.93	16.73	11.7	16.21	16.49	14.59		
	NT2RP2004488	10.21	10.37	13.58	8.53	5.46	7.65	8.97	6.18	4.15	*	*
10	NT2RP2004490	6.88	9.48	11.96	10.41	4.06	3.06	6.4	5.15	3.37		
	NT2RP2004495	59.84	40.86	52.11	47.08	29.44	39.52	53.9	45.74	40.44		
	NT2RP2004512	17.42	8.07	18.38	11.03	4.08	6.19	1.75	5.77	3.87	*	-
	NT2RP2004523	26.61	22.99	26.09	20.55	9.56	18.73	12.96	22.93	30.09		
	NT2RP2004524	21.22	18.85	29.36	17.14	12.55	10.77	11.27	10.59	14.51	*	-
	NT2RP2004536	39.58	17.04	37.57	26.29	26.05	14.38	14.91	28.86	19.32		
15	NT2RP2004538	145.51	113.79	134.59	95.27	89.81	81.41	118.33	103.7	132.33	*	-
	NT2RP2004548	21.33	25.87	20.88	16.6	11.36	9.17	14.62	15.2	15	*	**
	NT2RP2004551	8.55	11.05	18.95	8.38	5.63	4.59	5.77	5.04	6.54		
	NT2RP2004556	107.44	116.09	115.34	100.64	83.01	68.21	138.61	66.34	73.2	*	-
	NT2RP2004568	25.54	15.99	32.04	18.77	7.42	18.63	9.21	19.06	44.48		
	NT2RP2004580	28.48	22.84	30.46	23.04	12.01	15.3	24.34	30.63	24.49		
20	NT2RP2004585	104.19	75.97	102.59	102.16	96.71	82.97	64.51	65.78	63.06	*	-
	NT2RP2004587	7.64	7.71	10.73	6.38	2.94	4.03	2.08	3.66	11.64	*	-
	NT2RP2004594	9.49	13.7	13.53	10.94	10.06	5.96	7.18	7.17	14.25		
	NT2RP2004600	11.79	11.86	12.42	9.8	6.39	8.89	9.84	7.14	9.81	*	*
	NT2RP2004602	16.85	24.33	21.89	13.29	12.49	8.02	12.27	7.59	7.04	*	*
	NT2RP2004606	282.85	252.35	268.41	181.43	249.55	245.26	257.06	189.04	158.13		
25	NT2RP2004614	9.31	7.04	11.06	6.07	2.67	4.48	3.52	3.61	6.4	*	*
	NT2RP2004648	12.5	37.87	41.62	14.38	8.31	11.65	10.13	8.24	22.59		
	NT2RP2004655	27.02	40.5	41.28	26.01	23.69	13	4.9	10	13.87	**	-
	NT2RP2004664	12.3	12.14	15.06	9.64	6.17	5.52	2.65	4.39	2.54	*	**
	NT2RP2004670	9.81	11.79	9.6	6.17	5.86	2.45	3.26	4.14	2.42	*	**
	NT2RP2004675	22.26	31.4	25.45	19.55	10.99	11.73	17.4	17	31.58	*	-
30	NT2RP2004681	11.82	17.49	14.89	8.26	5.82	3.58	5.62	7.61	5.68	*	**
	NT2RP2004689	5.34	26.14	16.38	16.38	9.9	10.44	10.84	15.98	14.64		
	NT2RP2004709	38.28	22.19	35.75	22.32	11.28	19.42	7.33	20.31	16.27		
	NT2RP2004710	23.78	32.41	33.69	19.19	16.47	14	10.16	17.13	21.44	*	*
	NT2RP2004721	16.3	9.83	18.51	7.64	2.48	4.31	3.84	6.3	2.86	*	*
	NT2RP2004736	12.51	12.2	14.69	12.94	8.12	6.27	5.93	10.36	6.34	*	-
35	NT2RP2004743	18.86	18.19	16.11	11.52	9.54	6.56	6.31	8.72	9.61	**	**
	NT2RP2004750	59.2	56.12	63.52	47.6	43.74	38.38	59.22	63.07	62.81	**	-
	NT2RP2004755	27.3	33.26	34.09	17.59	21.76	19.12	17.05	12.23	8.96	**	**
	NT2RP2004767	16.81	19.28	18.07	14.61	10.15	10.32	11.83	8.67	9.96	*	**
	NT2RP2004768	39.27	17.22	28.44	49.02	23.23	30.46	23.63	20.93	17.76		
	NT2RP2004775	10.4	6.35	15.81	7.59	3.37	4.94	1.86	3.35	3.03	*	-
40	NT2RP2004791	35.3	37.93	43.25	33.95	20.1	16.04	17.4	29.11	27.1	*	-
	NT2RP2004794	54.46	52.25	59.56	37.23	24.39	16.04	14.21	17.04	17.83	*	**
	NT2RP2004795	16.82	13.04	16.28	12.97	8.52	3.96	6.33	6.26	8.64	**	-
	NT2RP2004799	16.76	14.17	14.52	9.03	7.47	5.55	2.73	2.76	3.58	**	**
	NT2RP2004802	42.99	46.43	41.16	46.78	39.32	30.76	28.53	29.92	38.26	*	-
	NT2RP2004810	18.3	18.68	17.35	9.03	6.57	4.19	8.85	4.21	4.39	**	**
45	NT2RP2004816	30.61	34.82	43.2	16.85	15.68	3.1	5.7	11.84	0.57	*	**
	NT2RP2004837	55.01	32.88	59.21	31.78	19.92	27.08	12.99	11.53	9.41	*	-
	NT2RP2004841	12.28	19.6	17.04	13.83	8.03	5.66	4.26	5.92	8.44	*	-
	NT2RP2004847	56	45.24	59.59	31.54	30.59	31.44	43.02	39.63	29.66	**	-
	NT2RP2004861	6.61	6.78	10.74	6.21	2.52	2.33	3.42	5.23	3.33		
	NT2RP2004897	8.06	8.52	10.02	7.86	4.8	3.34	2.33	3.07	4.66	**	-
50	NT2RP2004932	11.96	10.46	13.81	9.34	4.73	6.48	4.87	3.86	6	*	**
	NT2RP2004933	6.78	7.42	14.62	6.21	3.1	2.23	3.41	1.97	1.54	*	-
	NT2RP2004936	9.66	18.67	21.72	10.34	4.39	7.29	2.62	3.9	3.25	*	-
	NT2RP2004951	8.57	7.11	15.72	9.26	2.32	5.42	3.11	6.13	4.04		
	NT2RP2004959	12.5	13.69	22.18	6.53	5.09	6.63	3.92	5.67	5.43	*	*
	NT2RP2004961	15.97	14.64	23.99	12.05	7.35	8.71	10.28	8.72	8.04	*	-
55	NT2RP2004962	15.99	15.58	20.13	13.9	10.21	9.93	9.78	10.65	9.69	*	**
	NT2RP2004966	6.94	8.72	7.55	5.31	3.88	2.7	4.34	2.81	2.89	*	**

Table 433

	NT2RP2004967	18.8	14.08	15.99	13.12	6.04	9.98	11.43	12.91	9.85	*	*	-	-
	NT2RP2004974	8.02	8.78	7.74	5.74	3.27	3.73	5.44	2.35	2.1	**	*	-	-
	NT2RP2004978	14.12	27.31	13.7	11.96	4.65	6.79	4.16	9.57	4.35				
5	NT2RP2004982	4.88	6.54	10.22	4.28	1.48	0.85	1.99	1	1.83	*	*	-	-
	NT2RP2004985	209.85	195.75	215.75	166.58	153.94	208.41	198.37	224.84	192.82				
	NT2RP2004999	16.04	12.97	26.42	17.44	8.41	10.32	9.65	18.31	9.11				
	NT2RP2005000	9.18	10.25	11.07	6.99	2.87	3.26	5.46	4.95	3.42	*	**	-	-
	NT2RP2005001	18.08	20.79	40.06	15.62	11.69	13.08	12.25	15.19	13.27				
10	NT2RP2005003	15.88	14.42	15.05	11.32	5.53	6.52	11.83	11.19	8.75	*	*	-	-
	NT2RP2005012	40.61	57.66	43.61	20.05	11.76	16.65	21.02	13.16	20.53	**	**	-	-
	NT2RP2005018	6.29	10.32	12.32	7.2	3.34	4.91	3.54	5.22	4.18		*	-	-
	NT2RP2005020	138.98	109.02	105.29	97.72	59.61	79.54	117.66	175.16	138.64				
	NT2RP2005022	8.77	8.01	12.34	8.19	7.74	5.07	4.96	7.16	9.74				
	NT2RP2005027	53.46	62.9	53.33	58.43	50.24	56.5	33.74	38.11	31.82		**	-	-
15	NT2RP2005031	6.85	8.81	9.58	5.73	4.02	3.36	3.46	3.48	3.14	*	**	-	-
	NT2RP2005037	16.82	18.46	19.47	6.47	4.36	2.93	2.65	3.66	6.14	**	**	-	-
	NT2RP2005038	6.96	8.98	11.09	7.2	2.46	3.49	4.34	2.45	1.1		*	-	-
	NT2RP2005048	39.21	28.46	29.89	31.24	22.21	43.14	32.34	46.11	37.29				
	NT2RP2005069	79.3	47.14	64.37	36.64	18.08	20.34	23.96	33.08	29.72	*	*	-	-
20	NT2RP2005073	67.78	54.66	62.54	70.16	48.08	81.7	55.95	55.76	57.19				
	NT2RP2005097	10.25	7.51	14.59	6.49	1.21	4.7	3.75	2.8	2.35		*	-	-
	NT2RP2005108	13.57	11.63	13.11	6.87	5.69	6.68	5.31	6.56	5.73	**	**	-	-
	NT2RP2005116	11.75	10.87	12.14	10.24	4.17	4.29	7.43	5.88	6.2		**	-	-
	NT2RP2005126	21.43	28.84	28.25	14.77	6.89	5.64	7.77	5.68	5.93	*	**	-	-
	NT2RP2005135	10.21	11.92	11.29	12.06	3.02	7.4	9.29	7.72	6.92		*	-	-
	NT2RP2005139	4.47	5.9	6.41	5.94	3.02	9.46	4.16	4.52	4.09				
25	NT2RP2005140	10.93	7.52	7.44	7.58	3.55	5.44	3	4.22	2.26		*	-	-
	NT2RP2005144	13.73	10.54	13.89	8.29	4.49	7.83	1.84	3.98	2.4	*	**	-	-
	NT2RP2005147	22.69	15.06	21.74	11.07	5.61	11.36	5.53	13.64	8.82	*	*	-	-
	NT2RP2005148	19.34	14.98	12.3	16.32	7.5	14.47	18.68	18.99	24				
	NT2RP2005159	9.52	7.06	9.83	13.34	5.14	7.92	4.36	3.56	6.05		*	-	-
	NT2RP2005162	14.54	12.5	16.31	14.53	7.94	8	8.72	9.34	7.02		**	-	-
30	NT2RP2005163	25.5	37.52	33.86	15.82	13.92	18.66	24.95	23.28	21.32	*	*	-	-
	NT2RP2005168	10.58	6.62	14.16	11.05	5.89	4.43	4.83	6.74	4.36				
	NT2RP2005181	4.05	2.99	8.75	6.74	2.11	1.29	1.74	3.19	2.03				
	NT2RP2005204	14.87	10.24	20.73	15.12	7.06	10.51	11.01	6.88	10.24				
	NT2RP2005219	24.24	19.15	32.19	26.01	12.29	15.28	21.03	18.69	23.06				
35	NT2RP2005227	12.24	9.75	17.91	17.67	5.27	7.45	11.51	12.06	11.25				
	NT2RP2005237	103.35	89.54	103.29	128.64	70.44	96.83	81.16	75.94	83.42	*	*	-	-
	NT2RP2005239	4.86	6.22	9.52	8.57	2.23	3.55	3.5	4.01	4.35				
	NT2RP2005247	22.45	26.01	32.27	32.43	14.24	19.04	34.79	31.96	33.52				
	NT2RP2005254	36.5	15.86	25.1	17.04	11.36	15.24	5.51	13.65	13.69				
	NT2RP2005270	25.5	13.21	29.5	13.51	9.93	13.53	11.24	14.21	22.67				
40	NT2RP2005276	40.6	21.43	40.17	20.18	14.43	16.86	10.58	8.43	8.36	*	*	-	-
	NT2RP2005287	16.9	10.22	25.14	13.6	9.12	7.29	8.33	9.76	8.8				
	NT2RP2005288	6.35	8.09	8.85	7.18	3.2	3.43	4.54	4.39	3.3		*	-	-
	NT2RP2005289	19.76	15.26	21.43	14.2	10.57	10.92	15.53	14.93	15.73	*	*	-	-
	NT2RP2005293	9.79	11.07	10.95	8.57	5.47	3.14	6.98	5.79	5.74	*	**	-	-
	NT2RP2005315	15.84	21	21.65	20.97	8.72	12.4	13.48	9.21	11.44		*	-	-
45	NT2RP2005322	33.55	31.7	65.28	25.82	25.53	26.43	14.38	22.11	31.46				
	NT2RP2005325	54.2	44	55.99	38.68	30.92	29.07	18.94	27.07	30.65	*	**	-	-
	NT2RP2005336	20.36	12.98	27.96	11.35	7.87	9.01	10.99	13.9	14.17				
	NT2RP2005343	12.61	22.98	14.15	9.9	5.77	8.7	7.81	10.19	10.12				
	NT2RP2005344	6.04	8.8	10.41	6.82	3.18	3.71	4.76	3.86	3.88		*	-	-
	NT2RP2005347	7.59	13.3	8.99	7.33	4.35	4.03	4.9	3.27	3.77		*	-	-
50	NT2RP2005354	41.58	40.59	43.7	31.3	21.57	29.41	26.2	24.6	22.64	**	**	-	-
	NT2RP2005358	43.39	32.77	43.03	61.06	32.41	50.49	63.9	54.2	58.54		*	+	+
	NT2RP2005360	11.79	10	18.74	11.01	6.71	7.24	3.72	6.21	9.76				
	NT2RP2005378	29.24	21.46	29.8	11.99	9.12	7.48	6.73	9.68	15.33	**	*	-	-
	NT2RP2005391	8.87	18.64	25.48	15.21	9.76	9	4.05	7.34	6.04				
	NT2RP2005393	18.88	11.72	17.99	12.44	7.52	10.75	12.61	18.43	12.16				
55	NT2RP2005407	7.79	10.99	12.03	9.14	5.76	6.4	4.56	6.12	6.26		*	-	-
	NT2RP2005419	14.03	13.17	13.95	13.78	13.3	12.37	11.42	9.28	10.02		**	-	-
	NT2RP2005425	22.13	23.63	29.77	16.49	17.86	16.5	26.07	23.18	23.95	*	*	-	-

Table 434

	NT2RP2005429	20.77	21.25	24.75	28.87	19.9	22.9	31.5	41.11	27.5			
	NT2RP2005436	21.72	21.01	36.27	15.82	10.49	11.17	6.19	10.76	15.31			
5	NT2RP2005441	12.34	10.42	16.43	6.82	3.95	2.88	3.88	5.58	7.88	*	*	-
	NT2RP2005442	100.99	76.34	97.05	85.22	107.34	64.16	56.06	96.44	76.81			
	NT2RP2005444	44.56	42.84	50.52	45	41.48	37.39	33.32	34.33	40.3		*	-
	NT2RP2005453	6.3	5.27	7.3	6.26	2.81	2.81	2.27	2.79	2.65	**		-
	NT2RP2005457	65.08	106.4	103.3	51.25	79.76	59.93	40.37	56.9	47.82	*		-
	NT2RP2005458	19.63	18.76	13.48	12.24	12.61	6.33	8.23	12.39	11.01	*		-
10	NT2RP2005463	26.71	23.66	25.36	21.35	13.39	12.75	11.08	11.67	8.93	*	**	-
	NT2RP2005464	28.8	25.9	35.07	16.26	12.23	8.38	4.05	11.36	13.81	**	**	-
	NT2RP2005465	8.44	13.41	18.06	10.55	9.11	6.34	5.69	6.77	5.88			
	NT2RP2005472	156.47	127.25	179.85	146.2	122.26	139.88	141.98	194.05	159			
	NT2RP2005476	18.49	17.23	18.61	16.08	8.51	7.62	10.76	9.58	6.82	**		-
	NT2RP2005490	38.19	48.01	41.98	41.4	60.4	46.27	36.8	25.85	27.98	*		-
15	NT2RP2005491	79.97	62.21	87.46	43.7	46.69	33.15	42.26	41.55	39.38	*	**	-
	NT2RP2005495	8.67	12.67	12.73	8.05	5.23	3.12	3.29	2.22	4.63	*	**	-
	NT2RP2005496	40.82	33.68	40.13	35.53	16.36	22.99	49.27	41.88	52.93			
	NT2RP2005498	14.64	10.07	20.28	8.15	3.71	0.94	3.15	5.06	7.24	*	*	-
	NT2RP2005501	15.01	11.26	15.06	10.4	6.02	5.78	5.37	7.88	6.8	*	**	-
	NT2RP2005506	386.46	291.76	402.21	469.63	426.17	208.66	248.04	333.44	241.6			
20	NT2RP2005509	12.93	15.67	24.29	8.78	9.8	9.01	11.69	14.68	14.73			
	NT2RP2005514	15.12	18.77	16.43	9.09	7.1	7.44	5.07	6.13	3.95	**	**	-
	NT2RP2005520	125.71	88	119.54	107.31	84.59	104.73	102.45	122.23	104.75			
	NT2RP2005525	11.61	19.18	16.45	11.91	8.22	5.77	3.77	4.63	4.84	**		-
	NT2RP2005531	6.49	2.54	4.37	5.65	2.65	0.74	1.72	1.38	1.4			
25	NT2RP2005535	28.78	24.33	27.3	18.42	7.97	16.95	13.78	20.87	16.38	*	*	-
	NT2RP2005539	7.33	11.94	18.75	8.51	6.39	4.26	3.51	3.63	4.88			
	NT2RP2005540	16.33	11.75	18.94	9.77	17.11	5.41	9.79	8.14	4.41	*		-
	NT2RP2005541	14.69	11.15	19.91	13.02	7.16	8.12	7.95	8.57	7	*		-
	NT2RP2005549	11.12	11.63	18.04	9.08	7.83	5.49	4.23	4.44	5.21	*		-
	NT2RP2005555	16.74	21.24	18.63	10.59	10.43	7.67	9.05	5.08	3.67	**	**	-
30	NT2RP2005557	15.1	14.02	12.36	10.06	7.31	4.94	4.63	4.36	4.73	*	**	-
	NT2RP2005581	28.08	26.29	29.21	26.59	10.92	19.41	31.86	21.24	23.29			
	NT2RP2005586	16.13	21.05	17.82	8.84	4.94	6.39	4.6	7.07	6.9	**	**	-
	NT2RP2005597	6.89	6.97	9.77	7.01	1.89	3.66	2.71	4.02	1.82	*		-
	NT2RP2005600	10.61	7.34	12.5	8.41	8.29	5.16	5.14	5.97	3.47	*		-
	NT2RP2005605	53.68	52.91	55.5	30.27	27.97	29.06	25.09	21.21	26.25	**	**	-
35	NT2RP2005614	9.49	10.07	16.9	6.5	3.69	4.19	2.85	3.64	2.63	*	*	-
	NT2RP2005620	17.66	10.99	8.05	7.1	2.87	3.18	7.89	3.09	3.37			
	NT2RP2005622	16.16	16.55	15.71	9.98	5.85	5.98	5.01	2.43	3.54	**	**	-
	NT2RP2005632	24.79	21.59	16.99	24.01	11.37	16.72	22.78	10.85	12.69			
	NT2RP2005635	41.82	31.3	47.35	47.22	30.84	66.01	30.58	31.82	30.82			
	NT2RP2005637	8.32	23.19	12.21	8.57	5.9	4.47	3.6	7.75	5.54			
40	NT2RP2005640	15.46	12.6	16.31	14.33	9.36	13.4	14.45	17.32	12.67			
	NT2RP2005645	23.93	18.08	21.54	10.6	8.02	9.84	11.24	9.09	9.16	**	**	-
	NT2RP2005651	27.47	30.93	34.21	15.98	10.8	18.12	23.48	20.74	24.88	**	*	-
	NT2RP2005654	13.13	10.24	14.43	6.36	4.26	2.41	3.56	3.27	5.28	**	**	-
	NT2RP2005666	12.61	72.48	13.27	7.56	5.9	4.42	7.43	6.32	9.59			
	NT2RP2005669	15.23	15	15.44	12.86	8.17	11.55	8.81	7.49	8.17	*	**	-
45	NT2RP2005670	7.59	11.17	16.69	7.09	6.37	6.24	3.98	5.41	8.38			
	NT2RP2005671	8.66	9.38	12.5	6.17	4.27	6.41	3.39	7.42	4.35	*	*	-
	NT2RP2005675	53.41	58.69	56.21	73.47	47.08	88.08	46.13	47.46	45.27	**		-
	NT2RP2005683	12.5	14.86	22.54	12.03	8.9	11.13	12.51	11.13	11			
	NT2RP2005690	7.16	9.78	9.15	7.31	2.58	3.76	6.01	4.75	5.81	*		-
	NT2RP2005694	13.45	13.78	12.27	8.68	4.9	4.46	6.63	6.81	8.01	**	**	-
50	NT2RP2005701	21.29	27.54	24.8	13.54	7.14	7.23	9.96	8.67	7.38	**	**	-
	NT2RP2005712	5.67	6.5	6.73	7.41	2.31	3.04	4.59	2.86	2.66	*		-
	NT2RP2005719	17.92	12.64	12.02	8.92	5.92	13.08	4.64	11.29	9.06			
	NT2RP2005722	24.17	15.94	25.68	22.5	8.47	9.89	8.38	12.95	9.48	*		-
	NT2RP2005723	11.76	19.91	11.37	8.9	4.43	7.12	5.8	6.31	6.59	*		-
	NT2RP2005726	13.16	8.51	18.51	13.17	7.93	10.58	7.85	8.96	10.35			
55	NT2RP2005729	20.35	17.21	20.34	11.64	9.52	5.78	12.25	8.44	10.44	**	**	-
	NT2RP2005731	4.25	2.53	4.11	5.17	0	0.69	1.06	1.65	0.86	*	*	-
	NT2RP2005732	54.72	53.14	65.72	91.69	67.12	83.97	67.17	50.47	67.53	*	+	-

Table 435

	NT2RP2005737	61.08	46.51	54.73	57.66	30.52	54.9	80.55	70.19	69.8	*	†
	NT2RP2005741	8.17	4.22	11.68	8.13	3	5.42	3.62	4.85	3.95		
5	NT2RP2005748	8.36	5.27	13.52	8.19	3.71	6.33	3.46	4.51	7.44		
	NT2RP2005752	31.75	22.62	38.43	14.99	13.75	18.04	15.51	16.74	18.45	*	*
	NT2RP2005753	34.44	30.95	48.77	33.24	26.02	18.11	26.19	25.32	15.55		
	NT2RP2005763	8.78	7.62	12.88	6.76	3.85	3.68	4.32	5.6	4.17	*	-
	NT2RP2005767	8.89	8.69	15.86	7.42	5.16	5.67	6.13	4.89	5.16		
	NT2RP2005773	53.73	61.68	69.19	40.66	32.98	33.21	37.38	30.92	21.66	**	**
10	NT2RP2005774	13.75	12.5	18.48	16.31	7.06	7.63	18.33	17.56	17.06		
	NT2RP2005775	12.13	7.53	22.24	13.73	4.82	6.66	4.04	6.6	5.74		
	NT2RP2005781	39.68	23.61	38.05	24.73	22.45	22.65	9.91	16.91	23.06		
	NT2RP2005784	30.34	20	41.77	17.54	13.38	14.34	11.13	13.26	15.12		
	NT2RP2005789	16.92	16.55	24.71	17.16	13.64	7.39	8.95	14.02	9.78		
	NT2RP2005799	11.23	8.75	9.48	10.01	3.28	4.24	3.37	6.03	3.88	**	-
15	NT2RP2005804	106.7	97.93	105.55	76.62	70.98	67.98	110.4	84.7	108.91	**	-
	NT2RP2005812	6.56	9.52	8.36	6.62	4.2	4.89	5.32	2.9	2.58	*	-
	NT2RP2005815	2.76	4.98	5.71	6.34	2.94	2.66	4.39	4.52	4.97		
	NT2RP2005835	26.87	25.04	37.02	18.31	16.79	16.79	10.34	14.43	39.55	*	-
	NT2RP2005841	22.25	27.56	27.52	20.49	14.43	16.92	11.4	11.65	19.51	*	-
	NT2RP2005853	18.13	15.89	21.67	12.41	10.18	1.04	9.88	13.51	11.3	*	-
20	NT2RP2005857	11.03	8.75	10.83	7.42	4.51	1.32	4.21	5.92	5.5	*	**
	NT2RP2005859	12.15	11.97	15.23	11.24	7.93	4.86	8.29	8.94	6.43	*	-
	NT2RP2005860	0.96	5.77	2.68	4.74	2.31	1.31	1.34	1.77	1.13		
	NT2RP2005863	8.01	8.99	7.06	7.45	6.66	5.32	7.67	5.36	4.12		
	NT2RP2005868	5.66	10.09	8.76	11.28	4.39	6.75	7.63	5.42	5.14		
25	NT2RP2005876	29.94	9.36	44.21	25.04	19.27	15.81	14.52	17.33	37.26		
	NT2RP2005878	17.4	21.07	28.07	15.86	10.5	10.77	9.96	17.05	21.58		
	NT2RP2005883	9.58	9.62	13.3	8.93	6.54	7.61	3.43	11.45	8.28		
	NT2RP2005886	109.48	86.27	131.02	108.7	95.74	145.77	77.39	72	86.69		
	NT2RP2005887	12.65	18.34	15.15	9.59	5.47	2.19	3.8	5.68	5.07	*	**
	NT2RP2005890	11.6	13.15	14.84	6.76	5.32	5.53	4.7	5.77	4.32	**	**
	NT2RP2005901	11.96	15.27	14.95	10.18	6.55	8.12	6.42	5	5.8	*	**
30	NT2RP2005902	4.82	5.49	5.62	9.24	3.69	5.72	4.9	8.33	5.18		
	NT2RP2005908	24.41	23.56	59.06	23.37	17.17	15.35	18.41	25.09	27.9		
	NT2RP2005927	7.88	6.48	15.44	8.31	4.33	4.46	3.45	5.76	4.29		
	NT2RP2005933	14.92	15.67	28.13	12.37	6.74	6	4	6.32	4.28	*	-
	NT2RP2005941	10.69	8.58	13.22	7.84	3.9	3.96	2.9	4.82	2.65	*	**
	NT2RP2005942	10.35	10.52	11.7	8.52	4	3.46	3.66	4.6	2.9	*	**
35	NT2RP2005946	8.12	19.6	14.91	5.77	6.58	2.97	4.94	4.86	6.09		
	NT2RP2005970	73.5	72.19	81.01	50.77	49.15	40.53	67.44	62.72	62.64	**	*
	NT2RP2005980	7.01	5.07	5.9	6.68	2.11	2.14	3.31	3.86	4.51	*	-
	NT2RP2005994	12.99	9.14	13.53	7.59	4.09	0.3	2.32	3.71	4.52	*	**
	NT2RP2006004	7.54	4.47	13.06	6.53	2.59	2.1	2.72	2.9	3.13		
40	NT2RP2006013	11.06	6.58	20.3	11.12	5.96	2.47	2.76	11.94	3.04		
	NT2RP2006023	79.4	60.83	74.67	51.53	34.64	38.07	64.39	76.12	79.93	*	-
	NT2RP2006028	23.13	26.87	22.92	16.89	12.58	6.73	6.52	8.45	15.41	*	**
	NT2RP2006038	4.35	4.75	6.83	4.07	1.31	0.83	1.09	0.16	1.4	**	-
	NT2RP2006042	15.45	13.74	13.53	9.24	8.86	3.55	5.34	6.22	7.22	*	**
	NT2RP2006043	17.81	13.76	15.29	13.7	7.47	8.55	9.41	5.9	6.89	*	-
45	NT2RP2006052	12.36	8.55	16.5	5.69	3	4.31	2.78	3.7	3.31	*	*
	NT2RP2006057	7	6.58	13.05	6.99	3.77	3.67	1.75	3.57	2.95	*	-
	NT2RP2006064	31.45	32.66	33.8	25.4	15.66	8.71	6.36	7.35	7.36	*	**
	NT2RP2006068	7.85	6.5	16.27	7.3	3.64	3.64	2.88	4.02	3.43		
	NT2RP2006069	10.49	8.04	9.64	6.75	2.89	1.65	2.28	1.16	1.94	*	**
	NT2RP2006071	12.09	22.31	12.61	10.26	7.27	0.85	3.44	3.17	3.04	*	-
50	NT2RP2006090	10.61	10.59	22.59	7.62	4.75	0.57	5.24	4.28	5.3		
	NT2RP2006092	15.25	7.07	12.08	13.1	8.69	10.62	13.15	8.79	8.66		
	NT2RP2006097	52.21	101.2	64.35	48.63	48.31	38.97	25.59	53.43	52.7		
	NT2RP2006098	13.67	12.41	21.3	14.85	6.15	8.49	5.13	8.68	3.6	*	-
	NT2RP2006099	65.92	60.33	80.23	76.5	49.76	0.24	73.49	73.17	78.2		
	NT2RP2006100	14.09	12.17	17.63	9.6	8.02	0.77	4.01	5.07	4.89	**	-
55	NT2RP2006103	6.26	4.22	7.72	5.83	3.58	2.06	2.74	2.72	2.55	*	-
	NT2RP2006106	48	36	55.68	34.38	35.82	35.56	24.01	21.59	18.79	*	-
	NT2RP2006127	6.5	4.86	5.96	5.76	1.93	3.45	3.78	1.37	2.06	*	-



Table 436

	NT2RP2006134	9.57	6.53	12.45	11.76	2.26	6.54	9.28	6.55	5.96			
	NT2RP2006141	13.6	10.51	20.75	11.91	8.44	5.24	5.17	8.6	15.73			
5	NT2RP2006166	43.39	37.58	47.62	23.75	15.94	0.88	44.65	56.53	70.7	*		-
	NT2RP2006176	17.92	13.68	20.98	13.87	7.31	8.84	7.42	10.41	8.82	*	*	-
	NT2RP2006181	4.75	8.83	6.23	3.92	1.81	1.35	3.97	2.81	2.8	*		-
	NT2RP2006184	64.52	54.32	63.63	42.14	32.28	42.22	63.72	47.39	43.75	**		-
	NT2RP2006186	8.19	11.92	9.4	6.19	2.49	2.83	2.18	2.13	1.87	*	**	-
	NT2RP2006196	22.53	23.16	21.9	14.52	7.82	10.37	16.26	11.79	10.32	**	**	-
10	NT2RP2006199	9.01	9.11	8.26	8.72	4.43	4.65	6.19	4.21	5.05	**	**	-
	NT2RP2006200	7.28	4.32	9.53	5.05	3.47	3.37	3.59	4.46	2.65			-
	NT2RP2006210	90.78	69.8	53.22	55.44	37.83	25.49	20.22	40.51	30.76	*		-
	NT2RP2006219	11.28	20.39	17.51	8.1	14.35	6.63	11.34	9.44	19.6			-
	NT2RP2006224	12.75	19.13	21.38	12.72	10.81	3.64	17.87	16.61	1.85			-
	NT2RP2006237	7.47	20.77	9.96	5.08	2.48	0.88	3	2.56	0.6			-
15	NT2RP2006238	10.52	14.31	12.03	6.19	1.38	2.03	2.55	2.62	2.66	**	**	-
	NT2RP2006258	10.05	20.38	11.9	6.71	3.4	2.58	5.8	4.54	6.64	*		-
	NT2RP2006261	8.38	9.18	5.31	9.6	2.51	4.78	2.42	4.07	4.58	*	*	-
	NT2RP2006269	17.03	14.29	15.32	11	5.59	7.26	3.86	12.06	5.85	*	*	-
	NT2RP2006275	46.12	39	46.05	70.83	38.96	80.2	37.5	48.02	38.1			-
	NT2RP2006282	18.4	26.43	24.55	13.47	12.52	6.62	5.66	6.21	6.64	*	**	-
20	NT2RP2006302	17.18	26.6	32.5	13.26	6.56	8.01	5.28	4.17	5.65	*	*	-
	NT2RP2006312	31.59	23.04	41.51	9.42	5.96	4.21	6.1	4.79	7.53	*	**	-
	NT2RP2006320	41.28	41.71	36.93	24.86	13.12	15.23	28.98	37.1	32.63	**		-
	NT2RP2006321	10.41	9.33	12.86	10.26	2.43	5.6	7.6	9.6	8.78			-
	NT2RP2006323	7.58	5.4	4.29	6.62	1.35	3.01	7.41	4.95	4.91			-
	NT2RP2006333	5.03	7.52	4.99	6.18	1.44	5.34	2.1	4.81	3.82			-
25	NT2RP2006334	7.94	8.71	7.64	8.5	4.46	6.47	2.3	4.34	3.32	**		-
	NT2RP2006338	12.7	9.34	36.56	7.32	2.93	4.16	2.16	2.04	3.64			-
	NT2RP2006339	6.41	4.31	4.61	6.37	3.36	3.67	2.31	2.9	2.66	*		-
	NT2RP2006355	6.78	12.38	3.94	6.81	1.66	2.59	2.74	4.14	2.84			-
	NT2RP2006365	5.27	2.38	4.32	5.39	0.85	1.53	2.13	3.92	2.48			-
30	NT2RP2006374	123.01	124.5	151.43	183.62	144.52	148.4	137.08	112.64	166.86			-
	NT2RP2006393	22.69	18.53	23.1	17.79	6.84	13.61	27.67	23.54	25.74			-
	NT2RP2006394	15.6	11.55	17.73	16.97	12.66	13.34	9.59	13.69	11.86			-
	NT2RP2006400	8.82	4.99	12	10.48	4.15	11.24	9.88	11.64	10.5			-
	NT2RP2006411	4.42	4.9	11.08	5.28	2.3	3.07	2.25	3.04	3.21			-
	NT2RP2006429	2.69	1.8	8.38	6.1	1.17	1.68	2.03	2.68	1.46			-
35	NT2RP2006435	1.14	1.44	3.96	3.86	0	1.28	1.25	0.25	0.25			-
	NT2RP2006436	18.89	25.65	29.36	23.03	10	15.2	18.88	16.71	17.66			-
	NT2RP2006441	3.24	5.37	8.45	6.78	2.17	3.47	5.5	2.69	1.87			-
	NT2RP2006447	19.2	14.3	18.35	21.17	15.45	16.45	6.09	13.77	11.65			-
	NT2RP2006454	8.01	2.56	13.95	6.26	3.2	3.65	3.95	4.09	2.96			-
	NT2RP2006455	37.87	46.16	39.71	20.34	20.45	22.87	31.23	29.73	37.11	**		-
40	NT2RP2006456	12.66	10.34	20.88	11.22	5.29	5.49	7.54	4.09	3.92			-
	NT2RP2006464	49.31	38.6	70.84	30.42	38.8	32.65	22.89	19.33	15.74	*		-
	NT2RP2006467	7.41	7.72	13.37	8.13	6.48	4.56	10.4	4.81	8.63			-
	NT2RP2006472	17.27	35.33	39.96	36.59	25.1	29.12	15.84	31.69	29.65			-
	NT2RP2006474	5.31	10.55	8.31	9.45	5.79	7.02	7.91	11.16	8.64			-
	NT2RP2006475	14.67	7.33	18.42	13.4	5.52	5.53	5.81	10.03	7.38			-
45	NT2RP2006476	21.17	14.25	23.98	17.93	10.29	15.83	16.59	21.36	17.75			-
	NT2RP2006501	80.64	47.79	67.54	47.86	36.74	36.28	29.87	41.76	52.91			-
	NT2RP2006512	10.73	9.4	12.56	6.68	7.05	5.5	3.87	4.91	5.32	*	**	-
	NT2RP2006526	12.09	17.75	22.2	19.62	16.43	13.33	17.31	20.34	13.23			-
	NT2RP2006527	4.41	6.17	7.16	7.48	1.84	1.55	3.51	2.56	2.84	*		-
	NT2RP2006534	4.37	9.41	7.99	5.05	4.19	2.96	4.68	2.83	2.5			-
50	NT2RP2006537	5.9	9.98	11.68	11.28	5.12	7.83	10.34	5.58	8.5			-
	NT2RP2006543	12.11	8.37	13.04	12.23	3.26	11.04	6.8	5.53	9.23			-
	NT2RP2006554	7.01	5.37	13.82	7.47	2.64	2.23	3.56	4.89	9.98			-
	NT2RP2006565	14.34	12.69	22.07	6.94	4.33	4.74	3.36	7.61	8.3	*	*	-
	NT2RP2006571	65.34	49.49	69.38	45.6	41.55	34.63	47.98	65.86	43.88	*		-
	NT2RP2006573	12.86	9.58	16.76	8.82	7.97	5.87	5.7	4.86	5.46	*		-
55	NT2RP2006598	5.92	15.24	10.14	5.39	4.48	3.2	2.52	3.49	4.84			-
	NT2RP2006601	5.92	8.92	7.57	6.45	4.69	2.53	4.15	3.79	3.98	*		-
	NT2RP3000002	17.28	31.41	14.62	22.94	26.64	18.92	27.08	23.91	17.49			-

Table 437

	NT2RP3000011	14.9	6	15.29	9.33	4.35	7.79	4.33	10.84	6.28				
	NT2RP3000014	108.09	109.54	95.92	98.76	68.18	81.91	47.71	112.2	132.8				
5	NT2RP3000016	14.35	13.63	24.71	7.65	8.46	5.45	3.86	7.49	4.11	*	*	-	-
	NT2RP3000022	7.65	10.24	13.67	9.49	4.92	2.16	2.89	2.32	2.03	*	*	-	-
	NT2RP3000024	12.64	12.37	14.37	11.32	5.72	6.81	6.24	6.05	6.52	*	**	-	-
	NT2RP3000031	77.24	79.76	145.67	144.42	128.63	86.96	77.23	69.72	83.66				
	NT2RP3000034	6.27	6.62	8.74	6.38	3.4	3.43	4.64	3.79	2.96		*	-	-
	NT2RP3000037	17.58	19.44	20.81	11.72	11.55	13.9	18.45	10.67	14.15	**	*	-	-
10	NT2RP3000040	27.59	16.23	24.01	13.53	7.79	10.55	2.51	8.1	6.81	*	*	-	-
	NT2RP3000041	5.08	4.46	12.76	6.9	3.15	3.65	6.44	3	1.87				
	NT2RP3000046	7.63	5.75	15.27	8.29	3.02	2.83	2.71	4.54	5.05				
	NT2RP3000047	5.93	4.81	14.06	5.49	2.34	2.87	0.9	3.18	1.51				
	NT2RP3000049	6.45	8.2	10.35	6.13	1.6	1.78	2.62	3.99	1.9		*	-	-
15	NT2RP3000050	11.72	13.02	12.95	7.97	7.04	4.74	3.27	4.45	3.93	**	**	-	-
	NT2RP3000051	20.55	9.33	15.87	14.09	17.37	4.84	3.99	4.5	4.21		*	-	-
	NT2RP3000054	6.46	5.61	6.8	6.67	3.52	2.38	1.52	2.23	2.77		**	-	-
	NT2RP3000055	18.47	13.61	17.33	12.33	8.89	12.37	7.71	11.31	9.35	*	*	-	-
	NT2RP3000056	1.67	2.36	8.51	3.35	1.42	1.09	0.81	1.36	0.36				
	NT2RP3000059	7.89	7.9	22.29	10.9	7.16	5.13	2.59	4.88	2.31				
20	NT2RP3000063	1.84	4.14	7.63	4.56	1.09	0.43	0.47	0.97	0				
	NT2RP3000068	6.17	8.89	16.21	5.26	4.81	2.29	6.13	4.42	2.89				
	NT2RP3000069	9.15	8.31	8.75	6.58	4.56	4.92	4.17	3.76	6.03	**	**	-	-
	NT2RP3000072	32.05	40.26	39.15	31.11	26.2	25.34	26.47	26.26	26.37	*	*	-	-
	NT2RP3000080	25.2	23.2	22.56	18.48	15.53	13.5	21.79	14.38	13.52	**		-	-
25	NT2RP3000085	67.96	43.89	70.79	53.46	33.71	65.94	52.26	69.62	62.27				
	NT2RP3000087	111.9	96.79	117.72	81.88	54.53	62.52	49.82	71.54	66.46	*	**	-	-
	NT2RP3000092	9.87	12.43	24.83	8.97	4.39	4.92	2.95	7.36	3.67				
	NT2RP3000109	10.57	9.88	12.54	8.31	8.64	5.99	6.65	6.37	5.22	*	**	-	-
	NT2RP3000119	8.08	6.85	10.03	6.29	4.73	2.45	4.69	3.89	2.89		*	-	-
	NT2RP3000125	6.75	8.13	6.71	5.47	2.88	2.09	0.61	2.51	2.19	*	**	-	-
	NT2RP3000131	13.6	16.29	13.49	12.52	5.73	6.16	5.37	4.48	4.22		**	-	-
30	NT2RP3000134	18.43	21.97	18.23	9.28	9.9	8.55	6.96	2.89	3.6	**	**	-	-
	NT2RP3000137	10.23	18.11	17.39	15.98	4.55	11.71	4.48	6.98	5.44	*	*	-	-
	NT2RP3000142	35.53	27.58	35.61	21.77	15.45	19.48	21.05	30.25	26.9	*	*	-	-
	NT2RP3000148	26.32	39.38	34.66	19.53	19	15.35	18.54	17.46	14.71	*	*	-	-
	NT2RP3000149	32.9	38.83	27.1	14.1	20.26	8.54	10.04	7.73	9.34	*	**	-	-
	NT2RP3000163	8.85	9.04	13.21	8.67	3.56	5.95	3.7	3.77	3.35		**	-	-
35	NT2RP3000168	15.39	20.39	19.23	9.48	11.8	5.55	7.63	15.26	9.88	*	*	-	-
	NT2RP3000169	15.25	12.33	13.06	7.58	7.27	4.09	8.07	3.27	4.36	**	**	-	-
	NT2RP3000171	6.75	12.8	10.62	11.26	6.03	4.95	8.98	2.23	5.04				
	NT2RP3000172	40.04	25.12	32.12	25.17	9.97	24.6	26.83	33.18	37.52				
	NT2RP3000186	16.1	16.13	19.67	12.39	6.63	8.09	5.65	10.05	10.55	*	*	-	-
40	NT2RP3000197	50.94	62.27	70	34.47	33.63	20.62	34.62	48.18	55.04	*	*	-	-
	NT2RP3000201	14.53	11.88	22.5	7.11	4.59	3.11	5.14	5.79	5.41	*	*	-	-
	NT2RP3000204	4.16	4.96	6.59	4.48	1.18	2.3	2.66	1.7	2.27		*	-	-
	NT2RP3000207	95.59	249.91	234.63	30.21	59.19	29.76	35.62	12.46	31.91	*	*	-	-
	NT2RP3000216	7.95	7.31	6.95	6.17	2.69	2.5	2.94	3.29	3.98	*	**	-	-
	NT2RP3000220	22.18	29.86	28.92	10.43	5.88	15.01	13.77	5.33	14.12	**	*	-	-
	NT2RP3000221	10.31	9.17	11.73	12.25	5.03	10.36	5.52	10.77	5.91				
45	NT2RP3000232	46.66	42.43	53.26	15.69	8.2	7.9	5.53	11.37	6.25	**	**	-	-
	NT2RP3000233	8.3	12.35	2.97	7.16	16.65	2.19	9.24	3.42	2.51				
	NT2RP3000234	3.63	3.88	5.86	5.35	3.32	2.04	1.6	2.52	2.2		*	-	-
	NT2RP3000235	9.35	15.39	13.27	13.07	5.58	8.43	10.72	9.32	10.97				
	NT2RP3000239	18.63	25.23	22.23	15.58	11.06	7.77	9.06	9.28	12.71	*	**	-	-
	NT2RP3000247	32.06	44.16	41.62	22.89	17.24	20.67	24.3	20.29	19.85	**	*	-	-
50	NT2RP3000251	44.56	41.2	38.69	25.94	14.62	23.41	43.42	39.09	44.51	**		-	-
	NT2RP3000252	21.9	16.55	21.84	18.88	16.64	19.17	13.44	23.92	18.04				
	NT2RP3000255	18.67	16.02	17.43	18.73	10.56	14.35	9.36	10.73	8.47		**	-	-
	NT2RP3000262	17.74	15.84	18.49	25.1	16.29	24.75	12.36	12.76	13.36		**	-	-
	NT2RP3000266	37.8	22.61	54.63	46.91	29.06	37.64	30.75	39.28	44.8				
	NT2RP3000267	5.43	5.61	4.39	6.25	5.05	2.74	3.18	2.68	2.59		**	-	-
55	NT2RP3000271	4.92	10.2	10.62	7.08	4.11	3.49	3.88	5.36	2.72				
	NT2RP3000278	6.77	11.93	8.85	9.67	5.55	4.79	8.29	7.56	5.48				
	NT2RP3000281	32.19	29.94	32.48	16.28	8.76	14.6	16.94	10.41	13.64	**	**	-	-

Table 438

	NT2RP3000292	73.41	53.56	62.96	43.77	42.72	40.98	49.91	45.23	84.29	*	-	-
	NT2RP3000299	6.1	3.92	13.07	7.5	3.65	4.11	4.21	4.47	3.64			
5	NT2RP3000304	25.73	24.35	31.49	22.39	17.08	15.95	20.38	9.68	10.08	*	*	-
	NT2RP3000310	21.09	16.82	33.26	14.15	13.15	10.27	8.12	6.37	6.54	*		-
	NT2RP3000312	0.99	6.75	7.52	6.17	1.98	0.95	3.63	3.7	0.46			
	NT2RP3000320	11.54	11.91	24.03	15.6	10.14	7.39	6.78	13.07	6.3			
	NT2RP3000322	6.3	10.23	13.74	8.18	5.89	5.4	11.65	9.13	4.6			
	NT2RP3000324	3.35	4.35	17.76	5.33	3.9	3.91	1.03	4.83	1.94			
10	NT2RP3000326	64.19	41.44	38.83	20.52	19.15	16.6	15.62	30.96	63.08	*	-	
	NT2RP3000329	11.55	11.02	22.98	13.53	7.92	12.17	10.06	11.03	12.62			
	NT2RP3000330	7.65	5.98	10.92	7.41	2.84	4.65	3.07	4.04	3.9	*		-
	NT2RP3000333	5.32	5.01	9.94	8.43	4.88	3.17	4.98	3.48	4.27			
	NT2RP3000341	13.68	14.31	17.57	13.78	9.61	9.9	9.7	9.67	11.82	*		-
	NT2RP3000344	45.81	52.79	53.7	28.28	29.87	22.15	36.08	31.27	32.79	**	**	-
15	NT2RP3000345	9.05	22.29	17.79	14.81	9.64	10.42	11.7	5.94	6.21			
	NT2RP3000348	152.75	76.47	143.51	181.96	103.16	145.4	96.65	108.56	99.33			
	NT2RP3000350	14.44	9.79	17.94	12.6	7.91	9.69	10.66	15.9	13.61			
	NT2RP3000359	12.38	12.66	23.75	11.88	10.77	13.58	14.05	17.04	16.51			
	NT2RP3000361	30.21	20.92	25.69	12.5	10.99	10.9	7.28	12.88	9.35	**	**	-
	NT2RP3000366	69.71	53.96	58.74	44.82	38.68	40.33	27.58	41.09	30.61	*	*	-
20	NT2RP3000378	5.8	12.66	6.1	6.74	3.98	3.58	4.72	5.63	5.68			
	NT2RP3000384	26.45	19.42	18.46	13.21	9.98	7.79	8.34	6.32	5.93	*	**	-
	NT2RP3000389	22.1	25.13	28.16	17.61	19.95	18.45	23.81	18.85	25.81	*		-
	NT2RP3000393	33.85	14.06	19.19	10.32	8.44	17.76	6.01	7.4	12.32			
	NT2RP3000395	24.46	28.99	21.1	13.42	10.29	14.47	9.05	14.21	24.87	**		-
	NT2RP3000397	24.89	21.35	36.91	14.31	14.82	16.14	17.25	23.74	23.2			
25	NT2RP3000398	9.55	10.75	17.31	7.25	6.82	4.6	4.16	4.17	3.99	*		-
	NT2RP3000403	93.32	64.65	56.89	57.84	43.74	45.93	35.74	40.63	30.88	*		-
	NT2RP3000418	14.37	22.01	20.2	11.88	12.29	11.51	7.67	14.89	12.11	*		-
	NT2RP3000424	40.86	56.6	51.72	39.57	32.99	30.24	31.05	29.26	23.73	*	*	-
	NT2RP3000427	19.59	24.95	16.59	14.3	10.74	15.64	9.16	9.9	12.52	*		-
30	NT2RP3000431	16.18	14.67	25.82	11.73	10.4	20.33	8.15	16.47	13.08			
	NT2RP3000433	25.31	54.08	36.8	35.67	31.56	27.85	24.04	39.4	34.85			
	NT2RP3000436	9.62	10.09	16.49	6.56	4.89	5.29	2.88	5.01	2.75	*	*	-
	NT2RP3000439	44.72	47.78	44.4	50.96	50.94	30.43	33.38	44	42.05			
	NT2RP3000441	10.82	8.95	14.82	10.83	6.19	5.02	6.65	8.63	7.39			
	NT2RP3000444	17.45	14.75	26.3	14.55	11.35	9.32	12.21	11.85	12.68			
35	NT2RP3000448	6.61	7.47	11.97	6.37	5.01	4.15	4.85	3.6	5.55			
	NT2RP3000449	17.38	26.19	23.45	8.67	7.34	7.86	3.61	4.2	2.92	**	**	-
	NT2RP3000451	31.29	40.71	35.46	10.79	20.02	15.29	13.25	22.78	15.67	**	**	-
	NT2RP3000456	6.24	4.2	13.64	8.03	3.84	0	2.84	3.63	2.55			
	NT2RP3000460	10.33	10.39	17.07	7.27	4.9	3.93	5.19	5.56	4.78	*	*	-
	NT2RP3000471	11.88	7.85	23.63	10.17	6.71	3.54	3.68	5.28	5.09			
40	NT2RP3000477	49.73	54.72	58.77	38.09	33.82	22.58	25.2	26.62	28.76	*	**	-
	NT2RP3000478	6.95	4.02	8.07	5.51	2.95	1.38	1.83	1.8	1.91	*		-
	NT2RP3000481	11.03	7.58	11.93	11.71	8.13	6.39	6.65	9.77	6.96			
	NT2RP3000484	25.46	33.21	34.57	19.56	15.47	13.67	14.97	11.89	12.9	*	**	-
	NT2RP3000487	21.14	29.38	33.76	13.62	12.2	14.9	5.33	12.46	12.14	*	*	-
	NT2RP3000512	12.44	14.88	14.98	11.55	7.87	5.16	5.05	7.04	5.14	*	**	-
45	NT2RP3000523	93.94	104.88	80.32	71.64	44.61	35.48	20.12	30.84	18.65	*	**	-
	NT2RP3000526	7.94	7.79	12.87	7.19	2.92	3.56	4	5.42	4.09	*		-
	NT2RP3000527	42.97	38.74	42.72	25	28.15	22.19	19.81	21.07	11.92	**	**	-
	NT2RP3000531	20.64	13.92	14.48	12.89	10.75	4.81	8.04	4.79	4.56	*		-
	NT2RP3000532	5.33	6.65	5.17	4.82	3.38	2.17	2.24	1.62	4.13	*		-
	NT2RP3000542	21.28	18.32	16.2	8.3	8.11	6.12	3.53	3.83	3.8	**	**	-
50	NT2RP3000554	11.71	17.67	14.03	9.45	3.02	6.99	4.57	4.9	5.09	*	**	-
	NT2RP3000561	21.04	16.88	23.96	14.27	9.57	9.4	4.67	15.18	7.79	*	*	-
	NT2RP3000562	56.42	51.6	61.28	47.36	46.18	42.62	32.74	44.25	48.68	*		-
	NT2RP3000578	19.29	21.22	25	14.6	13.72	9.4	9.07	9.7	10.06	*	**	-
	NT2RP3000582	9.4	7.64	13.09	8.29	5.67	6.43	5.12	6.71	5.65			
	NT2RP3000584	22.71	44.85	35.97	15.47	26.23	10.78	9.11	11.41	6.79	*		-
55	NT2RP3000586	8.23	4.88	7.14	6.37	3.31	2.97	3.91	1.9	2.63	*		-
	NT2RP3000590	7.21	5.97	5.97	5.32	2.92	1.94	4.92	2.84	1.77	*		-
	NT2RP3000592	69.63	37.92	90.02	128.75	103.66	125.15	70.02	69.72	60.26	*	+	-

Table 439

	NT2RP3000596	8.71	11.87	13.23	5.92	4.35	3.28	4.65	3.35	4	*	**	-	-
	NT2RP3000599	39.3	60.28	67.05	35.1	44.12	24.38	35.82	36.31	35.96				
5	NT2RP3000603	69.47	91.4	87.14	91.5	86.56	93.49	64.94	61.32	72.5				
	NT2RP3000605	22.45	27.45	25.73	13.14	8.89	13.46	17.63	11.14	9.76	**	*	-	-
	NT2RP3000607	10.48	11.53	16.41	10.77	7.11	9.56	5.29	9.79	8.32				
	NT2RP3000616	11.96	13.13	17.29	7.98	6.33	4.22	6.69	4.25	4.27	*	**	-	-
	NT2RP3000621	218.49	188.17	246.49	222.59	168.47	221.1	202.08	168.53	186.24				
	NT2RP3000622	11.99	8.26	9.27	9.15	3.89	5.28	6.73	6.59	3.57				
10	NT2RP3000624	27.07	18.6	22.96	16.72	12.03	13.8	17.33	23.33	18.89	*		-	
	NT2RP3000628	27.69	34.41	73.45	22.73	20.51	22.18	15.98	19.75	18.56				
	NT2RP3000631	6.03	12.91	11.07	11.79	9.91	5.14	4.52	6.12	7.95				
	NT2RP3000632	16.5	21.72	26.01	18.26	13.03	16.89	15.73	14.14	13.67				
	NT2RP3000638	31.94	42.93	38.07	22.76	17	20.23	24.56	32.44	30.42	**		-	
	NT2RP3000644	26.66	26.83	24.84	16.68	14.97	15.79	28.13	27.03	30.11	**		-	
15	NT2RP3000645	12.37	13.95	21.96	14.87	10.1	8.68	7	6.44	7.2	*		-	
	NT2RP3000652	20.17	23.26	25.45	12.67	9.39	13.26	9.11	9.19	15.37	**	*	-	-
	NT2RP3000658	6.96	4.69	8.52	6.05	2.7	4.41	2.15	3.59	3.85	*		-	
	NT2RP3000660	21.94	12.21	11.63	11.36	9.42	9.56	9.02	8.73	8.05				
	NT2RP3000661	15.39	18.23	27.58	11.62	4.78	9.25	6.26	7.03	6.07	*	*	-	-
20	NT2RP3000665	34.94	43.07	59.18	27.69	16.86	21.15	16.2	20.9	14.32	*	*	-	-
	NT2RP3000676	11.53	4.79	8.95	6.6	4.34	2.4	4.94	2.78	3.68				
	NT2RP3000677	12.19	14.6	7.18	13.97	4.51	9.55	9.82	11.58	12.06				
	NT2RP3000681	7.72	7.98	7.04	6.12	2.54	4.33	4.62	3.23	3.26	*	**	-	-
	NT2RP3000683	16.43	8.63	13.69	14.68	12.94	13.49	5.83	9.27	7.59				
	NT2RP3000685	8.41	6.46	7.19	10.24	3.04	4.6	5.55	3.8	3.45	*		-	
25	NT2RP3000690	11.52	7.55	10.23	15.03	9.13	13.25	14.85	17.96	14.92	*		+	
	NT2RP3000698	6.94	6.35	7.8	8.41	2.13	5.63	3.39	7.51	5.51				
	NT2RP3000708	9.74	10.33	12.77	11.25	8.14	10.39	9.73	10.17	12.86				
	NT2RP3000719	9.86	16.24	14.31	8.23	2.38	5.7	5.89	3.68	4.39	*	*	-	-
	NT2RP3000721	8.23	3.7	5.33	7.95	1.94	5.33	6.54	5.47	6.13				
	NT2RP3000728	4.68	4.59	4.86	7.19	1.44	3.15	5.16	3.82	3.57				
30	NT2RP3000730	14.89	15.22	17.78	16.76	11.05	11.99	16.08	10.04	9.6				
	NT2RP3000733	62.46	50.63	81.88	55.7	39.3	45.85	39.59	39.01	40.88				
	NT2RP3000735	4.91	3.22	9.89	6.52	1.99	3.91	2.03	3.65	2.09				
	NT2RP3000736	6.36	3.45	10.98	8.89	2.09	4.31	3.75	3.03	2.56				
	NT2RP3000739	40.42	44.03	40.83	24.77	27.39	34.23	25.37	20.3	32.14	*	*	-	-
	NT2RP3000742	4.84	6.47	8.58	7.03	4.15	2.9	3.28	5.74	3.55				
35	NT2RP3000753	8.3	6.8	12.66	10.6	4.35	5.47	5.99	5.75	7.45				
	NT2RP3000759	36.84	70.63	56.01	36.02	19.41	27.88	8.09	6.25	5.44	**		-	
	NT2RP3000789	45.54	27.39	34.07	33.12	27.39	34.54	20.51	27.67	27.21				
	NT2RP3000815	22.33	13.62	22.75	12.02	10.68	14.79	18.74	20.82	19.96				
	NT2RP3000818	30.57	21.11	33.63	24.24	17.69	21.68	13.73	17.32	15.5	*		-	
	NT2RP3000820	35.87	28.12	43.92	32.81	27.98	25.05	21.15	26.93	23.2				
40	NT2RP3000821	3.51	4.2	7.15	6.21	2.3	3.01	3.82	2.8	1.62				
	NT2RP3000825	16.22	23.18	33.6	11.67	17.67	13.25	9.13	8.99	16.22				
	NT2RP3000826	57.22	56.7	80.61	55.4	48.67	48.17	57.78	64.97	54.17				
	NT2RP3000836	3.1	3.53	3.85	7.53	2.33	2.42	3.69	4.81	2.68				
	NT2RP3000838	14.56	14.22	18.93	20.92	12.46	10.78	11.08	17.41	54.13				
	NT2RP3000839	45.25	36.9	44.36	35.78	27.32	20.79	19.28	33.14	25.15	*	*	-	-
45	NT2RP3000841	12.21	10.37	21.1	12.42	10.04	9.18	8.34	11.21	7.12				
	NT2RP3000845	8.59	31.26	15.5	9.69	12.93	10.25	5.37	12.21	8.92				
	NT2RP3000847	12.91	10.6	18.85	11.05	8.9	9.57	6.7	5.47	6.54	*		-	
	NT2RP3000848	11.47	16.2	11.34	8.1	7	4.83	3.86	7.4	3.83	*	*	-	-
	NT2RP3000850	21.09	31.1	29.31	19.76	12.79	16.25	10.7	10.54	5.19	*	**	-	-
	NT2RP3000852	2.73	3.9	3.17	7.51	3.17	2.39	4.15	2.97	3.66				
50	NT2RP3000859	32.3	21.43	36.02	18.9	21.77	13.31	16.61	18.23	32.52				
	NT2RP3000861	15.56	12.49	16.59	9.02	5.36	4.49	4.53	5.88	27.25	**		-	
	NT2RP3000862	12.15	10.89	17.99	10.36	6.14	6.17	5.59	8.92	5.21	*		-	
	NT2RP3000865	9.02	6.17	10.68	7.46	4.29	4.01	2.73	4.35	3.2	*		-	
	NT2RP3000866	43.46	38.1	57.47	39.52	40.18	44.87	37.48	37.57	27.56				
	NT2RP3000868	10.55	23.22	17.15	7.33	6.65	4.58	6.64	9.1	10.81	*		-	
55	NT2RP3000869	5.78	11.8	14.52	9.41	10.86	7.13	6.87	5.05	7.12				
	NT2RP3000871	194.48	190.18	141.72	252.15	170.88	170.92	247.35	193.7	214.46				
	NT2RP3000875	14.37	14.46	23.84	13.76	12.05	11.47	7.45	6.27	6.52	*		-	

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	NT2RP3000895	2.84	2.51	12.27	4.16	1.17	2.03	1.28	3.4	1.59			
	NT2RP3000900	10.4	8.3	14.31	18.92	3.45	5.38	4.15	13.51	4.93			
5	NT2RP3000901	14.3	18.5	22.78	13.03	13.47	11.77	11.97	9.53	14.53			
	NT2RP3000903	5.01	6.85	6.69	5.82	1.64	3.35	1.28	1.92	1.35	**	-	
	NT2RP3000904	108.6	100.47	123.83	118.07	108.3	100.81	97.74	77.69	108.28			
	NT2RP3000907	84.64	90.19	89.66	84.77	80.01	92.59	125.26	82.21	80.83			
	NT2RP3000913	19.19	19.49	20.62	24.35	9.57	18.44	17.39	14.75	19.21			
	NT2RP3000917	16.28	18.3	30.01	16.96	15.22	12.11	11.68	16.63	14.88			
10	NT2RP3000919	9.33	7.65	14.92	9.52	7.41	6.8	4.46	8.2	5.92			
	NT2RP3000921	112.89	136.59	133.65	119.03	103.41	74.11	25.71	35.79	29.01	**	-	
	NT2RP3000942	67.7	68.21	86.84	75.24	51.25	30.13	38.31	52.76	48.83	*	-	
	NT2RP3000968	50.83	31.86	37.11	29.89	24.92	14.66	9.86	11.81	12.71	**	-	
	NT2RP3000974	8.96	8.74	9.35	9.04	12.66	5.51	4.39	4.92	2.99	**	-	
	NT2RP3000980	52.51	65.55	64.13	24.76	40.04	30.49	19.39	8.08	16.43	**	-	
15	NT2RP3000984	21.27	24.19	17.57	32.72	12.14	21.58	18.47	14.77	17.87			
	NT2RP3000994	13.76	10.35	18.12	10.02	5.77	7.25	4.5	8.07	7.2	*	-	
	NT2RP3001001	26.43	28.79	25.4	17.26	14.54	13.11	11.19	38.41	33.45	**	-	
	NT2RP3001004	4.86	4.98	10.62	7.73	3.07	4.03	3.13	4.4	2.41			
	NT2RP3001007	7.65	8.96	16.59	12.13	9.28	3.44	5.05	6.53	5.77			
	NT2RP3001012	29.74	22.53	33.06	15.24	16.46	13.42	12.28	11.59	13.53	*	-	
20	NT2RP3001042	8.82	8.59	12.15	8.9	5.69	3.5	3.15	4.09	3.65	**	-	
	NT2RP3001044	9.07	11.65	10.99	8.25	9.28	5.59	7.83	7.51	5.88	*	-	
	NT2RP3001048	6.16	7.8	4.48	10.05	2.76	3.93	4.91	5.32	6.21			
	NT2RP3001050	13.37	10.61	15.08	10.7	4.83	9.6	6.34	11.26	9.4			
	NT2RP3001055	13.05	10.48	21.89	13.3	7.76	7.17	10.39	12.83	10.26			
25	NT2RP3001057	402.89	324.38	250.29	272.31	285.99	209.38	216.17	328.86	144.63			
	NT2RP3001061	7.38	5.55	10.57	7.56	3.5	2.09	3.67	3.84	2.18	*	-	
	NT2RP3001069	5.39	4.71	9.6	4.84	1.4	2.62	2.39	2.57	3.49			
	NT2RP3001074	12.1	8.82	12.25	8.96	3.61	6.95	9.25	6.39	6.94			
	NT2RP3001078	13.01	11.28	14.67	14.05	9.24	8.9	10.46	7.65	9.46	*	-	
	NT2RP3001081	8.54	6.06	5.96	10.22	3.89	7.03	6.21	3.36	4.4			
	NT2RP3001084	37.48	37.33	40.93	15.51	10.29	21.45	23.22	30.25	29.17	**	-	
30	NT2RP3001095	7.76	24.69	13.38	9.04	3.7	5.9	3.38	7.52	4.23			
	NT2RP3001096	10.65	10.08	12.53	7.44	5.06	4.16	3.27	5.66	3.18	*	-	
	NT2RP3001097	16.83	38.99	30.48	15.02	9.07	10.26	12.7	8.94	6.97	*	-	
	NT2RP3001107	28.61	24.48	44.48	22.05	25.16	18.26	10.04	8.83	11.02	*	-	
	NT2RP3001109	17.96	17.48	18.06	10.7	9.3	6.66	7.73	5.5	3.91	**	-	
	NT2RP3001111	10.67	15.58	14.57	9.33	6.41	6.38	8.41	3.97	4.53	*	-	
35	NT2RP3001112	31.69	26.22	26.11	22.8	9.31	16.42	16.88	9.36	14.31	**	-	
	NT2RP3001113	14.44	9.43	17.91	10.99	5.21	10.46	6.16	6.79	9.04			
	NT2RP3001115	254.68	276.58	258.3	135.39	153.31	123.7	118.47	299.67	339.02	**	-	
	NT2RP3001116	5.38	8	8.83	6.23	4.02	2.69	4.29	3.33	3.99	*	-	
	NT2RP3001119	18.64	22.98	19.35	7.26	6.2	5.92	8.84	7.37	9.08	**	-	
	NT2RP3001120	6.46	9.54	10.55	5.21	2.06	2.39	3.48	2.35	2.85	*	-	
40	NT2RP3001126	20.13	19.18	15.24	6.77	6.2	4.55	4.46	2.87	5.52	**	-	
	NT2RP3001127	348.14	574.68	264.45	161.21	220.83	168.52	563.89	269.72	342.5			
	NT2RP3001133	93.42	110.06	112.43	155.23	89.96	123.37	108.06	86.85	85.22			
	NT2RP3001140	96.94	96.61	111.2	55.83	46.1	51.01	55.61	103.28	84.66	**	-	
	NT2RP3001147	4.72	7.64	8.71	6.37	2.09	3.65	2.74	3.66	2.93	*	-	
45	NT2RP3001150	11.47	12.3	12.64	9.98	10.24	3.21	4.96	7.94	6.36	**	-	
	NT2RP3001152	36.54	72.08	61.62	66.57	55.9	58.11	48.19	41.6	53.56			
	NT2RP3001155	19.7	23.76	17.71	11.79	7.15	8.62	14.02	11.36	10.16	**	-	
	NT2RP3001156	19.46	20.53	21.5	20.77	20.49	12.08	20.09	17.5	18.2			
	NT2RP3001159	18.55	19.29	22.76	15.71	9.43	11.61	19.86	20.4	20.19	*	-	
	NT2RP3001170	16.8	14.86	12.69	11.85	4.5	6.68	9.82	3.85	4.53	*	-	
	NT2RP3001176	17.96	17.32	14.24	8.81	7.86	12.88	9.17	14.49	11.22	*	-	
50	NT2RP3001195	197.73	229.27	190.42	299.15	260.22	386.11	194.62	191.1	184.16	*	+	
	NT2RP3001209	74.83	67.88	81.64	88.53	60.41	90.53	81.32	84.97	83.11			
	NT2RP3001214	17.39	13.69	27.12	17.15	13.89	13.51	7.67	14.21	13.2			
	NT2RP3001216	18.74	16.38	19.13	19.54	12.84	10.16	26.01	26.17	21.52	*	+	
	NT2RP3001221	6.31	7.39	8.65	9.62	5.18	6.37	8.56	6.05	7.92			
55	NT2RP3001226	22.75	26.78	31.16	8.49	9.07	6.76	11.49	9.21	9.9	**	-	
	NT2RP3001230	6.51	6.56	3.99	9.46	3.93	5.31	7.3	6.36	5.9			
	NT2RP3001232	6.36	3.81	12.04	7.09	3.34	3.56	1.97	4.41	3			

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	NT2RP3001236	30.11	19.17	30.67	17.48	11.33	17.06	7.98	12.61	12.49	*	-
	NT2RP3001239	12.58	7.93	16.69	7.8	5.43	5.92	7.31	5.36	3.8		
5	NT2RP3001240	16.64	15.42	32.69	20.34	13.57	11.75	7.09	11.44	8.12		
	NT2RP3001245	8.04	12.54	22.57	10.74	8.24	10.53	7.27	7.75	6.31		
	NT2RP3001253	5.41	9.93	13.75	5.39	2.74	1.6	4.68	3.73	2.31		
	NT2RP3001259	278.9	310.98	327.25	256.7	262.84	274.28	334.89	289.89	242.91		
	NT2RP3001260	18.94	14.44	22.33	34.17	17.19	23.22	21.96	25.77	20.83		
	NT2RP3001264	67.04	56.89	77.24	82.42	71.22	82.52	43.6	44.18	61.74		
10	NT2RP3001268	54.13	43.25	63.3	45.53	25.93	35.18	39.08	48.29	54.07		
	NT2RP3001271	7.61	5.79	12.88	6.16	2.76	3.69	3.87	7.7	5.38		
	NT2RP3001272	23.18	22.6	31.48	18.93	15.25	15.77	18.56	19.39	20.08	*	-
	NT2RP3001274	143.91	121	164.35	135.41	115.24	154.69	133.08	136.37	139.51		
	NT2RP3001275	7.03	7.19	20.08	7.2	8.45	4.21	4.17	4.56	3.94		
	NT2RP3001280	14.64	18.72	19.46	9.93	11.17	5.67	7.5	8.91	6.46	*	**
15	NT2RP3001281	0.38	2.63	0.7	4.71	1.73	1.17	1.88	0.77	0.6		
	NT2RP3001288	43.86	21.34	42.34	25.62	18.43	26.29	27.01	32.19	37.1		
	NT2RP3001297	77.1	64.75	81.93	35.55	27.23	38.6	12.09	28.24	29.77	**	**
	NT2RP3001300	9.48	9.06	13.81	7.61	5.56	4.66	4.6	5.82	8.28		
	NT2RP3001301	5.4	3.52	7.37	3.86	1.62	1.26	1.66	3.26	1.26		
	NT2RP3001307	13.22	10.36	15.55	10.66	10.08	6.04	5.09	8.17	7.35	*	-
20	NT2RP3001310	9.88	12.87	16.58	11.85	7.95	6.71	4.27	4.42	3.89	*	-
	NT2RP3001318	7.4	8.54	9.21	7.25	6.79	6.73	5.34	5.32	3.43	*	-
	NT2RP3001322	11.09	11.38	14.04	15.94	12.19	11.47	14.66	6.17	7.73		
	NT2RP3001325	1201.7	1025	1099	286.93	377.86	405.84	75.06	206.06	219.63	**	**
	NT2RP3001338	162.73	132.54	198.96	171.74	181.83	241.04	134.27	161.16	143.19		
	NT2RP3001339	16.04	11.7	17.8	11.35	7.84	6.88	2.83	5.64	4.58	*	**
25	NT2RP3001340	35.84	31.42	47.79	30.03	31.99	45.26	31.64	27.19	27.6		
	NT2RP3001341	37.44	66.22	47.17	33.31	24.96	24.34	25.96	38.56	34.37		
	NT2RP3001354	42.85	32.23	43.99	23.31	23.56	19.16	13.01	13.77	11.4	*	**
	NT2RP3001355	2.26	7.76	10.15	5.3	3.13	3.72	4.66	3.96	2.91		
	NT2RP3001356	43	54.12	51.32	62.98	37.84	46.81	81.45	50.61	59.12		
	NT2RP3001359	34.72	29.05	42.17	41.55	33.32	37.07	21.86	23.34	24.66		
30	NT2RP3001364	19.26	26.46	29.33	17.86	11.52	13.89	13.78	18.18	15.95	*	*
	NT2RP3001373	16.79	12.24	26.6	10.58	10.1	9.34	9.17	17.19	12.49		
	NT2RP3001374	95.59	73.12	108.77	136.19	114.69	107.19	68.33	56.48	69.32		
	NT2RP3001383	12	19.08	15.5	12.1	5.75	6.51	13.27	9.62	6.82		
	NT2RP3001384	22.91	17.21	30.7	33.57	22.7	20.56	19.13	14.74	15.12		
	NT2RP3001388	9.38	9.17	7.78	9.06	5.69	4.27	7.73	5.71	5.18	*	-
35	NT2RP3001392	4.64	4.2	2.65	5.43	2.03	2.78	2.37	2.94	3.1		
	NT2RP3001396	47.27	37.6	60.04	23.62	14.23	34.71	12.93	30.54	38.42		
	NT2RP3001398	13.09	9.85	15.48	8.92	6.22	7.1	4.4	8.04	6.53	*	*
	NT2RP3001399	17.91	14.49	24.37	16.05	7.15	6.8	6.07	7.51	6.62	*	-
	NT2RP3001402	30.22	31.51	33.24	60.13	23.85	9.5	15.21	24.77	23.82	*	-
	NT2RP3001407	72.56	60.86	88.74	96.01	74.06	85.12	43.61	63.39	61.28		
40	NT2RP3001416	18.88	22.22	16.48	16.79	17.16	5.73	3.31	4.98	5	**	-
	NT2RP3001420	5.88	3.11	4.79	4.91	2.62	1.74	1.34	1.67	2.52	*	-
	NT2RP3001425	11.74	10.47	11.8	11.91	6.37	9.11	8.4	4.94	6.04	*	-
	NT2RP3001426	12.17	11.79	16.88	9.1	9.64	6.43	5.51	9.62	7.81	*	-
	NT2RP3001427	10.81	11	21.59	12.3	6.43	8.87	17.63	22.78	19.89		
	NT2RP3001428	7.7	10.58	20.16	8.58	3.38	6.04	5.05	8.84	8.9		
45	NT2RP3001429	4.55	6.04	12.09	5.05	1.79	1.93	2.26	1.46	1.89		
	NT2RP3001432	20.32	18.99	30.96	16.39	14.24	12.25	16.49	28.23	11.89		
	NT2RP3001439	31.43	37.32	28.95	26.93	25.44	19.21	14.96	11	10.21	**	-
	NT2RP3001441	34.77	41.28	46.38	53.64	42.72	50.36	30.69	23.25	24.74	*	-
	NT2RP3001446	4.24	2.49	4.94	4.53	3.01	2.2	2.82	2.01	1.51		
	NT2RP3001447	22.35	21.24	25.11	13.3	8.65	15.94	13.67	37.08	14.99	*	-
50	NT2RP3001449	139.79	126.76	203.02	199.4	166.47	178.45	131.32	106.74	139.38		
	NT2RP3001453	31.6	35.5	49.48	34.98	29.3	36.04	28.49	31.86	35.69		
	NT2RP3001457	13.38	17.23	17.13	11.75	10.12	6.15	5.98	6.75	6.92	*	**
	NT2RP3001459	11.29	13.84	13.09	7	3.75	5.3	5.53	4.44	5.41	**	**
	NT2RP3001463	6.65	4.84	3.81	4.67	1.94	1.07	1.96	2.08	0.69	*	-
55	NT2RP3001466	5.28	4.9	5.4	5.77	2.51	1.55	2.18	1.94	1.06	**	-
	NT2RP3001472	5.37	5.26	7.06	12.24	7.01	3.59	1.12	2.87	2.9	*	-
	NT2RP3001475	230.39	301.8	150.57	92.73	106.13	95.77	29.54	68.35	93.78	*	*

Table 442

	NT2RP3001479	6.51	3.77	10.27	6.45	4.18	2.2	2.6	4.56	5.3			
	NT2RP3001490	15.72	6.25	23.45	15.28	5.31	6.47	7.24	7.84	8.04			
5	NT2RP3001492	14	14.91	21.99	13.76	7.53	9.81	14.28	13.21	12.48			
	NT2RP3001495	18.56	21.11	19.03	12.08	9.76	9.93	15.89	18.33	21.35	**	-	
	NT2RP3001497	36.57	27.99	40.31	47.7	28.75	36.07	23.59	21.43	24.3	*	*	-
	NT2RP3001501	16.76	28.67	29.3	12.62	8.54	7.31	11.78	2.93	8.97	*	*	-
	NT2RP3001527	5.54	5.56	5.02	7.34	2.65	3.31	4.71	3	2.59	*	*	-
	NT2RP3001529	21.9	27.01	22.29	20.64	12.59	16.78	7.77	18.39	18.96			
10	NT2RP3001538	80.06	67.26	76.24	89.51	76.4	114.47	59.99	77.08	72.65			
	NT2RP3001539	4.24	4.99	8.09	6.1	3.34	4.14	3.58	5.72	3.56			
	NT2RP3001542	17.53	25.89	26.44	14.74	14.15	8.68	14.26	12.41	17.97	*	-	
	NT2RP3001549	6.14	6.2	5.77	5.79	1.73	1.92	2.67	2.05	1.89	**	-	
	NT2RP3001554	28.4	40.66	43.76	10.47	10.16	7.96	15.92	6.96	13.22	**	**	-
	NT2RP3001560	79.18	91.03	86.96	84.47	48.32	76.97	115.31	93.32	84			
15	NT2RP3001561	3.47	3.93	2.29	6.28	2.06	3.29	2.23	2.16	2.49			
	NT2RP3001564	34.74	32.97	34.99	17.25	16.65	19.41	10.11	30.58	15.23	**	-	
	NT2RP3001568	23.08	14.44	30.67	16.92	14.73	6.11	7.97	12.05	7.85			
	NT2RP3001575	34.43	18.91	39.8	19.69	12.66	21.53	16.47	22.21	25.65			
	NT2RP3001580	17.53	21.3	27.37	11.9	7.8	11.25	7.5	7.41	8.67	*	**	-
	NT2RP3001587	14.32	16.9	20.18	11.06	6.6	9.89	19.28	18.65	20.31	*	-	
20	NT2RP3001589	6.31	5.44	5.39	5.29	2.4	2.48	2.34	4.87	3.41			
	NT2RP3001592	37.3	61.22	57.18	30.41	23.17	28.18	46.3	38.66	32.65	*	-	
	NT2RP3001607	11.49	11.68	9.02	7.34	3.49	8.45	5.15	2.53	3.96	**	-	
	NT2RP3001608	30.61	24.16	28.98	15.14	18	18.45	9.66	10.92	10.91	**	**	-
	NT2RP3001613	55.34	46.31	54.71	81.86	48.17	86.77	51.11	48.11	44.78			
	NT2RP3001619	162.64	181.38	185.09	152.03	118.43	125.85	144.48	167.59	158.06	*	-	
25	NT2RP3001621	29.97	24.25	25.08	33.83	16.83	30.34	32.22	27.66	24.11			
	NT2RP3001629	28	13.33	26.21	16.28	12.69	19.85	19.79	23.48	12.56			
	NT2RP3001630	3.51	2.38	4.56	4.63	1.01	2.11	3.79	2.64	3.67			
	NT2RP3001631	64.16	51.12	67.22	112.91	65.5	60.67	59.38	50.82	71.84			
	NT2RP3001634	3.71	4.65	2.94	7.85	2.25	2.09	4.62	2.51	1.18			
	NT2RP3001642	29.24	22.78	34.25	25.21	18.32	21.46	34.78	35.92	40.14			
30	NT2RP3001646	18.72	13.31	23.84	17.34	7.46	8.49	11.13	12.12	12.05			
	NT2RP3001650	4.88	6.33	12.48	7.77	5.89	4.37	3.47	3.76	3.82			
	NT2RP3001667	17.36	19.67	39.76	21.84	7.89	10.07	11.81	14.81	13.16			
	NT2RP3001671	13.32	10.22	13.86	10.05	5.86	9.27	7.9	6.32	3.97	*	-	
	NT2RP3001672	56.18	72.22	87.94	28.72	18.36	21.55	10.7	4.04	14.95	**	**	-
	NT2RP3001676	11.94	10.66	12.76	8.88	5.99	6.36	7.09	3.31	6.98	*	*	-
35	NT2RP3001678	368.4	207.45	268.13	268.3	249.2	237.9	189.86	337.31	274.16			
	NT2RP3001679	19.45	8.41	17.68	13.47	5.77	7.99	3.71	6.54	7.99			
	NT2RP3001682	115.37	82.43	118.94	71.89	66.26	91.02	56.88	114.15	137.5			
	NT2RP3001685	4.91	3.52	11.94	5.16	2.78	2.73	5	2.99	2.91			
	NT2RP3001688	4.75	1.41	4.66	3.33	0.27	0.64	0.99	2.07	0			
	NT2RP3001690	8.33	10.1	11.83	11.07	4.69	5.02	5.74	5.13	6.32	*	-	
40	NT2RP3001693	2.22	6.17	10.5	5.55	2.56	2.65	2.84	2.33	2.39			
	NT2RP3001696	7.34	11.29	11.31	6.93	5.94	11.43	6.97	3.31	6.44			
	NT2RP3001698	780.45	572.31	725.4	616.13	658.96	0.94	533.83	1241.6	1289.4			
	NT2RP3001708	348.43	297.84	257.74	514.57	355.27	1.82	148.2	628.13	519.33			
	NT2RP3001712	32.9	21.37	35.65	18.32	14.72	16.28	22.44	33.16	22.67	*	-	
	NT2RP3001716	13.86	9.55	15.36	8.27	11.28	8.27	5.55	15.45	9.22			
45	NT2RP3001724	28.26	21.7	18.91	32.47	31.93	25.73	16.65	23.86	18.15			
	NT2RP3001727	27.92	15.82	33.03	16.01	12.47	12.24	8.97	9.14	8.89	*	-	
	NT2RP3001729	2.64	5.64	5.12	5.09	2.61	2.56	2.6	2.88	1.65			
	NT2RP3001730	421.81	524.98	490.91	328.42	274.16	316.08	179.32	117.74	101.94	**	**	-
	NT2RP3001733	1.54	1.62	4.9	4.53	0	1.49	0.54	0.39	1.87			
	NT2RP3001737	7.85	25.52	17.42	10.76	4.14	4.59	3.35	7.04	17.36			
50	NT2RP3001738	28.07	24.45	41.36	18.76	13.82	15.18	12.56	15.63	32.84	*	-	
	NT2RP3001739	2.19	2.42	9.16	4.78	1.8	1.62	1.06	2.07	0.9			
	NT2RP3001742	11.1	11.43	14.41	9.77	5.51	6.65	7.73	6.52	8.12	*	*	-
	NT2RP3001751	1.19	3.87	3.32	5.53	0.3	1.67	1.29	0.92	0.82			
	NT2RP3001752	2.48	4.8	2.87	3.47	0.21	1.52	1.75	2.38	0.9			
	NT2RP3001753	3.96	5.83	5.77	7.82	4.31	2.86	4.73	5.28	2.61			
55	NT2RP3001754	3.14	1.28	9.55	3.89	0.47	2.48	0.99	1.82	0.86			
	NT2RP3001756	4.67	4.56	13.42	7.12	2.77	3.58	2.62	4.94	3.56			

Table 443

	NT2RP3001764	3.84	4.67	12.85	4.07	1.87	1.79	1.19	3.02	2.08			
	NT2RP3001771	10.53	6.71	15.52	12	8.69	4.55	2.42	4.06	4.07	*		-
5	NT2RP3001777	40.65	47.79	33.95	47.7	28.57	21.63	29.91	18.82	40.09			
	NT2RP3001782	18.47	18.59	14.66	13.14	8.87	10.49	5.89	13.23	9.56	*	*	-
	NT2RP3001792	51.98	43.73	63.18	42.18	33.54	33.35	80.48	61.45	65.58			
	NT2RP3001799	7.5	9.23	9.91	6.52	4.07	3.35	7.42	5.61	3.54	*		-
	NT2RP3001819	9.21	8.05	11.94	7.62	3.17	5.23	2.57	7.27	6.12			
	NT2RP3001829	0.79	0.98	6.7	3.6	0.17	1.25	3.26	1.13	0.11			
10	NT2RP3001836	16.84	18.26	30.32	14.13	7.32	15.63	6.9	7.75	7.46	*		-
	NT2RP3001839	6.81	9.19	13.79	8.6	4.4	4.34	2.3	5.79	3.54			
	NT2RP3001844	5.94	4.03	11.89	5.39	1.37	2.09	2.04	1.24	1.53			
	NT2RP3001848	53.13	36.02	38.27	40.15	39.26	28.02	46.65	51.58	51.5			
	NT2RP3001854	53.05	46.79	83.54	47.02	38.11	28.76	72.37	61.23	74.82			
	NT2RP3001855	8.77	9.33	11.43	9.53	8.22	8.62	9.1	7.34	5.15			
15	NT2RP3001857	2.78	1.95	7.57	5.8	0.8	2.63	1.53	2.14	0.96			
	NT2RP3001858	1.48	1.77	7.55	6.01	1.18	1.83	0	1.41	1.37			
	NT2RP3001861	4.86	3.76	12.83	6.03	2.09	1.54	1.75	2.42	0.53			
	NT2RP3001866	4.29	4.19	8.56	7.38	2.36	3.86	2.27	2.97	2.71			
	NT2RP3001871	4.11	2.37	11.14	4.75	0.71	0.4	0.62	1.36	0.06			
	NT2RP3001874	10.44	5.38	11.3	5.07	2.46	1.93	2.08	3.65	5.3	*		-
20	NT2RP3001878	6.84	8.82	7.25	6.09	2.26	2.81	4.01	2.14	3.46	*	**	-
	NT2RP3001885	6.75	5.91	9.28	7.33	5.82	5.26	4.29	3.86	3.96		*	-
	NT2RP3001896	15.8	9.61	18.78	10.19	5.77	12.23	2.88	7.21	8.15			
	NT2RP3001898	10.12	6.81	17.59	9.29	3.83	4.48	2.35	4.36	3.15			
	NT2RP3001899	4.46	3.48	9.66	6.74	4	4.77	3.33	4.46	3.02			
	NT2RP3001901	2.97	2.49	8.51	4.89	2.11	2.05	1.6	0.22	0.74			
25	NT2RP3001915	21.98	18.4	24.23	18.83	15.46	12.75	6.48	6.95	5.98	**		-
	NT2RP3001926	42.5	70.22	59.74	46.58	37.18	35.96	45.08	32.42	25.88			
	NT2RP3001929	7.68	7.59	9	5.33	1.89	5.28	3.26	1.47	1.63	*	**	-
	NT2RP3001931	7.03	5.58	8.39	8.57	1.83	4.32	4.68	3.69	4.06	*		-
	NT2RP3001938	0.69	0.54	7.42	4.87	0	1.52	0	1.16	0.26			
30	NT2RP3001943	188.81	183.6	152.87	80.5	86.76	128.25	85.31	121.73	115.26	*	*	-
	NT2RP3001944	17.12	20.99	26.58	14.69	15.73	4.63	10.12	15.18	9.75		*	-
	NT2RP3001945	39.73	40.32	37.82	24.74	26.95	28.23	17.61	14.81	14.26	**	**	-
	NT2RP3001947	47.48	38.36	48.19	30.55	15.52	22.26	24.69	18.23	25.96	*	**	-
	NT2RP3001949	37.29	38.85	47.2	29.25	26.76	28.05	30.76	28.58	28.74	*	*	-
	NT2RP3001952	10.17	10.07	6.99	3.68	1.57	0.37	2.44	1.18	1.17	**	**	-
	NT2RP3001954	9.56	18.54	17.64	8.37	4.32	7.01	11.86	5.36	4.75	*		-
35	NT2RP3001956	3.88	4.98	8.37	7.17	1.4	2.11	0.35	2.86	1.91			
	NT2RP3001967	7.48	3.68	9.02	8.89	3.53	3.86	3.05	4.36	2.97			
	NT2RP3001969	2.15	1.05	4.78	4.72	1.42	2.2	1.63	2.56	0.82			
	NT2RP3001976	1.89	2.22	5.25	5.93	1.38	2.82	1.33	1.09	1.87			
	NT2RP3001986	3.89	3.3	6.39	4.22	1.46	2.65	3.43	6.44	2.42			
40	NT2RP3001989	6.56	8.64	5.36	8.05	1.81	1.73	3.37	1.97	1.12	*	*	-
	NT2RP3002002	7.76	11.38	8.57	5.38	2.01	2.22	6.25	3.04	6.16	*	**	-
	NT2RP3002004	7.76	12.41	12.06	6.85	3.16	4.05	3.73	2.48	3.6	*	*	-
	NT2RP3002007	14.2	10.34	19.96	11.2	4.92	6.67	4.6	9.34	6.75			
	NT2RP3002014	2.11	1.84	5.64	7.64	3.81	2.33	1.74	3.76	3.1			
	NT2RP3002015	10.24	10.71	16.79	11.66	11.36	10.59	8.67	8.67	11.36			
	NT2RP3002033	8	5.97	11.92	6.98	3.29	5.92	6.91	8.34	8.48			
45	NT2RP3002045	7.45	16.7	16.88	5.97	3.53	4.5	4.78	3.11	3.05	*	*	-
	NT2RP3002054	292.36	495.82	456.61	206.09	224.87	171.66	441.79	291.3	543.12	*		-
	NT2RP3002056	3.09	3.6	0.88	3.45	0.32	0.79	0.92	1.02	0.67			
	NT2RP3002057	10.26	15.21	13.61	7.78	1.9	3.69	8.33	6.11	3.21	*	*	-
	NT2RP3002061	3.7	2.82	3.37	5.14	1.22	2.6	0	1.37	0.53		**	-
50	NT2RP3002062	14.95	11.22	12.96	12.28	11.33	13.44	7.88	11.32	11.12			
	NT2RP3002063	3.07	0.91	3.18	5.76	3.45	2.53	1.35	2.57	1.94			
	NT2RP3002064	4.75	4.07	6.06	8.44	3.11	3.26	2.69	6.61	3.66			
	NT2RP3002071	2.99	2.02	2.84	4.58	1.41	2.26	2.09	2.02	0.69			
	NT2RP3002073	4.16	1.73	3.01	5.39	0.35	0	3.4	1.98	3.29			
	NT2RP3002074	3.97	4.7	9.59	5.64	1.52	1.74	2.26	2.79	1.06			
55	NT2RP3002075	115.61	136.72	152.03	61.15	60.41	66.84	138.08	127.44	140.01	**		-
	NT2RP3002077	1.88	1.37	7.12	4.73	0	2.99	1.52	0.95	1.4			
	NT2RP3002081	9.52	4.64	17.43	9.04	2.14	3.36	6.77	6.6	8.59			



Table 444

	NT2RP3002086	9.1	5.64	14.68	7.72	4.13	4.75	9.35	9.69	7.69				
	NT2RP3002094	3.34	2.83	6.44	4.61	2.06	2.3	2.41	5.92	1.29				
5	NT2RP3002096	12.33	8.92	11.73	8.59	3.97	5.5	5.94	5.18	4.01	*	**	-	-
	NT2RP3002097	23.91	20.85	34.1	19.75	11.2	19.57	12.95	19.73	14.4				
	NT2RP3002098	5.03	5.84	6.49	7.72	2.61	2.62	5.48	4.78	3.63				
	NT2RP3002102	13.2	5.06	15.39	11.41	5.66	7.42	3.96	4.11	3.36				
	NT2RP3002106	10.36	7.3	14.64	10.63	8.57	6.26	3.35	4.87	10.6				
	NT2RP3002108	4.96	2.64	12.49	5.65	1.44	2.35	2.54	2.99	5.43				
10	NT2RP3002109	40.98	15.02	38.55	15.39	16.89	11.31	8.11	16.82	8.14				
	NT2RP3002110	5.34	2.87	6.32	5.23	2.17	1.37	2.33	2.43	0.38				
	NT2RP3002113	9.48	7.75	15.49	10.55	5.09	3.01	6.14	4.67	6.08				
	NT2RP3002120	7.73	8.74	11.8	6.57	3.91	2.89	5.04	3.74	4.99	*	*	-	-
	NT2RP3002121	1.11	4.94	1.77	5.17	1.32	0.68	2.8	1.37	1.2				
	NT2RP3002126	64.09	54.26	55.37	40.43	28.8	44.09	33.92	65.97	39.23	*		-	
15	NT2RP3002128	8.94	4.6	9.8	7.18	4.51	3.23	4.1	5.32	11.38				
	NT2RP3002130	45.15	21.81	38.29	25.97	19.96	17.62	5.74	23.29	23.75				
	NT2RP3002133	713.78	729.07	666.05	842.53	766.78	697.72	544.62	1065.2	813.76				
	NT2RP3002136	99.29	50.26	79.88	69.55	58.35	39.45	17.4	37.71	52.59				
	NT2RP3002140	3.69	7.52	7.94	5.4	2.45	3.08	2.99	3.81	3.42				
	NT2RP3002142	9.07	12.94	11.89	8.33	6.6	5.19	5.4	5.06	2.64	*	**	-	-
20	NT2RP3002146	9.3	10.61	11.18	9.37	7.32	7.23	12.19	11.03	8.72				
	NT2RP3002147	11.07	11.26	19.71	10.63	7.44	5.02	4.38	6.88	4.67		*	-	
	NT2RP3002151	15	10.97	25.17	14.01	7.18	7.82	7.02	15.09	18.04				
	NT2RP3002155	53.25	66.04	47.55	73.17	43.36	52.61	36.35	94.67	86.47				
	NT2RP3002156	3.79	2.7	6.74	4.59	0.75	1.4	1.04	0.59	1.13		*	-	
	NT2RP3002160	9.08	10.25	12.47	12.87	7.96	7.04	2.86	3.65	6.87		*	-	
25	NT2RP3002163	13.64	21.03	16.3	10.69	7.06	4.19	9.73	11.32	12.78	*		-	
	NT2RP3002165	6.75	7.58	8.41	6.08	1.96	1.96	2.6	3.84	1.9	*	**	-	-
	NT2RP3002166	5.43	5.03	4.69	5.27	1.55	0.67	2.88	6.31	2.47				
	NT2RP3002173	517.9	446.69	509.69	297.97	240.6	253.29	44.66	135.22	128.7	**	**	-	-
	NT2RP3002174	130.22	107.95	156.75	150.48	138.99	121.68	76.48	86.96	88.77		*	-	
	NT2RP3002181	5.97	4.69	12.81	5.8	2.39	3.23	1.84	5.23	1.34				
30	NT2RP3002185	44.31	38.54	51.77	25.79	16.42	22.4	38.06	52.39	48.7	**		-	
	NT2RP3002193	7.33	7.63	13.87	8.26	3.71	3.99	4.19	5.78	8.23				
	NT2RP3002204	41.05	45.66	52.03	45.02	28.36	25.63	28.31	47.28	47.76				
	NT2RP3002244	12.8	20.63	18.31	13.33	15.24	10.05	9.17	7.08	5.13		*	-	
	NT2RP3002248	7.98	7.8	12.04	10.57	4.97	3.5	9.37	6.63	3.98				
	NT2RP3002253	17.21	11.16	18.79	9.56	7.33	7.05	3.72	10.84	9.39	*		-	
35	NT2RP3002255	3.26	2.63	8.57	4.41	1.55	2.02	1.36	3.59	1.93				
	NT2RP3002254	81.68	74.91	64.3	98.72	70.97	43.12	54.37	98.78	53.26				
	NT2RP3002267	2.25	3.31	8.07	3.82	0.82	1.41	0.79	1.35	0.88				
	NT2RP3002273	20.4	16.49	19.5	15.02	8.97	5.71	10.11	9.27	13.28	*	**	-	-
	NT2RP3002276	3.97	2.93	8.36	4.35	0.7	1.55	1.24	0.89	0.84				
	NT2RP3002281	13.35	12.31	15.77	11.45	7.06	7.28	10.16	10.76	11.32	*	*	-	-
40	NT2RP3002286	16.62	19.5	20.21	12.28	6.1	7.69	4.25	3.16	1.57	**	**	-	-
	NT2RP3002297	94.9	98.81	132.4	64.72	33.84	39.98	11.41	37.45	29.98	*	**	-	-
	NT2RP3002301	11.34	12.34	18.57	7.11	3.98	4.21	2.56	4.64	4.68	*	*	-	-
	NT2RP3002303	7.54	10.15	16.1	7.32	5.62	4.17	5.05	6.82	7.85				
	NT2RP3002304	91.67	49.25	50.79	81	77.65	34.95	31.29	39.07	25.04				
	NT2RP3002309	4.32	3.35	10.38	4.01	1.44	1.07	2.59	1.36	0.22				
45	NT2RP3002311	9.65	9.45	12.73	9.08	6.57	4.41	3.9	4.09	5.31		**	-	
	NT2RP3002315	16.31	24.1	16.79	7.96	7.42	8.29	9.67	8.19	10.65	*	*	-	-
	NT2RP3002319	8.49	14.45	9.47	9.99	3.2	4.43	5.43	3.04	5.3		*	-	
	NT2RP3002324	18.48	20.79	21.07	16.08	9.05	11.92	2.65	9.16	8.78	*	**	-	-
	NT2RP3002330	14.44	26.39	29.36	13.92	12.3	11.42	5.88	11.72	10.72		*	-	
50	NT2RP3002333	41.51	67.04	49.57	36.81	41.81	35.64	33.68	44.76	37.87				
	NT2RP3002337	4.44	8.96	11.93	5.8	1.82	3.91	2.32	2.11	2.55		*	-	
	NT2RP3002342	25.61	22.15	24.13	19.61	11.87	9.75	11.85	13.94	20.4	*	*	-	-
	NT2RP3002343	3.99	7.39	7.92	5.18	2.92	2.42	2.4	1.77	3.64		*	-	
	NT2RP3002351	20.96	17.51	19.58	6.79	4.97	3.6	9.93	4.83	3.54	**	**	-	-
	NT2RP3002352	29.92	68.54	51.75	25.45	36.1	22.42	47.8	10.88	7.27				
55	NT2RP3002353	26.94	28.46	26.72	23.44	18.05	15.48	14.2	29.02	22.52	*		-	
	NT2RP3002362	18.42	12.38	24.27	11.02	6.28	7.66	12.53	15.38	16.92				
	NT2RP3002363	11.71	14.02	21.35	9.9	11.24	7.29	10.05	11.93	6.97				

Table 445

	NT2RP3002377	20.63	15.78	16.8	13.04	9.6	12.99	16.42	23.7	18.15	*	-	-
	NT2RP3002397	5.32	9.77	13.16	6.81	2.98	3.19	4.39	2.85	3.63			
5	NT2RP3002404	6.54	8.21	7.65	4.33	1.3	1.29	2.68	0.69	1.15	*	**	-
	NT2RP3002410	7.62	4.7	8.02	3.73	3.33	1.2	3.81	3.45	2.67	*	*	-
	NT2RP3002414	5.43	4.93	6.03	6.64	1.85	2.91	4.09	1.68	3.33	*	*	-
	NT2RP3002430	5.86	5.44	9.44	4.78	1.52	1.85	3.2	1.23	1.16	*	*	-
	NT2RP3002448	12.97	9.25	9.52	5.21	1.95	1.81	2.67	2	4.7	**	**	-
	NT2RP3002454	12.06	19.92	16.37	13.74	7.64	12.02	13.75	9.17	8.67			
10	NT2RP3002455	4.76	3.53	5.11	6.77	1.51	4.71	3.7	5.48	5.26			
	NT2RP3002456	58.03	38.92	43.81	27.96	14.69	15.06	14.57	36.86	33.26	*	-	-
	NT2RP3002462	20.18	13.39	21.5	10.24	9.33	4.6	3.9	5.28	3.19	*	**	-
	NT2RP3002469	3.83	1.84	6.7	6.03	3.37	1.62	2.45	1.7	0.82			
	NT2RP3002470	35.44	35.5	72.47	34.81	21.72	19.39	33.8	20.85	19.08			
	NT2RP3002484	3.62	2.13	4.4	4.15	1.03	1.2	2.28	1.6	1.75			
15	NT2RP3002491	13.97	21.34	15.21	12.05	5.93	4.04	5.95	7.05	7.23	*	*	-
	NT2RP3002494	24.09	40.78	35.02	15.6	8.77	12.21	26.54	16.61	15.03	*	-	-
	NT2RP3002497	1.45	2.72	2.12	3.96	0.95	2.47	1.03	1.64	2.67			
	NT2RP3002500	16.58	14.89	20.26	24.82	15.49	27.1	14.57	11.42	19.8			
	NT2RP3002501	32.52	29.62	45.43	41.64	21.97	31.25	12.71	18.89	18.63	*	-	-
	NT2RP3002512	5.61	3.7	5.13	8.12	4.35	5.53	3.81	5.5	5.08			
20	NT2RP3002529	570.71	676.56	723.55	824.94	401.81	698.08	438.95	899.52	707.21			
	NT2RP3002533	33.09	38.94	36.28	44.79	15.69	31.1	9.54	21.79	17.75	**	-	-
	NT2RP3002539	6.02	8.36	9.74	6.07	3.74	0.01	2.47	0	0.12	**	-	-
	NT2RP3002540	4.32	7.97	5.52	9.08	2.78	5.47	9.44	4.32	6.18			
	NT2RP3002543	12.62	4.6	12.88	12.84	5.24	6.49	9.1	11.85	10.42			
25	NT2RP3002545	2.99	1.16	9.33	6.12	1.46	2.25	2.07	3.55	0.82			
	NT2RP3002549	6.99	4.28	13.6	7.32	1.84	2.44	4.48	4.56	2.91			
	NT2RP3002552	4.39	5.59	10.04	7.03	1.31	2.23	3.66	3.6	2.29			
	NT2RP3002558	34.53	21.49	27.53	25.41	11.35	21.08	37	39.71	40.69	*	+	-
	NT2RP3002565	13.64	7.8	14.18	11.1	3.88	9.31	11.41	13.37	16.44			
	NT2RP3002566	7.8	8.76	13.33	16.41	6.98	8.51	6.63	7.76	8.89			
	NT2RP3002571	8.13	11.03	10.93	9.57	4.89	4.39	4.63	2.67	3.9	**	-	-
30	NT2RP3002572	74.15	45.74	56.76	41.43	36.41	30.38	19.06	45.1	46.35			
	NT2RP3002573	32.62	15.75	29.51	19.71	16.82	14.99	13.13	13.23	21.22			
	NT2RP3002577	47.28	29.36	41.83	19.87	14.5	21	17.59	15.85	17.3	*	*	-
	NT2RP3002579	8.63	6.06	12.6	7.23	3.12	4.38	5.33	4.66	5.1			
	NT2RP3002582	6.19	3.82	10.45	7.84	3.56	3.38	4.87	4.78	3.74			
	NT2RP3002587	10.07	10.45	15.76	10.84	6.77	7.46	4.8	4.74	3.88	*	-	-
35	NT2RP3002590	544.94	699.14	857.26	489.72	627.82	453.24	363.97	273.66	582.87			
	NT2RP3002602	7.18	7.63	10.58	10.16	7.38	6.68	4.87	4.34	6.16	*	-	-
	NT2RP3002603	14.44	13.52	18.75	16.38	10.66	15.03	8.16	15.4	88.12			
	NT2RP3002621	6.81	5.15	9.83	8.56	3.04	3.97	3.12	5.17	6.09			
	NT2RP3002622	6.75	5.01	13.82	8.8	3.27	3.73	2.74	4.44	11.45			
40	NT2RP3002624	26.96	16.99	21.5	17.24	10.36	13.21	17.97	25.27	18.08			
	NT2RP3002628	6.59	5.38	9.7	6.43	2.65	4.46	4.24	5.21	2.97			
	NT2RP3002629	5.76	11.73	14.59	10	6.43	5.93	6.71	4.48	3.96			
	NT2RP3002631	48.35	45.23	46.18	26.1	22.1	27.75	26.27	23.38	21.25	**	**	-
	NT2RP3002647	12	15.89	13.32	16.2	15.29	15.81	10.24	7.5	7.23	*	-	-
	NT2RP3002649	9.3	7.92	12.59	9.96	4.23	5.01	3.45	5.1	5.57	*	-	-
45	NT2RP3002650	26.86	18.53	27.47	18.25	9.68	13.45	17.35	20.46	18.82			
	NT2RP3002652	5.52	5.57	14.03	5.61	3.76	3.01	2.75	4.84	3.27			
	NT2RP3002654	20.14	13.49	14.7	11.91	10.11	6.69	5.42	7.8	5.1	*	-	-
	NT2RP3002657	16.5	15.29	20.85	14.05	6.31	13.07	15.2	14.6	14.98			
	NT2RP3002659	15.92	19.34	18.66	13.66	10.7	8.74	4.85	10.09	6.73	*	**	-
	NT2RP3002660	5.66	10.19	9.81	8.43	3.68	4.95	6.72	4.39	3.92			
50	NT2RP3002663	10.53	17.57	11.68	14.14	15.43	9.63	19.1	11.04	8.75			
	NT2RP3002664	28.81	23.63	39.16	18.72	11.43	13.27	7.92	17.21	15.51	*	*	-
	NT2RP3002667	32.83	27.15	33.62	23.94	18.84	19.81	15.18	21.3	26.19	*	-	-
	NT2RP3002671	38.88	30.21	40.39	24.11	15.4	14.74	30.8	35.93	33.74	*	-	-
	NT2RP3002682	8.45	6.51	13.68	7.64	3.93	4.02	2.41	3.04	2.62	*	-	-
	NT2RP3002684	20.03	14.16	18.81	8.9	8.81	5.51	4.13	6.96	4.79	*	**	-
55	NT2RP3002687	9.25	11.21	13.71	14.12	8.33	10.78	7.86	7.74	7.01	*	-	-
	NT2RP3002688	168.35	106.47	188.15	190.36	164.88	199.08	153.97	87.55	117.43			
	NT2RP3002698	8.07	8.3	9.14	8.34	5.8	6.56	5.59	5.87	4.73	**	-	-

Table 446

	NT2RP3002701	11.4	8.8	15.19	9.64	4.21	7.04	4.79	10.11	7.18			
	NT2RP3002705	30.23	29.89	43.68	30.05	23.71	23.42	20.15	25.03	27.52			
5	NT2RP3002708	25.52	23.92	35.27	19.02	13.81	19.8	19.34	22.92	17.32			
	NT2RP3002711	87.34	128.24	131.86	149.35	126.88	84.65	16.56	37.78	36.54	**	-	
	NT2RP3002712	11.51	9.81	14.14	7.18	5.15	2.41	5.29	7.06	4.76	*	*	-
	NT2RP3002713	17.13	13.75	17.42	8.41	9.55	4.36	13.41	9.28	8.38	*	*	-
	NT2RP3002721	70.06	117.72	122.3	101.88	70.22	94.12	113.7	122.46	107.46			
	NT2RP3002722	20.45	20.54	15.56	16.97	11.11	10.65	14.55	10.8	10.74	*	*	-
10	NT2RP3002723	12.21	14.76	21.14	7.75	4.55	7.76	4.96	7.72	6.61	*	*	-
	NT2RP3002737	4.67	4.9	12.9	7.24	2.22	4.66	2.62	1.49	3.15			
	NT2RP3002738	122.73	88.31	164.33	156.37	134.11	152.93	81.07	85.63	82.42			
	NT2RP3002742	4.62	5.31	8.06	6.59	2.59	2.11	2.29	3.26	2.78	*		-
	NT2RP3002744	11.76	7.9	17.24	10.03	4.45	6.38	6.88	8.18	6.87			
	NT2RP3002756	8.91	6.64	6.82	7.81	5.13	2.63	2.84	1.31	1.38	**	-	
15	NT2RP3002757	18.22	14.86	15.65	13.62	6.41	8.83	10.99	9.29	10.38	*	**	-
	NT2RP3002758	16.5	15.69	16.85	13.98	8.17	9.33	15.83	11.78	10.47	*		-
	NT2RP3002762	6.55	8.17	14.93	9.33	2.38	7.36	4.56	5.11	6			
	NT2RP3002763	6.01	4.94	14.86	7.96	3.26	4.46	4.15	2.77	3.35			
	NT2RP3002770	13.79	15.86	20.19	13.26	7.67	4.65	6.38	6.79	5.16	**	-	
	NT2RP3002771	6.48	3.94	12.36	8.16	4.01	1.77	3.51	4.07	2.45			
20	NT2RP3002785	7.93	7.61	12.09	7.52	4.23	4.31	4.14	3.39	4.41	*	-	
	NT2RP3002790	12.74	8.68	16.54	10.03	4.49	9.67	11.67	8.3	11.43			
	NT2RP3002799	44.32	36.15	61.61	71.32	40.17	61.97	38.77	29.46	32.11			
	NT2RP3002801	9.13	7.96	8.02	8.82	3.17	7.55	6.99	2.43	2.63	*	-	
	NT2RP3002802	6.6	5.16	13.06	9.48	2.83	4.69	3.71	3.1	3.55			
25	NT2RP3002810	21.61	13.43	30.89	15.94	9.02	13.72	15.57	16.49	23.18			
	NT2RP3002818	12.26	21.33	22.29	12.03	10.84	9.9	12.06	10.85	7.02			
	NT2RP3002821	3.08	2.76	7.5	5.13	0.98	2.74	3.88	1.7	1.96			
	NT2RP3002823	5.94	5.9	9.87	7.27	1.84	2.08	2.79	3.12	3.09	*	-	
	NT2RP3002825	46.16	68.1	69.32	16.84	16.8	11.22	9.52	7.53	4.62	**	**	-
	NT2RP3002829	36.39	46.01	39.22	22.92	16.02	11.21	24.02	7.98	9.64	**	*	-
30	NT2RP3002831	9.11	9.95	10.41	14.39	9.89	8.12	9.96	4.98	9.9			
	NT2RP3002836	16.68	11.51	17.27	10.91	4.09	9.65	4.06	4.72	7.36	**	-	
	NT2RP3002845	38.76	32.47	30.9	12.04	7.1	5.17	5.18	12.27	9.29	**	**	-
	NT2RP3002852	27.07	21.18	24.92	24.24	10.22	18.18	20.47	22.49	18.97			
	NT2RP3002861	6.45	10.44	9.71	7.81	2.41	4.65	6.77	4.65	5.14			
	NT2RP3002869	6.19	9.1	10.7	6.8	3.23	3.7	4.89	3.27	3.99	*	-	
35	NT2RP3002874	12.63	13.11	17.2	9.07	5.37	6.1	8.08	3.93	8.06	*	*	-
	NT2RP3002876	143.63	148.27	181.51	254.93	163.87	216.77	137.83	99.6	141.63			
	NT2RP3002877	16.65	19.83	22.97	18.33	13.19	15.19	13.02	8.47	12.29	*	-	
	NT2RP3002887	11.91	8.65	14.58	12.86	6.78	9.6	8.16	11.65	6.83			
	NT2RP3002900	24.9	40	47.49	50.72	36.64	57.77	42.16	46.86	41.82			
	NT2RP3002902	50.68	50.65	63.54	17.78	28.94	15.05	19.17	20.83	23.73	**	**	-
40	NT2RP3002909	5.43	3.6	6.73	6.91	1.07	4.91	4.39	3.43	4.07			
	NT2RP3002911	32.27	38.37	39.37	37.75	22.31	32.66	41.96	41.35	47.38			
	NT2RP3002948	97.24	122.54	134.73	183.88	103.17	110.98	109.55	85.09	95.2			
	NT2RP3002953	130.69	155.36	174.07	145.08	99.42	98.1	201.22	181.14	165.58			
	NT2RP3002955	11	13.27	12.07	9.74	5.71	6.63	7.47	5.75	5.17	*	**	-
	NT2RP3002958	11.7	7.18	10.81	11.8	6.8	11.76	8.8	13.15	14.41			
45	NT2RP3002969	10.47	5.67	11.5	11.46	3.57	3.82	2.62	3.28	4.09	*	-	
	NT2RP3002972	9.18	3.34	9.31	7.48	3.85	0.87	5.21	5.53	7.19			
	NT2RP3002978	17.8	13.14	17.07	16.61	7.47	16.55	15.56	17.59	21.66			
	NT2RP3002983	14.39	16.02	14.98	15.99	6.52	11.68	18.52	16.38	19.45	*	+	
	NT2RP3002985	4.55	5.27	7.26	6.46	1.04	3.38	4.84	3.07	3.43			
	NT2RP3002988	8.52	6.19	9.46	9	4.1	8.27	7.55	8.24	9.04			
50	NT2RP3003000	3.67	3.71	3.5	6.2	1.26	2.48	2.37	2.4	2.73	**	-	
	NT2RP3003008	10.96	2.67	10.84	10.43	9.08	7.16	5.31	8.35	5.42			
	NT2RP3003012	2.33	3.47	10.69	4.62	0.4	1.73	0.84	1.69	1.54			
	NT2RP3003015	94.04	42.5	71.87	52.22	37.75	51.79	66.36	44.43	66.31			
	NT2RP3003018	4.14	3.97	9.63	5.98	1.6	1.48	2.56	2.43	2.26			
	NT2RP3003028	3.8	4.39	9.49	7.13	4.25	1.98	3.07	2.68	1.64			
55	NT2RP3003029	10.59	12.64	16.85	9.46	5.29	7.18	11.38	8.45	12.28			
	NT2RP3003032	18.44	16.02	27.77	16.77	11.22	12.42	15.36	17.44	10.46			
	NT2RP3003041	9.55	9.82	9.95	12.39	5.66	4.67	6.47	4.02	3.62	**	-	

Table 447

	NT2RP3003044	20.51	12.05	18.28	17.95	10.92	17.93	12.47	17.92	24.95				
	NT2RP3003047	318.58	233.21	307.78	283.91	158.8	215.31	289.99	339.63	305.02				
5	NT2RP3003050	6.01	3.67	13.67	6.04	1.27	2.97	2.45	4.04	3.78				
	NT2RP3003053	4.73	4.39	9.42	5.4	1.52	3.2	1.65	2.69	4.02				
	NT2RP3003059	3.4	2.18	5.45	4.75	1.77	1.03	2.8	1.96	1.97				
	NT2RP3003061	3.92	4.63	10.62	7.14	5.71	3.17	3.68	3.67	3.35				
	NT2RP3003068	13.64	16.72	19.09	13.94	11.08	9.11	15.51	9.65	9.79				
	NT2RP3003071	501.47	582.68	529.35	407.82	335.95	447.01	379.51	122.11	170.7	*	*	-	-
10	NT2RP3003076	11.52	4.82	12.85	9.77	5.93	5.76	7.19	9.4	27.45				
	NT2RP3003078	14.69	14.12	17.86	9.88	7.71	7.1	3.81	7.38	11.24	**	*	-	-
	NT2RP3003081	14.34	14.21	20.22	13.69	9.02	9.23	12.85	17.91	10.55				
	NT2RP3003090	4.38	6.96	9.84	6.19	3.29	2.43	4.26	4.05	2.94				
	NT2RP3003097	14.02	15.06	14.8	11.66	5.57	6.77	8.05	9.19	6.11	*	**	-	-
	NT2RP3003098	6.1	7.46	9.23	6.48	4.67	4.01	3.99	4.01	3.93		*	-	-
15	NT2RP3003101	11.04	12.95	14.52	11.99	6.27	8.65	11.09	9.21	8.98				
	NT2RP3003109	27.77	29.32	24.18	32.49	26.06	31.9	22.67	12.21	14.33		*	-	-
	NT2RP3003121	14.74	6.75	15.15	12.65	4.66	5.96	4.11	5.09	12.75				
	NT2RP3003133	8.34	7.45	12.11	8.93	5.28	6.18	2.52	4.07	7.32				
	NT2RP3003137	4.53	5.11	11.1	4.41	2.55	1.77	1.57	3.58	2.61				
20	NT2RP3003138	14.49	14.02	31.57	15.47	8.83	7.42	8.07	6.92	9.16				
	NT2RP3003139	17.72	13.28	16.88	11.32	8.97	7.87	7.6	10.95	5.4	*	*	-	-
	NT2RP3003145	29.81	27.36	41.27	37.92	28.86	28.23	19.57	16.3	17.5		*	-	-
	NT2RP3003150	3.07	5.2	3.99	5.23	1.85	1.66	3.17	2.46	1.85				
	NT2RP3003157	36.91	28.34	31.25	37.59	20.43	24.91	16.55	12.31	12.99		**	-	-
	NT2RP3003185	12.88	12.16	22.32	13.29	10.08	11.04	7.56	13.67	13.84				
	NT2RP3003193	56.79	51.34	61.74	61.27	47.04	47.44	61.96	79.57	80.02				
25	NT2RP3003197	14.34	9.96	23.45	8.85	5.2	5.54	6.63	9.8	4.5				
	NT2RP3003203	13.42	14.29	19.75	14.19	7.85	8.04	8.52	12.56	10.13				
	NT2RP3003204	19.08	17.04	30.4	16.33	10.47	7.75	7.19	12.58	11.16				
	NT2RP3003210	6.33	8.19	12.29	9.16	9.84	6.29	6.27	7.36	5.46				
	NT2RP3003212	8.37	8.5	11.56	8.16	5.18	3.57	6.2	5.26	6.14		*	-	-
	NT2RP3003213	5.67	4.05	5.85	6.17	2.96	2.21	4.78	3.56	3.34				
30	NT2RP3003224	55.68	53.67	56.74	16.3	18.72	16.37	11.98	29.14	26.24	**	**	-	-
	NT2RP3003226	4.57	3.58	10.67	6.47	2.35	3.36	2.91	2.15	2.81				
	NT2RP3003230	7.29	5.28	14.91	8.17	2.63	3.43	3.72	2.45	3.81				
	NT2RP3003235	79.63	66.15	103.5	95.3	92.56	60.75	55.64	70.39	55.23				
	NT2RP3003242	73.44	66.48	77.54	45.7	33.8	25.86	41.52	43.2	38.85	**	**	-	-
	NT2RP3003251	104.1	73.55	126.64	135.43	95.34	99.58	79.05	81.02	71.32				
35	NT2RP3003252	10.37	11.27	12.13	9.17	5.92	6.54	5.47	5.61	2.73	*	**	-	-
	NT2RP3003258	15.2	11.75	13.65	15.47	7.62	6.38	7.6	4.08	5.36		**	-	-
	NT2RP3003260	20.33	21.23	23.55	13.01	8.75	11.13	14.98	15.72	16.47	**	**	-	-
	NT2RP3003264	39.02	33.18	49.85	37.17	29.58	23.32	18.19	26.52	25.18		*	-	-
	NT2RP3003273	4.51	4.91	15.07	7.81	4.36	2.59	2.42	2.45	2.99				
40	NT2RP3003278	10.07	13.81	15.32	10.69	5.74	4.93	4.88	5.26	3.08		**	-	-
	NT2RP3003280	8.01	8.36	9.74	5.35	2.41	1.56	1.8	2.02	2.23	*	**	-	-
	NT2RP3003282	6.34	4.14	6.3	6.51	1.72	3.27	3.2	1.42	0.91		*	-	-
	NT2RP3003290	5.35	4.64	5.82	6.64	2.67	3.3	2.13	0.74	2.31		**	-	-
	NT2RP3003301	10.24	13.13	10.58	8.04	5.22	4.9	4.68	1.19	1.93	*	**	-	-
	NT2RP3003302	44.6	31.52	44.49	25.69	16.4	28.65	36.54	47.16	60.3	*		-	-
45	NT2RP3003311	4.75	4.55	11.5	8.43	3.14	4.46	2.2	3.71	1.64				
	NT2RP3003312	24.36	35.16	29.14	9.01	9.9	12.13	5.11	5.46	5.49	**	**	-	-
	NT2RP3003313	11.85	10.76	12.83	7.95	5.85	3.91	3.77	4.31	3.7	*	**	-	-
	NT2RP3003327	9.48	7.49	11.81	7.32	3.83	2.99	4.61	4.57	4.3		*	-	-
	NT2RP3003330	28.77	45.14	40.86	24.02	22.59	18.95	15.05	12.99	8.77	*	**	-	-
	NT2RP3003344	7.42	9.51	10.17	9.56	3.26	4.53	3.31	3.26	4.42		**	-	-
50	NT2RP3003346	7.58	7.33	10.55	7.96	3.11	4.95	5.04	6.17	6.71				
	NT2RP3003349	77.06	82.34	60.61	59.72	39.01	41.31	20.2	47.64	67.66	*		-	-
	NT2RP3003353	5.79	9.35	12.49	5.84	3.66	3.54	2.78	3.58	3.64		*	-	-
	NT2RP3003354	50.09	93.38	122.44	53.2	56.67	30.98	100.88	61.77	52.32				
	NT2RP3003368	10.01	14.26	18.12	8.66	5.26	5.87	4.9	3.64	2.35	*	*	-	-
	NT2RP3003375	13.81	11.33	19.09	11.92	5.85	11.47	12.29	9.6	11.66				
55	NT2RP3003377	8.13	11.7	14	6.42	2.73	1.97	7.35	4.71	8.09	*		-	-
	NT2RP3003384	15.97	18.59	24.94	10.9	5.8	5.57	11.93	4.66	4.64	*	*	-	-
	NT2RP3003385	10.44	16.16	15.37	14.39	15.35	10.89	10.54	6.35	9.2				

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	NT2RP3003396	16.4	12.74	16.94	16.32	6.79	16.93	14.73	19.34	18.49			
	NT2RP3003403	3.1	2.78	7.09	5.18	1.78	3.29	1.96	3.43	3.41			
5	NT2RP3003409	7.35	11.81	12.63	9.44	12.96	4.77	6.95	7.18	6.37			
	NT2RP3003411	11.06	12.25	14.86	7.42	4.83	5.8	7.12	7.74	6.44	**	**	-
	NT2RP3003420	19.06	32.9	36.55	21.71	11.78	14.57	23.43	20.87	21.3			
	NT2RP3003425	6.27	5.68	8.42	5.84	2.62	3.03	4.29	2.39	4.38	*		-
	NT2RP3003426	7.48	8.53	6.3	7.22	3.59	4.34	6.93	6.05	8.2			
	NT2RP3003427	28.71	32.12	28.4	30.38	20.54	27.6	31.57	21.98	21.07			
10	NT2RP3003433	4.33	3.61	3.8	5.72	1.58	3.56	2.47	5.63	2.76			
	NT2RP3003437	3.79	2.73	8.27	7.3	2.16	3.14	2.83	3.31	4.36			
	NT2RP3003448	50.3	43.28	42.61	71.29	41.3	73.4	51.67	39.73	51.96			
	NT2RP3003455	10.05	10.38	13.46	9.15	4.03	7.96	7.2	5.64	6.56	*		-
	NT2RP3003462	10.37	9.93	17.25	9.92	5.42	4.43	5.52	5.56	5.82	*		-
	NT2RP3003464	14.66	13.89	13.26	12.87	7.49	6.91	18.26	16.54	18.68	**		+
15	NT2RP3003469	17.22	14.94	13.68	14.5	4.68	9.94	19.05	18.28	19.4	*		+
	NT2RP3003473	10.99	11.83	10.53	13.09	12.46	13.39	10.9	7.59	8.71	*	+	-
	NT2RP3003474	3.37	3.95	4.83	6.73	2.05	5.69	2.42	1.56	2.61	*		-
	NT2RP3003475	25.58	23.74	27.15	19.96	21.31	0.35	11.64	10.85	19.52	*		-
	NT2RP3003490	6.09	2.59	4.63	5.62	1.54	3.26	2.21	16.1	3.36			
	NT2RP3003491	18.8	17.56	17.3	22.58	14.42	27.63	10.64	13.18	15.87	*		-
20	NT2RP3003493	4.17	0.67	1.27	6.14	0.62	2.97	3.62	2.46	1.88			
	NT2RP3003500	5.9	4.89	5.02	7.76	1.8	6.18	6.6	5.32	6.99			
	NT2RP3003527	7.67	4.85	6.47	6.19	2.35	4.17	6.12	6.18	4.88			
	NT2RP3003532	10.61	16.22	14.72	12.47	4.81	8.89	14.42	12.45	12.16			
	NT2RP3003535	38.7	29.85	32.07	25.66	21.86	25.49	14.16	14.9	18.19	*	**	-
	NT2RP3003536	5.83	2.22	11.18	6.74	1.99	4.05	4.59	4.1	3.31			
25	NT2RP3003543	83.01	76.4	71.54	99.52	61.99	69.1	35.13	38.35	47.54	**		-
	NT2RP3003549	5.05	3.61	9.39	4.68	1.49	3.34	2.95	6.92	3.73			
	NT2RP3003552	5.72	3.03	6.03	6.81	1.98	1.74	4.06	3.11	1.34			
	NT2RP3003555	7.3	5.08	11.06	9.46	2.64	6.2	9.1	6.02	7.32			
	NT2RP3003559	16.08	18.05	20.35	13.82	7.72	7.64	10.69	7.28	10	*	**	-
	NT2RP3003564	21.9	11.18	19.14	32.64	13.35	24.42	5.9	11.04	13.84			
30	NT2RP3003572	4.45	3.71	12.53	6.23	1.91	3.3	2.99	5.76	5.28			
	NT2RP3003576	10.13	4.39	10.89	7.2	4.48	6.35	2.89	3.48	6.99			
	NT2RP3003587	4.99	3.94	10.87	4.59	3.45	2.48	4.61	2.31	2.5			
	NT2RP3003589	8.81	6.29	8.93	5.98	6.78	3.45	8.93	5.16	5.31			
	NT2RP3003592	16.97	13.2	13.23	12.11	9.09	12.9	9.83	6.59	9.69	*		-
	NT2RP3003593	8.95	15.57	14.21	12.38	7.8	13.05	6.6	6.07	15.06			
35	NT2RP3003614	16.19	15.38	25.69	16.13	12.3	18.94	17.5	16.33	15.44			
	NT2RP3003621	23.31	9.78	21.55	19.16	8.76	10.65	10.2	15.44	18.25			
	NT2RP3003625	30.15	13.92	27.9	27.09	17.35	16.31	10.08	25.7	26.09			
	NT2RP3003627	13.85	10.22	17.05	10.88	8	10.73	7.14	16.59	27.58			
	NT2RP3003636	43.56	19.06	24.94	24.57	26.12	25.77	9.71	16.11	10.76			
40	NT2RP3003642	9.55	5.41	10.21	6.42	5.7	4.71	4.31	4.84	5.36	*		-
	NT2RP3003645	11.93	7.13	13.91	10.67	5.31	7.85	4.02	4.25	4.25	*		-
	NT2RP3003648	6.56	6.34	9.24	8.44	4.41	4.52	4.4	2.95	3.73	*		-
	NT2RP3003649	26.09	26.77	29.81	22.55	18.26	23.64	34.18	24.81	32.1	*		-
	NT2RP3003650	12.61	11.46	21.64	12.68	5.46	10.24	6.28	12.27	13.31			
	NT2RP3003656	6.54	4.65	10.33	8.68	1.7	4.51	3.42	4.72	11.15			
45	NT2RP3003659	9.46	5.9	15.28	7.57	5.1	6.1	4.35	6.43	5.32			
	NT2RP3003662	8.5	8.39	10.9	5.37	1.92	5.94	1.35	3.6	1.87	*	**	-
	NT2RP3003664	4.6	5.97	8.27	6.79	3.03	4.25	2.14	1.93	3.82	*		-
	NT2RP3003665	11.75	13.45	13.25	12.32	5.11	5.74	4.75	7.06	5.47	**		-
	NT2RP3003671	70.45	72.23	46.58	69.47	88.76	53.27	45.85	13.94	22.44	*		-
	NT2RP3003672	12.42	9.87	13.46	13.04	14.86	11.85	11.18	14.12	13.48			
50	NT2RP3003673	8.49	4.06	14.72	9.56	3.98	4.91	4.97	6.88	5.68			
	NT2RP3003679	10.33	6.46	20.68	8.71	5.36	8.11	4.9	8.58	8.08			
	NT2RP3003680	13.23	15.82	26.63	9.67	11.59	10.92	6.46	10.89	9.67			
	NT2RP3003686	3.02	3.35	12.97	5.63	1.59	1.88	2.06	1.47	1.07			
	NT2RP3003689	9.23	7.33	11.82	8.17	6.77	3.83	2.32	5.97	3.24	*		-
	NT2RP3003697	6.83	7.26	6.91	7.08	5.61	6.06	2.11	3.71	4.84	*		-
55	NT2RP3003701	9.67	9.01	11.76	7.31	4.84	5.19	3.31	2.62	4.46	*	**	-
	NT2RP3003704	10.73	9.76	12.38	10.7	7.93	10.02	15.67	9.66	12.47			
	NT2RP3003714	6.87	2.51	9.56	7.86	2.41	3.23	1.8	2.83	0.8			

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	NT2RP3003716	7.01	8.27	14.18	5.47	2.75	3.52	6.58	5.29	3.83			
	NT2RP3003721	13.04	10.15	23.8	10.64	5.81	9.58	11.26	11.19	10.89			
5	NT2RP3003722	3.89	8.42	15.57	8.33	6.34	5.67	3.09	6.47	3.17			
	NT2RP3003726	9.91	10.2	12.37	9.7	5.8	5.18	6.04	11.22	5.51			
	NT2RP3003729	15.24	10.41	15.84	9.27	8.89	4.46	6.77	7.5	6.93		*	-
	NT2RP3003731	21.75	24.76	24.08	12.03	11.65	6.88	4.57	8.08	5.08	**	**	-
	NT2RP3003740	6.25	8.21	13.85	9.2	5.84	6.01	5.86	5.22	4.61			
	NT2RP3003746	8.07	4.76	18.45	7.1	1.15	4.58	3.94	4.56	4.9			
10	NT2RP3003749	12.41	10.83	19.25	6.47	8	6.02	6.17	7.75	8.42			
	NT2RP3003754	6.51	6.89	16.88	6.39	6.73	2.6	13.69	10.54	7.77			
	NT2RP3003759	5.04	4.82	10.4	5.36	1.64	1.95	2.96	2.71	1.17			
	NT2RP3003764	37.79	25.83	53.35	42.39	40.22	42.13	25.68	27.55	28.87			
	NT2RP3003766	53.84	52.07	31.23	39.67	26.34	21.22	14.6	22.88	28.5		*	-
	NT2RP3003767	8.01	8.08	7.88	8.43	4.34	4.24	4.39	2.88	4.34		**	-
15	NT2RP3003778	24.16	27.96	20.47	21.14	16.84	15.25	32.15	22.31	26.7			
	NT2RP3003779	12.68	5.29	15.64	10.68	4.35	10.53	3.1	5.95	4.41			
	NT2RP3003783	21.6	12.18	19.59	7.99	4.9	7.06	6.28	6.7	5.9	*	*	-
	NT2RP3003787	6.7	5.75	13.41	6.04	3.64	1.85	4.2	4.99	1.46			
	NT2RP3003789	8.11	11.36	13.5	7.92	6.55	6.67	5.52	5.69	3.28		*	-
	NT2RP3003795	28.23	17.85	14.78	13.94	17.1	12.18	13.09	11.24	13.99			
20	NT2RP3003799	7.73	3.87	9.64	5.67	2.6	3.17	2.83	1.93	2.55			
	NT2RP3003800	80.77	76.75	98.8	62.18	49.64	73.93	101.61	58.63	58.22			
	NT2RP3003805	19.72	20.08	15.07	17.29	8.51	14.67	17.48	12.39	11.94			
	NT2RP3003809	8.63	14.84	28.37	7.81	4.06	5.86	6.78	7.04	6.7			
	NT2RP3003819	19.91	12.71	21.8	8.29	12.89	15.12	8.35	11.58	14.32			
25	NT2RP3003824	4.44	5.34	16.42	6	3.26	2.18	5.16	4	3.14			
	NT2RP3003825	15.83	8.99	17.57	10.52	9.35	8.99	8.88	7.14	8.67			
	NT2RP3003828	7.18	6.66	13.27	7.4	5.95	4.81	5.75	3.03	3.24			
	NT2RP3003831	49.77	38.05	46.92	12.19	13.59	13	11.7	8.2	8.68	**	**	-
	NT2RP3003833	7	12.76	5.52	6.51	1.52	3.02	3.01	1.46	3.08			
	NT2RP3003836	22.92	45.16	37.16	16	14.78	18.49	26.73	7.91	11.58	*		-
	NT2RP3003842	3.09	1.45	4.55	4.66	0.91	2.25	1.5	2.49	0.97			
30	NT2RP3003843	23.17	13.66	18.94	21.62	11.25	18.44	16.81	22.17	19.21			
	NT2RP3003844	11.64	8.51	12	9.56	4.9	7.1	7.94	10.02	13.51			
	NT2RP3003846	11.56	8.88	8.25	8.42	3.89	7.04	8.15	6.21	10.88			
	NT2RP3003849	5.16	5.61	9.2	5.16	1.5	2.43	2.36	2.09	1.97		*	-
	NT2RP3003862	8.43	6.43	11.03	6.94	2.53	2.38	2.84	2.47	3.72		*	-
	NT2RP3003870	9.39	14.91	15.6	7.42	3.58	2.61	4.29	2.22	5.4	*	*	-
35	NT2RP3003874	8.27	8.06	7.54	6.09	3.19	3.65	2.59	2.64	5.21	*	**	-
	NT2RP3003876	6.84	5.28	7.66	10.08	2.52	6.72	2.11	6.22	4.3			
	NT2RP3003880	11.2	8.02	13.91	8.47	2.77	7.12	3.7	8.83	6.95			
	NT2RP3003889	6.9	11.63	11.35	8.75	7.41	9.51	7.37	8.06	5.22			
	NT2RP3003891	13.51	11.29	17.94	8.42	7.04	7.49	10.43	12.21	12.8	*		-
40	NT2RP3003914	2.72	1.62	6.58	5.33	2.56	2.54	2.7	1.4	2.69			
	NT2RP3003915	13.41	9.97	16.94	9.16	3.88	5.29	7.39	4.87	7.36	*	*	-
	NT2RP3003918	7.35	6.41	5.09	8.06	2.84	2.93	4.26	2.94	4.43		*	-
	NT2RP3003920	10.75	6.92	10.79	7.41	1.85	6.22	6.71	4.36	3.03		*	-
	NT2RP3003924	33.52	17.52	18.55	12.63	9.6	13.46	9.41	16.84	13.76			
	NT2RP3003932	13.16	5.83	7.58	6.21	2.22	4.38	1.9	2.22	2.59		*	-
	NT2RP3003939	11.85	14.76	15.54	9.97	7.98	8.34	3.34	3.94	3.84	*	**	-
45	NT2RP3003940	12.22	9.19	12.29	11.49	8.56	4.42	7.78	12.51	10.79			
	NT2RP3003943	7.2	4.68	6.57	7.12	5.58	5.18	4.42	3.92	6.05			
	NT2RP3003959	7.72	13.55	11.27	9.14	1.71	5.64	6.69	7.88	9.75			
	NT2RP3003963	75.69	75.77	72.03	129.26	82.85	106.1	81.78	51.98	65.78			
	NT2RP3003965	18.74	14.24	13.95	14.48	9.03	12.62	20.67	19.68	26.47			
50	NT2RP3003972	4.57	5.37	14.74	8.17	2.14	5.46	5	3.91	5.17			
	NT2RP3003973	6.48	6.48	12.61	7.2	3.25	3.55	3.26	4.26	5.78			
	NT2RP3003979	4.45	3.72	9.63	4.82	2.41	2.62	1.15	1.72	1.66			
	NT2RP3003980	146.06	117.79	158.74	103.46	88.31	102.32	155.94	132.47	147.6	*		-
	NT2RP3003982	7.33	5.76	16.01	6.18	2.48	3	4.61	2.79	5.02			
	NT2RP3003989	10.71	10.02	27.87	8.13	4.12	8.61	5.84	9.52	13.56			
55	NT2RP3003992	46.04	43.58	55.68	31.62	22.83	36.4	32.87	30.71	18.85	*	*	-
	NT2RP3004000	75.38	38.37	57.12	93.25	54.67	51.6	36.78	36.39	33.4			
	NT2RP3004001	14.94	10.16	22.03	15.95	8.73	15.13	13.16	15.23	21.06			

Table 450

	NT2RP3004005	23.75	15.81	26.46	14	10.64	14.12	16.28	18.58	18.43				
	NT2RP3004013	22.54	11.33	21.98	6.11	3.13	3.73	3.05	4.94	3.43	*	*	-	-
5	NT2RP3004016	7.39	7.18	13.3	10.92	9.82	5.35	6.27	5.44	4.76				
	NT2RP3004025	22.82	15.93	25.25	22.37	10.03	12.12	21.2	17.91	21.7				
	NT2RP3004030	4.66	4.65	8.61	4.83	3.44	3.8	4.36	2.41	1.96				
	NT2RP3004041	4.1	2.26	3.06	5.03	2.28	1.57	2.62	0.7	0.71				
	NT2RP3004042	2602.1	1724.7	1778.2	2098.3	1690	1795.1	1947.3	2828.9	2085.3				
	NT2RP3004044	32.34	21.11	30.01	12.91	11.29	11.35	7.18	15.29	26.2	**		-	
10	NT2RP3004051	19.22	22.27	34.06	33.29	21.4	25.83	12.31	39.18	27.89				
	NT2RP3004052	20.9	17.89	21.89	18.39	15.57	16.97	13.27	17.39	19.16				
	NT2RP3004053	19.14	11.65	20.87	15.13	10.18	12.84	3.1	7.99	5.77	*		-	
	NT2RP3004055	5.06	6.81	8.6	5.35	3.54	2.7	2.8	3.03	2.13	*		-	
	NT2RP3004059	26.03	28.01	36.98	19.3	19.54	21.1	20.16	18	15.03	*	*	-	-
	NT2RP3004063	29.14	22.42	34.14	23.83	23.28	19.51	31.01	26.64	12.72				
15	NT2RP3004067	7.95	8.62	20.76	10	4.39	4.65	3.75	4.12	8.39				
	NT2RP3004070	905.61	934.59	965.28	291.19	622.85	595.78	278.31	1360.6	1279.5	*		-	
	NT2RP3004075	11.59	15.27	23.01	8.7	5.82	8.89	3.95	5.77	5.73	*		-	
	NT2RP3004078	13.83	11.53	17.13	13.53	5.08	9.69	12.68	11.48	12.45				
	NT2RP3004083	33.39	27.25	43.84	12.1	13.49	7.53	6.38	6.07	6.79	*	**	-	-
20	NT2RP3004084	25.34	24.44	39.2	27	15.25	16.2	38.67	47.1	47.33				
	NT2RP3004087	13.47	17.06	17.12	15.44	8.85	8.53	10.22	10.37	8.13	*		-	
	NT2RP3004090	72.24	81.09	78.4	57.09	57.97	55.36	77.78	70.88	90.98	**		-	
	NT2RP3004093	28.49	18.68	45.95	14.41	12.09	18.33	8.92	23.19	25.5				
	NT2RP3004095	33.26	26.66	48.11	23.16	21.66	33.49	19.24	23.44	21.47				
	NT2RP3004102	34.73	35.32	40.77	25.98	17.76	24.22	15.74	23.36	12.18	*	**	-	-
	NT2RP3004110	7.05	4.57	10.07	7.67	1.49	3.89	2.25	3.65	1.62	*		-	
25	NT2RP3004119	11.05	7.96	13.76	6.77	3.42	4.11	3.84	3.73	1.51	*	*	-	-
	NT2RP3004125	3.06	3.32	9.52	6.05	1.93	1.78	1.81	1.49	1				
	NT2RP3004129	11.05	13	16.54	13.66	11.08	8.18	7.67	3.97	5.87	*		-	
	NT2RP3004130	6.85	5.7	8.22	6.11	4.3	3.04	1.91	3.1	2.41	**		-	
	NT2RP3004133	8.31	5.24	20.22	8.3	3.21	4.09	3.33	4.08	3.29				
30	NT2RP3004145	5.99	4.29	13.16	5.33	2.78	2.69	2.63	4.11	3.14				
	NT2RP3004148	53	37.5	49.88	32.7	23.92	15.17	30.82	36.4	44.13	*		-	
	NT2RP3004155	8.18	8.86	12.7	12.14	3.98	4.25	2.59	2.94	3.13	**		-	
	NT2RP3004165	77.97	53.41	68.62	51.37	46.12	31.89	49.51	25.55	55.19				
	NT2RP3004179	9.55	6.18	11.2	6.95	2.94	2.88	4.01	3	3.7	*		-	
	NT2RP3004185	6.31	5.21	6.12	9.04	2.95	2.38	1.55	0.61	2.3	**		-	
	NT2RP3004188	6.31	7.01	6.86	7.94	4.08	2.67	3.74	2.3	1.82	**		-	
35	NT2RP3004189	15.63	7.3	21.16	9.58	5.21	8.89	4.83	8.4	6.14				
	NT2RP3004190	64.52	34.39	57.67	48.45	40.38	53.55	47.37	42.21	45.49				
	NT2RP3004191	122.58	123.5	136.79	74.78	46.86	44.19	48.51	70.16	47.4	**	**	-	-
	NT2RP3004202	18.55	13.31	21.41	14.01	15.47	6.42	10.97	12.13	10.67				
	NT2RP3004205	10.59	7.33	14.79	6.1	4.73	2.92	2.52	2.35	2.6	*		-	
40	NT2RP3004206	15.55	12.16	17.94	7.47	8.64	7.63	5.69	7.13	12.18	*		-	
	NT2RP3004207	8.65	8.42	9.24	5.53	2.88	3.67	2.31	1.22	2.02	**	**	-	-
	NT2RP3004209	27.4	23.65	14.82	17	13.67	16.8	19.95	17.39	12.49				
	NT2RP3004215	22.45	23.53	27.86	11	7.75	10.82	4.22	8.07	7.54	**	**	-	-
	NT2RP3004219	5.58	5.12	13.51	6.61	2.08	4.81	3.19	3.17	3.09				
	NT2RP3004242	4.18	6.26	13.02	6.15	3.05	4.41	4.72	3.98	3.45				
45	NT2RP3004246	3.85	4.1	9.37	4.89	2.24	1.94	1.48	3.04	2.11				
	NT2RP3004253	7.46	3.55	9.07	5.38	2.69	1.44	2.57	2.47	3.21				
	NT2RP3004258	8.43	4.33	9.6	7.18	4.84	3.38	6.14	4.76	3.41				
	NT2RP3004262	5.75	6.49	6.12	6.38	2.36	2.74	4.69	0.6	2.65	*		-	
	NT2RP3004275	5.37	6.56	6.47	6.33	1.33	2.3	2.5	1.89	3.75	**		-	
	NT2RP3004282	4.86	27.86	18.63	6.39	3.74	5.05	2.71	3.54	3.27				
	NT2RP3004289	6.43	5.13	10.92	5.92	2.79	3.35	2.25	2.59	3.21				
50	NT2RP3004294	4.71	4.44	6.56	4.95	2.62	3.32	2.88	6.45	3.88				
	NT2RP3004298	64.72	55.93	73.74	63.66	58.3	70.43	70.1	51.46	68.44				
	NT2RP3004309	10	7.69	11.97	7.21	2.5	3.75	5.84	3.48	5.36	*	*	-	-
	NT2RP3004321	23.29	38.14	42.57	12.44	16.53	8.76	14.14	5.43	9.71	*	*	-	-
	NT2RP3004322	4.19	4.29	4.98	4.8	1.3	0.91	2.93	1.84	2.18	**		-	-
	NT2RP3004332	9.53	11.83	11.13	7.92	3.85	4.05	4.3	2.24	2.92	*	**	-	-
55	NT2RP3004334	14.9	13.13	17.93	15.28	11.06	7.25	6.62	11.71	9.43	*		-	
	NT2RP3004336	9.94	8.5	13.66	9.26	7.37	6.68	4.73	8.17	4.32				

Table 451

	NT2RP3004338	20.15	16.11	15.61	11.35	11.45	16.93	14.61	18.8	16.46			
	NT2RP3004341	45.52	46.06	66.9	30.5	32.86	24.48	35.75	44.1	42.23	*	-	
5	NT2RP3004345	5.41	7.27	12.03	7.28	2.26	2.19	5.01	3.58	4.59			
	NT2RP3004348	8.2	11.9	19.15	6.37	5.32	6.29	9.92	4.97	6.08			
	NT2RP3004349	46.27	44.89	52.77	25.21	14.4	28.82	51.32	39.58	50.42	**	-	
	NT2RP3004355	13.69	17.95	13.45	12.62	8.18	11.72	10.41	5.58	7.23	*	-	
	NT2RP3004356	6.56	4.92	9.79	7.46	3.18	5.93	2.87	5.09	3.61	*	-	
	NT2RP3004360	11.41	7.43	12.2	11.26	4.38	7.34	4.62	4.39	7.23	*	-	
10	NT2RP3004361	22.43	16.96	27.29	12.91	14.7	16.73	18.55	21.02	26.27			
	NT2RP3004374	6.08	4.11	5.92	5.52	2.91	4.87	2.31	2.56	2.6	*	-	
	NT2RP3004378	50.03	39.45	48.92	39.78	39.18	55.24	61.97	46.46	63.83			
	NT2RP3004399	25.24	30.84	27.39	23.98	13.72	17.1	23.05	19.32	24.46	*	-	
	NT2RP3004405	5.46	2.89	3.95	6.86	3.8	2.54	2.58	3.57	3.49			
	NT2RP3004406	48.02	80.1	76.06	27.26	18.49	29.22	40.17	40.49	25.13	*	*	-
15	NT2RP3004411	21.84	13.45	15.39	11.3	8.55	12.78	6.83	10.8	17.8			
	NT2RP3004424	12.83	9.11	14	10.53	6.29	12.31	8.49	6.86	11.07			
	NT2RP3004428	9.06	4.59	7.61	7.92	3	6.19	2.13	2.45	2.73	*	-	
	NT2RP3004432	41.77	40.01	43.16	46.87	29.7	37.75	43.11	55.91	45.48			
	NT2RP3004434	6.59	6.36	9.2	19.42	10.09	11.41	8.35	8.97	10.87			
	NT2RP3004446	5.55	1.31	2.23	5.8	1.27	2.52	2.84	1.81	2.66			
20	NT2RP3004451	28.05	27.38	35.9	43.9	34.57	29.99	27.84	20.66	27.06			
	NT2RP3004454	3.04	4.95	3.07	5.17	2.65	2.97	3.32	1.95	4.76			
	NT2RP3004466	17.88	12.48	17.63	17.19	13.76	19.32	8.38	10.38	11.73	*	-	
	NT2RP3004470	6.58	4.48	12.1	9.37	2.81	3.83	6.66	6.76	5.57			
	NT2RP3004472	4.96	8.32	13.71	7.25	5.54	4.58	2.83	3.65	3.08			
	NT2RP3004475	9.27	6	11.18	8.66	2.73	3.48	3.79	5.2	3.34	*	-	
25	NT2RP3004480	22.33	15.69	32.46	17.18	10.83	15.46	12.05	10.67	10.95			
	NT2RP3004481	7.51	6.36	10.91	7.96	3.04	6.85	8.17	5.21	5.83			
	NT2RP3004490	1.96	3.67	4.31	5.07	2.67	3.48	2.86	2.05	1.78			
	NT2RP3004496	29.05	43.68	52.3	32.37	24.7	28.45	17.59	12.79	20.95	*	-	
	NT2RP3004498	6.1	6.29	10.2	8.29	5.15	5.43	3.36	4.35	5.77			
30	NT2RP3004503	13.34	8.17	15.98	13.28	6.98	13.95	9.69	13.04	16.21			
	NT2RP3004504	26.86	13.87	24.17	16.13	11.34	13.03	8.55	9.71	9.3	*	-	
	NT2RP3004505	60.88	42.22	65.16	60.93	61.18	59.93	38.93	40.66	35.92			
	NT2RP3004507	6.96	5.95	8.15	5.81	3.02	3.27	2.74	2.78	2.24	**	-	
	NT2RP3004519	3.09	3.32	8.34	4.29	1.92	0.77	1.76	0.64	1.58			
	NT2RP3004524	22.27	16.91	24.46	12.8	14.38	10.78	10.59	7.77	17.02	*	-	
	NT2RP3004527	31.26	36.6	41.52	32.19	22.11	22.1	23.08	21.05	18.57	**	-	
35	NT2RP3004534	1954.5	1225.4	1438.4	1526.7	1505.7	1779.6	777.34	2507.5	2418.6			
	NT2RP3004539	4.71	4.69	10.04	5.61	3.18	4.71	4.15	5.52	6.25			
	NT2RP3004541	14.72	10.14	22.05	12.49	7.26	9.05	8.78	11	10.96			
	NT2RP3004544	17.32	13.37	16.21	16.43	8.76	13.79	6.55	10.61	10.66	*	-	
	NT2RP3004551	12.43	7.15	13.73	9.94	5.53	6.65	10.18	9.42	7.62			
	NT2RP3004552	19.37	11.98	21.3	18.2	12.57	16.98	18.98	16.22	18.63			
40	NT2RP3004557	11.18	12.99	15.15	12.15	8.14	12.54	12.08	12.56	14.07			
	NT2RP3004561	2.52	4.37	4.66	6.9	2.44	3.94	3.97	3.31	3.2			
	NT2RP3004566	16.46	13.14	29	10.83	7.99	8.15	3.35	6.43	21.27			
	NT2RP3004569	20.41	16.28	28.7	14.13	11.71	13.43	13.97	16.78	16.75			
	NT2RP3004572	12.48	13.38	19.74	11.19	9.39	9.67	3.98	9.35	8.35	*	-	
	NT2RP3004578	6.49	6.06	8.06	7.21	4.59	4.3	5.13	4.76	4.1	*	-	
45	NT2RP3004584	8.34	6.1	9.57	5.07	2.29	4.9	3.85	3.5	2.08	*	*	-
	NT2RP3004588	4.64	4.62	7.46	7.78	2.88	3.22	3.01	5.54	3.28			
	NT2RP3004594	18.77	25.61	21.44	21.59	19.15	22.94	29.86	27.19	18.84			
	NT2RP3004603	4.79	6.26	5.77	8.8	3.9	4.9	5.46	7.72	5.82			
	NT2RP3004612	6.46	6.92	12.58	12.71	4.69	5.32	2.31	10.42	14.75			
50	NT2RP3004617	8.05	8.14	15.39	8.87	3.8	5.79	3.78	6.88	7.16			
	NT2RP3004618	36.56	23.11	37.29	24.87	25.7	22.47	22.39	33.72	29.91			
	NT2RP3004625	19.69	16.42	18.21	11.76	10.91	14.71	6.25	8.76	11.12	*	**	-
	NT2RP3004635	11.6	9.72	13.73	7.06	5.4	4.21	3.68	2.39	2.94	*	**	-
	NT2RP3004640	4.25	10.31	12.87	7.49	7.74	5.34	4.28	3.2	9.33			
	NT2RP3004642	15.02	23.4	27.93	15.96	15.92	16.39	17.49	17.88	14.1			
	NT2RP3004647	10.52	11.7	14.69	13.69	6.27	6.34	18.22	14.86	18.18	*	*	+
55	NT2RP3004652	28.1	24.38	41.76	13.95	14.47	12.02	4.02	12.27	12.65	*	*	-
	NT2RP3004669	7.74	7.41	20.24	7.31	6.69	6.49	4.02	6.68	4.21			



Table 452

	NT2RP3004670	5.78	5.9	15.55	5.95	8.77	4.78	1.73	4.19	3.14				
	NT2RP4000008	4.28	3.76	9.74	7.01	3.13	2.8	0.87	1.61	1.16				
5	NT2RP4000018	777.26	720.79	779.71	458.85	552.02	180.81	608.14	341.39	573.73	*	*	-	-
	NT2RP4000023	12.08	13.49	11.95	6.59	4.27	3.03	5.43	2.46	2.58	**	**	-	-
	NT2RP4000025	10.92	10.01	10.19	8.87	3.46	6.52	5.55	3.38	7.2		*	-	-
	NT2RP4000035	13.64	12.06	18.1	13.28	10.2	10.62	12.01	14.28	15.16				
	NT2RP4000041	7.95	4.85	12.17	6.47	2.4	5.6	2.83	2.55	3.55				
	NT2RP4000049	5.5	8.69	14.31	6.89	4.49	2.04	3	3.25	4.73				
10	NT2RP4000050	7.92	6.2	13.4	9.91	4.4	3.61	2.52	5.2	2.39				
	NT2RP4000051	11.64	12.9	17.08	9.37	6.75	7.7	7.83	11.79	8.18	*		-	-
	NT2RP4000063	9.36	7.43	9.4	6.21	2.66	4.7	2.12	2.88	2.29	*	**	-	-
	NT2RP4000065	8.57	5.45	7.62	5.43	1.38	3.74	3.79	2.44	1.14		*	-	-
	NT2RP4000070	8.9	10.6	11.32	10.92	5.17	4.74	3.9	3	5.41		**	-	-
	NT2RP4000074	7.09	6.56	7.33	6.07	3.64	2.14	2.7	1.95	3.11		**	-	-
15	NT2RP4000078	10.64	7.98	15.22	9.04	4.02	9.72	4.12	7.85	6.44				
	NT2RP4000080	39.53	29.48	35.07	14.73	7.78	7.51	7.13	12.84	8.56	**	**	-	-
	NT2RP4000099	17.27	15.29	21.59	9.54	12.81	6.62	5.87	6.72	3.64	*	**	-	-
	NT2RP4000102	8.52	8.93	15.05	7.45	6.98	5.31	5.6	5.59	5.12				
	NT2RP4000103	20.66	29.01	31.17	15.7	16.08	13.47	20.04	13.58	12.68	*	*	-	-
20	NT2RP4000108	10.35	7.66	11.54	5.11	5.39	5.22	4.96	2.69	3.44	*	**	-	-
	NT2RP4000109	9.73	11.84	8.78	8.41	4.9	6.21	6.7	3.67	4.98		*	-	-
	NT2RP4000111	9.68	7.22	7.83	10.68	5.18	7.24	9.51	4.5	2.88				
	NT2RP4000112	16.91	11.4	24.28	20.79	19.36	22.3	16.09	13.49	17.44				
	NT2RP4000115	7.34	4.25	10.98	5.53	2.81	4.32	2.76	2.51	2.27				
	NT2RP4000129	24.84	25.48	33.51	13.19	12.49	13.21	12.38	15.5	12.9	**	**	-	-
25	NT2RP4000137	20.7	16.54	14.08	10.11	6.13	6.89	9.81	6.38	10.47	*	*	-	-
	NT2RP4000138	7.91	6.25	8.72	5.36	2.95	3.73	3.09	3.11	5.54	*	*	-	-
	NT2RP4000141	11.63	7.1	7.39	5.05	2.2	2.55	3.83	2.34	1.67	*	*	-	-
	NT2RP4000147	7.8	8.75	6.46	5.67	2.45	1.71	3.71	1.66	2.95	*	**	-	-
	NT2RP4000150	22.83	40.43	32.64	26.18	18.45	19.86	24.1	13.63	20.82				
	NT2RP4000151	5.35	2.77	7.92	5.7	2.57	4.58	2.81	1.73	3.64				
30	NT2RP4000157	5.03	3.17	7.55	5.12	2.41	3.03	2.61	4.59	2.88				
	NT2RP4000159	7.7	6.21	14	7.81	5.43	9.16	5.02	7.93	7.16				
	NT2RP4000163	11.36	16.35	22.24	7.82	6.7	5.1	11.58	8.66	14.17	*		-	-
	NT2RP4000167	5.72	10.76	11.28	6.86	1.93	2.94	6.09	1.64	2.98				
	NT2RP4000171	17.67	20.8	16.76	13.24	7.81	11.48	17.22	11.6	13.85	*		-	-
	NT2RP4000175	7.68	11.5	9.21	7.19	5.94	7.44	5.84	4.86	6.71		*	-	-
35	NT2RP4000180	8.25	9.87	9.45	8.5	4.86	7.21	9.47	6.55	7.72				
	NT2RP4000185	3.44	9.69	9.07	5.25	3.82	5.08	3.89	5.51	9.51				
	NT2RP4000192	3.66	2.3	7.85	7.16	4.58	3.22	2.99	2.89	2.84				
	NT2RP4000194	4.94	3.92	6.27	5.67	6.92	4.33	4.73	3.32	6.3				
	NT2RP4000196	4.44	3.86	8.22	4.42	2.19	1.89	2.14	2.44	1.01				
	NT2RP4000210	4.32	3.9	5.46	5.03	2.17	1.97	3.56	2.52	3.91				
40	NT2RP4000212	10.41	10.12	9.74	6.43	6.54	3.07	4.86	4.69	2.44	*	**	-	-
	NT2RP4000214	21.41	28.56	31.47	14.93	12.43	12.75	14.71	10.53	11	*	**	-	-
	NT2RP4000216	18.56	17.54	17.8	9.05	3.32	6.3	7.12	4.66	4.69	**	**	-	-
	NT2RP4000218	20.76	13.22	21.73	16.85	12.17	21.91	12.16	18.58	23.33				
	NT2RP4000223	11.85	6.5	8.31	9.5	4.18	9.75	8.04	7.05	11.94				
	NT2RP4000243	10.56	9.93	12.96	11.2	9.86	11.7	8.64	9.69	10.23				
45	NT2RP4000246	7.12	5.86	5.64	5.65	4.43	4.42	2.37	2.31	3.27		**	-	-
	NT2RP4000250	11.29	8.98	12.39	10.04	3.49	5.45	5.46	5.81	5.67		**	-	-
	NT2RP4000256	3.26	5.13	6.67	4.51	2.18	2.56	3.11	2.41	2.48				
	NT2RP4000257	23.54	23.13	30.8	34.24	27.3	37.51	26.44	19.58	27.22				
	NT2RP4000259	5.19	5.55	3.54	8.67	2.13	4.17	4.34	3.84	5.01				
	NT2RP4000261	4.72	2.05	7.37	6.8	1.48	3.76	2.37	3.23	3.88				
50	NT2RP4000262	2.93	2.46	11.12	5.21	1.63	2.61	2.49	2.62	2.71				
	NT2RP4000263	8.03	5.82	13.8	7.33	4.75	4.76	8.35	4.63	5.93				
	NT2RP4000280	36.69	25.69	34.43	21.81	13.93	11.89	23.3	25.5	21.75	*		-	-
	NT2RP4000286	7.96	5.71	10.34	8.48	4.4	5.47	4.56	4.72	2.93				
	NT2RP4000290	6.28	5.27	10.35	7.67	3.77	4.58	5.45	2.24	4.35				
	NT2RP4000291	23.37	31.04	45.88	29.65	20.44	28.9	16.58	13.08	6.43	*		-	-
55	NT2RP4000301	9.06	21.31	16.13	18.84	21.42	12.52	13.04	8.64	8.86				
	NT2RP4000312	7.37	5.86	10.71	6.75	4.45	5.45	4.08	4.23	5.32				
	NT2RP4000321	14.11	6.64	13.51	10.77	5.65	7.11	6.38	8.75	12.76				

Table 453

	NT2RP4000323	42.99	31.25	39.68	23.73	23.52	24.08	25.22	26.31	20.02	*	*	-	-
	NT2RP4000324	28.87	20.72	25.53	23.74	16.73	21.66	28.32	24.57	21.68				
5	NT2RP4000334	11.51	10.77	15.15	9.55	9.47	9.13	6.39	6.12	5.89	**		-	
	NT2RP4000343	20.88	12.62	32.18	18.49	14.22	8.72	14.98	17.89	14.7				
	NT2RP4000348	12.35	14.21	17.96	11.42	8.77	9.63	12.1	7.85	8.02				
	NT2RP4000349	8.77	16.24	12.89	11.44	12.7	9.21	11.37	7.34	11.23				
	NT2RP4000355	253.25	117.6	189.34	264.37	149.78	254.47	257.02	316.08	192.79				
	NT2RP4000356	61.98	36.7	79.91	60.03	57.95	82.79	39.95	40.28	37.12				
10	NT2RP4000360	38.52	30.1	36.81	28.77	30.27	34.86	22.5	29.04	23	*		-	
	NT2RP4000367	5.32	7.72	13.11	9.15	7.75	6.58	5.65	7.52	4.05				
	NT2RP4000370	6.13	3.8	7.29	7.4	4.81	4.6	4.29	3.27	2.44				
	NT2RP4000373	52.16	35.56	49.83	33.3	22.86	20.18	8.95	13.1	7.55	*	**	-	-
	NT2RP4000376	4.35	4.76	3.85	5.98	2.55	3.6	3.64	2.24	1.76	*		-	
	NT2RP4000381	4.21	7.62	7.46	8.53	4.41	5.48	6.16	4.44	4.11				
15	NT2RP4000388	15.3	8.64	28.13	9.56	6.37	8.78	3.98	7.28	10.59				
	NT2RP4000390	9.32	12.91	21.1	9.57	7.3	6.9	4.45	8	7.73				
	NT2RP4000393	4.73	6.04	14.2	5.91	3.76	3.4	2.49	4.28	1.61				
	NT2RP4000398	15.1	12.32	17.4	15.43	7.99	12.09	10.09	7.98	7.95	*		-	
	NT2RP4000406	6.93	7.1	10	7.22	4.81	7.48	4.73	7.43	4.16				
	NT2RP4000407	14.2	8.65	18.88	9.39	7.38	7.23	8.05	7.66	8.08				
20	NT2RP4000413	6.36	8.44	8.74	7.32	6.23	4.25	14.9	11.64	8.91				
	NT2RP4000415	5.58	6.36	5.25	8.19	3.66	6.69	6.61	5.43	4.11				
	NT2RP4000417	4.81	3.78	14.82	6.27	2.89	2.96	1.78	3.56	2.97				
	NT2RP4000423	8.56	11.85	52.11	7.59	6.28	6.14	5.59	8.25	4.46				
	NT2RP4000424	5.63	6.45	12.56	7.04	3.08	2.9	3.66	4.14	1.14				
	NT2RP4000447	7.22	11.02	14.44	6.8	2.54	3.42	2.02	2.94	1.68	*		-	
25	NT2RP4000448	10.44	4.78	12.49	7.44	5.19	4.9	2.34	3.11	4.18				
	NT2RP4000449	14.23	13.95	15.79	8.35	8.81	8.15	9.09	11.62	7.03	**	*	-	-
	NT2RP4000453	9.01	6.07	14.02	7.74	5.15	4.89	6.56	4.27	8.08				
	NT2RP4000455	9.03	10.34	8.68	7.99	5.45	3.17	4.44	4.36	4.13	**		-	
	NT2RP4000456	7.04	6.17	17.02	5.76	3.52	4.72	1.66	2.58	3.46				
	NT2RP4000457	13.26	8.71	17.6	8.13	4.23	7.52	11.15	9.14	8.56				
30	NT2RP4000461	55.44	37.43	46.46	34.13	24.48	24.96	29.53	26.44	29.5	*	*	-	-
	NT2RP4000462	42.85	30.75	56.94	75.69	50.54	40.64	52.98	43.57	42.53				
	NT2RP4000463	85.58	62.21	92.77	65.01	52.99	43.38	67.48	75.6	83.4				
	NT2RP4000471	25.28	34.12	24.81	15.24	25.16	15.87	19.6	16.58	11.2	*		-	
	NT2RP4000472	7.71	9.85	9.52	10.37	5.54	5.62	6.84	6.67	3.82				
	NT2RP4000476	14.81	18.77	16.55	11.79	4.98	3.82	5.79	4.35	2.67	*	**	-	-
35	NT2RP4000480	12.42	10.39	22.37	9.71	8.11	7.69	2.98	6.14	7.56				
	NT2RP4000481	7.17	5.4	16.93	6.71	1.97	4.16	2.54	3.59	3.12				
	NT2RP4000483	21.87	12.5	29.34	14.63	7.41	9.82	17.08	21.67	14.93				
	NT2RP4000487	11.87	8.84	15.81	9.26	6.43	6.73	8.06	10.31	7.08				
	NT2RP4000496	16.33	41.67	19.05	11.91	7.25	5.15	7.41	10.6	17.63				
	NT2RP4000497	5.81	3.81	10.08	3.87	3.09	2.81	2.48	1.77	2.22				
40	NT2RP4000498	26.54	11.6	46.3	21.94	11.56	20.83	11.71	6.48	8.74				
	NT2RP4000500	16.19	14.2	13.24	21.4	11.25	11.2	15.02	6.9	5.02				
	NT2RP4000507	14.47	9.74	21.49	11.59	12.91	17.96	12.44	18.01	18.95				
	NT2RP4000515	34.88	29.88	36.21	23.73	25.4	27.6	24.2	28.54	29.19	*		-	
	NT2RP4000516	8.8	4.78	15.95	7.22	3.73	6.26	5.56	4.23	5.23				
	NT2RP4000517	6.93	4.39	11.92	5.6	2.28	2.95	2.26	2.51	3.47				
45	NT2RP4000518	5.66	5.23	9.62	6.13	3.29	2.14	2.66	2.57	2.25	*		-	
	NT2RP4000519	11.25	13.8	9.43	7.22	5.12	6.11	9.96	4.77	2.74	*		-	
	NT2RP4000524	3.66	2.61	3.66	4.66	0.22	1.66	1.44	0.06	0.23	**		-	
	NT2RP4000528	9.85	11.61	11.68	7.98	5.49	4.94	7.65	1.72	3.24	*	*	-	-
	NT2RP4000537	22.62	26.04	23.49	9.39	8.19	12.07	6.5	9.43	12.67	**	**	-	-
	NT2RP4000541	6.77	5.01	14.31	6.57	5.43	3.77	2.53	4.6	6.37				
50	NT2RP4000543	7.3	6.98	11.29	8.27	7.56	3.29	6.55	3.66	5.22				
	NT2RP4000545	22.52	30.13	32.57	13.3	16.56	19.62	18.71	21.42	13.96	*	*	-	-
	NT2RP4000546	4.78	4.57	9.21	6.74	1.72	3.53	3.64	0.82	4.41				
	NT2RP4000549	11.61	18.79	20.98	6.99	2.21	3.33	4.79	2.09	3.96	*	*	-	-
	NT2RP4000556	15.54	16.2	17.27	7.73	3.7	5.61	5.6	2.76	4.84	**	**	-	-
	NT2RP4000557	11.07	12.42	10.89	8.61	4	8.57	12.02	7.59	12.85				
55	NT2RP4000558	14.08	10.84	18.04	10.75	6.08	12.87	11.5	16.9	20.52				
	NT2RP4000560	6.31	4.01	7.32	5.77	2.76	5.36	5.37	6.37	4.62				

Table 454

	NT2RP4000568	23.22	25.79	25.36	10.18	10.21	8.47	12.24	9.65	11.67	**	**	-	-
	NT2RP4000583	5.85	2.98	7.97	6.46	2.06	2.6	3.62	4.57	3				
5	NT2RP4000585	9.33	19	28.37	6.6	3.13	5.64	10.5	7.96	7.04				
	NT2RP4000588	7.43	10.21	10.68	6.68	2.44	1.85	5.44	2.87	5.6	*	*	-	-
	NT2RP4000590	6.55	7.08	8.76	6.12	1.79	2.53	5.82	2.45	2.62		*	-	-
	NT2RP4000599	40.85	42.1	36.12	25.51	13.35	23.08	24.88	16.83	13.91	*	**	-	-
	NT2RP4000603	16.26	11.07	12.79	9.86	5.09	7.92	5.61	11.76	8.02	*		-	-
	NT2RP4000607	18.04	30.52	24.32	19.53	17.65	25.01	23.84	28.13	28.14				
10	NT2RP4000614	10.28	8.25	15.91	8.83	8.89	11.93	10.16	9.95	16.38				
	NT2RP4000634	6.36	4.3	5.27	7.5	2.83	3.42	3.64	2.83	2.88		*	-	-
	NT2RP4000638	23.34	31.48	44.47	17.42	11.63	10.92	16.58	9.75	15.96	*	*	-	-
	NT2RP4000648	20.24	25.67	26.97	19.17	9.45	12.88	31.67	25.66	31.95	*		-	-
	NT2RP4000657	29.17	33.57	37.98	49.46	41.57	42.06	36.04	23.15	32.67	*		+	-
	NT2RP4000691	5.59	4.16	3.63	5.96	2.37	3.18	5.01	2.34	4.68				
15	NT2RP4000697	6.38	8.16	10.53	9.34	4.77	12.75	6.26	6.22	8.11				
	NT2RP4000704	1.95	1.59	2.11	5.91	1.47	3.12	1.95	2.78	2.48				
	NT2RP4000710	20.97	14	15.55	13.68	8.51	18.99	7.53	9.31	11.22		*	-	-
	NT2RP4000713	4.84	3.26	2.49	5.57	2.13	4.31	3.32	1.62	2.08				
	NT2RP4000724	3.62	3.53	2.74	6.31	1.65	2.66	3.33	4.03	5.81				
20	NT2RP4000725	3.89	2.42	3.21	6.35	1.7	3.24	4.75	1.9	3.76				
	NT2RP4000728	11.56	10.9	20.97	12.34	10.22	7.45	16.8	22.52	15.47				
	NT2RP4000737	13.76	11.71	16.21	12.21	6.25	7.06	13.63	12.39	10.01				
	NT2RP4000739	8.74	4.93	10.91	9.95	3.76	6.63	5.46	5.27	7.1				
	NT2RP4000749	16.46	11.21	22.1	13.84	13.31	13.35	10.75	11.02	11.19				
	NT2RP4000769	9.99	10.26	18.79	12.18	3.6	7.13	3.73	5.86	5.05				
	NT2RP4000774	9.26	8.05	14.72	7.64	2.48	6.01	4.16	4.89	5.59				
25	NT2RP4000781	4.81	3.97	6.84	6.54	2.43	3.37	3.39	2.48	3.03				
	NT2RP4000783	17.33	30.73	35.46	25.7	13.51	13.28	15.68	13.86	21.97				
	NT2RP4000788	24.76	10.56	23.27	26.79	17.17	17.48	11.21	13.65	10.18				
	NT2RP4000792	5.04	4.94	10.96	8.67	1.86	4.24	2.65	4.16	5.52				
	NT2RP4000809	342.08	122.2	157.03	126.01	165.45	173.36	118.64	164.8	122.66				
	NT2RP4000817	8.94	6.91	14.48	7.71	3.01	5.35	5.37	3.63	4.85				
30	NT2RP4000821	136.37	90.35	131.55	91.69	114.89	72.17	100.95	73.86	85.69				
	NT2RP4000822	14.55	12.26	20.9	11.12	8.44	15.29	16.17	13.27	18.76				
	NT2RP4000823	2939.8	2567.2	3305.2	1530.8	2690.7	2293.4	1706.4	1550.9	2562.9				
	NT2RP4000831	78.61	54.25	90.69	72.05	94.12	99.31	70.64	58.37	82.02				
	NT2RP4000833	27.77	14.49	23.94	22.19	7.07	21.11	19.12	24.88	29.44				
	NT2RP4000837	6.72	4.87	9.85	8.02	2.92	3.66	2.57	4.16	7.79				
35	NT2RP4000839	145.23	125.82	232.83	173.61	169.29	177.66	124.91	117.96	102.54				
	NT2RP4000846	29.27	18.32	20.88	21.05	17.61	12.28	9.05	14.78	13		*	-	-
	NT2RP4000848	18.2	11.65	15.75	19.15	9.44	13.53	19	14.72	12.39				
	NT2RP4000855	6.13	7.14	11.29	10.66	4.62	6.62	4.65	3.21	3.53				
	NT2RP4000863	6.72	6.6	6.48	8.17	4.81	5.97	4.42	5.29	3.77		**	-	-
	NT2RP4000865	45.32	26.52	38.54	39.71	38.1	49.51	43.48	35.35	41.09				
40	NT2RP4000873	144.06	68.9	135.34	139.48	79.72	155.93	87.22	97.84	116.06				
	NT2RP4000874	10.17	6.06	16.44	7.29	2.79	4.52	3.81	5.9	8.53				
	NT2RP4000875	14.13	12.82	21.34	9.26	7.3	7.14	8.99	11.91	13.22	*		-	-
	NT2RP4000878	36.06	33.12	27.77	33.84	31.46	17.83	20.58	24.01	24.14		*	-	-
	NT2RP4000879	8.38	6.53	9.14	6.87	3.51	3.32	2.85	3.36	3.88		**	-	-
	NT2RP4000880	35.09	26.71	47.85	50.74	42.76	41.2	29.03	30.06	33.07				
45	NT2RP4000891	701.32	715.69	430.85	696.54	840.24	746.75	898.32	324.76	792.55				
	NT2RP4000894	21.41	14.41	21.14	15.13	8.85	12.55	11.08	19.34	17.24				
	NT2RP4000898	2.97	2.72	11.52	4.95	1.01	2.82	2.18	3.29	4.66				
	NT2RP4000899	44.53	41.78	65.07	39.31	37.51	42.09	31.81	35.26	42.89				
	NT2RP4000907	4.19	4.02	10.25	6.24	3.94	2.33	1.69	3.11	0.94				
	NT2RP4000908	14.45	17.63	18.1	10.04	7.21	5.31	4.66	6.8	4.87	**	**	-	-
50	NT2RP4000910	216.22	171.01	317.29	253.37	286.44	240.15	188.21	180.84	183.37				
	NT2RP4000918	3.56	6.94	4.06	7.07	6.01	6.69	5.32	2.08	2.17				
	NT2RP4000925	5.57	5.14	8.28	6.79	4.75	4.89	3.2	5.18	4.02				
	NT2RP4000927	3.1	2.26	4.02	4.89	1.52	0.68	2.5	1.38	1.2				
	NT2RP4000928	9.4	7.34	14.03	9.56	4.86	8.73	4.09	5.17	5.52				
	NT2RP4000929	3.84	3.91	13.46	5.95	2.85	3.04	2.12	4.29	1.99				
55	NT2RP4000946	6.59	6.92	14.08	8.15	4.03	3.77	3.48	3.97	1.29				
	NT2RP4000947	3.36	4.07	10.59	4.84	0.29	0.97	0.36	0.58	0				

Table 455

	NT2RP4000949	10.71	9.2	16.65	6.86	2.65	3.74	2.78	1.39	2.41	*	*	-	-
	NT2RP4000955	5.81	4.35	6.4	6.28	2.77	1.08	2.31	3.19	3.37	*	*	-	-
5	NT2RP4000959	46.28	46.79	57.49	28.43	49.02	25.11	20.47	30.52	16.93	**	*	-	-
	NT2RP4000962	11.98	9.47	12.39	11.59	10.69	8.83	6.01	4.92	5.77	**	*	-	-
	NT2RP4000973	21.72	16.11	23.28	13.29	14.47	13.18	9.73	13.42	15.34	*	*	-	-
	NT2RP4000975	12.7	11.46	22.76	9.51	5.19	6.19	5.82	10.95	9.25			-	-
	NT2RP4000979	15.15	9.34	21.99	15.27	12.98	9.04	9.28	10.97	8.24			-	-
	NT2RP4000984	6.41	8.08	14.46	6.57	1.97	3.73	2.22	3.31	3.09			-	-
10	NT2RP4000986	6.86	5.41	12.86	6.12	4.31	1.27	1.5	2.5	1.16	*	*	-	-
	NT2RP4000988	17.65	11.88	13.93	10.42	7.43	7.63	9.24	12.28	11.72	*	*	-	-
	NT2RP4000989	4.65	7.43	6.1	6.61	2.52	1.81	2.98	2.09	3.85	*	*	-	-
	NT2RP4000990	6.25	7.92	5.23	9.42	4.63	4.12	5.36	2.51	2.44			-	-
	NT2RP4000994	8.9	9.21	16.92	10.87	4.94	9.69	11.79	23.69	21.99			-	-
	NT2RP4000996	77.3	49.17	79.6	45.61	34.69	39.35	32.71	38.95	46.1	*	*	-	-
15	NT2RP4000997	122.55	129.24	107.05	94.09	70.8	26.94	46.25	80.17	57.14	**	*	-	-
	NT2RP4001001	12.46	18.44	15.8	14.39	8.88	9.17	8.14	8.28	5.33	*	*	-	-
	NT2RP4001004	5.22	3.76	7.06	6.01	1.06	2.64	1.83	1.39	1.05	*	*	-	-
	NT2RP4001006	13.89	13.25	17.25	8.9	7.61	7.07	7.25	6.36	7.3	**	*	-	-
	NT2RP4001009	16.48	20.86	24.07	12.83	13.33	10.38	13	7.19	7.56	*	*	-	-
	NT2RP4001010	12.07	13.64	9.65	9.47	5.84	7.62	5.8	4.44	3.25	**	*	-	-
20	NT2RP4001013	109.49	147.49	90.54	50.6	80.74	63.83	38.95	52.28	51.67	*	*	-	-
	NT2RP4001029	20.54	17.68	29.5	9.58	9.72	9.68	7.27	4.7	8.7	*	*	-	-
	NT2RP4001036	9.27	12.23	13.79	8.52	7.63	4.92	8.03	6.75	4.44	*	*	-	-
	NT2RP4001041	36.4	40.27	32.69	14.35	15.64	11.72	23.48	9.92	16.78	**	*	-	-
	NT2RP4001042	15.67	10.3	17.88	10.18	7.53	8.42	5.86	5.84	7.9	*	*	-	-
	NT2RP4001046	36.69	45.09	54.4	22.18	26.84	16.1	31.95	24.71	14.49	*	*	-	-
25	NT2RP4001050	14.02	22.04	12.83	10.97	2.91	3.84	9.37	3.59	3.94	*	*	-	-
	NT2RP4001051	21.06	26.13	23.41	17.4	11.41	16.25	15.66	11.32	18.06	*	*	-	-
	NT2RP4001057	5.02	3.25	6.98	7.18	2.13	3.82	4.33	2.83	3.14			-	-
	NT2RP4001063	6.13	4.37	7.2	7.29	2.91	4.39	2.87	3.18	3.35	*	*	-	-
	NT2RP4001064	9.3	9.96	15.17	12.02	5.98	5.07	7.19	9.48	7.97			-	-
	NT2RP4001067	10.58	14.37	13.96	6.93	4.54	4.48	7.26	9.16	8.36	**	*	-	-
30	NT2RP4001078	4	5.51	5.6	4.49	1.94	2.06	3.66	2.7	1.04	*	*	-	-
	NT2RP4001079	8.77	14.47	11.97	8.98	3.49	1.98	7.36	2.56	7.44			-	-
	NT2RP4001080	8.56	8.71	5.39	7.24	5.74	5.86	5.43	5.54	6.58			-	-
	NT2RP4001086	8.1	13.85	11.2	8.73	5.59	7.65	7.59	3.27	6.54			-	-
	NT2RP4001095	21.9	10.2	20.98	20.1	8.21	22.42	25.97	28.91	25.72			-	-
	NT2RP4001098	9.87	7.14	14.73	8.69	4.17	6.42	4.56	7.67	4.16			-	-
35	NT2RP4001100	87.64	83.13	87.53	54.87	47.17	71.93	63.14	104.74	100.86	*	*	-	-
	NT2RP4001105	4.62	5.85	6.18	8.6	3.1	3.62	2.72	2.96	3.35	**	*	-	-
	NT2RP4001110	4.35	3.52	3.95	6.4	1.65	2.39	2.86	1.95	2.46	*	*	-	-
	NT2RP4001115	9.9	15.92	16.54	12.73	4.3	5.05	12.1	7.78	11.14			-	-
	NT2RP4001117	47.61	50.63	46.56	30.24	19.2	17.67	37.4	37.77	12.69	**	*	-	-
	NT2RP4001122	7.49	13.49	11.17	8.93	3.06	4.64	5.55	4.07	4.81	*	*	-	-
40	NT2RP4001123	15.99	10.87	15.29	13.96	11.8	8.64	4.92	11.31	11.27			-	-
	NT2RP4001126	32.2	22.75	27.43	23.25	13.48	17.12	8.86	11.87	13.23	**	*	-	-
	NT2RP4001127	5.7	5.54	5.37	7.61	3.72	4.66	3.57	2.2	3.61	**	*	-	-
	NT2RP4001138	6.95	3.88	7.12	9.78	5.56	5.09	4.09	4.44	3.91			-	-
	NT2RP4001143	12.5	11.65	11.43	11.35	7.29	7.76	9.34	8.18	11.45			-	-
45	NT2RP4001148	6.15	6.48	10.09	9.86	3.88	5.87	3.55	2.98	4.94			-	-
	NT2RP4001149	10.56	12.29	14.62	14.76	6.44	4.57	8.21	6.46	7.23	*	*	-	-
	NT2RP4001150	2.08	2.58	2.6	5.53	2.21	2.02	2.86	2.61	5.29			-	-
	NT2RP4001159	28.55	18.66	30.75	17.14	15.33	13.97	7.91	12.94	18.83			-	-
	NT2RP4001162	19.05	7.92	22.71	10.51	6.28	6.36	7.29	6.36	7.28			-	-
	NT2RP4001170	4.82	3.9	7.97	5.23	1.81	3.87	2.53	3.13	2.09			-	-
50	NT2RP4001174	28.66	24.87	30.19	18.62	12.05	22.33	28.65	25.07	34.84	*	*	-	-
	NT2RP4001175	41.57	44.74	48.16	32.54	33.99	41.64	26.8	24.72	38.38	*	*	-	-
	NT2RP4001176	940.52	839.83	1091.9	860.36	609.5	960.82	721.44	858.51	780.83			-	-
	NT2RP4001184	63.86	45.01	63.95	60.3	52	64.4	59.44	58.17	76.19			-	-
	NT2RP4001198	36.14	14.18	33.12	25.99	15.11	24.84	10.23	17.15	15.95			-	-
	NT2RP4001199	7.47	5.66	10.86	10.65	3.07	4.16	4.96	7.07	8.52			-	-
55	NT2RP4001206	64.73	49.7	69.67	51.07	49.14	54.08	37.12	41.91	43.36	*	*	-	-
	NT2RP4001207	7.32	3.58	10.38	7.77	2.4	3.4	3.22	3.79	1.65			-	-
	NT2RP4001210	10.03	7.34	12.93	9.04	5.66	7.56	3.96	6.73	5.83			-	-

Table 456

	NT2RP4001213	7.81	5.05	8.73	8.57	3.73	3.8	4.8	3.72	3.86			
	NT2RP4001214	3.93	5.31	4.9	6.79	4.2	2.68	6.35	2.95	4.56			
5	NT2RP4001219	16.88	22.36	19.11	23.96	11.89	15.23	12.2	5.76	8.23	*		-
	NT2RP4001228	31.68	26.26	28.99	28.25	18.75	24.21	24.62	30.13	29.4			
	NT2RP4001235	19.17	16.01	20.65	14.75	7.88	8.31	4.98	7.75	11.8	*	*	-
	NT2RP4001256	7.87	5.89	15.98	8.52	4.59	3.98	3.22	7.66	6.44			
	NT2RP4001257	10.17	7.29	12.91	9.33	4.43	6.16	4.58	7.66	4.3			
	NT2RP4001260		9	7.35	9.45	7.52	2.82	3.63	1.87	4.5	2.81	**	-
10	NT2RP4001261	14.73		14	19.92	14.97	13.67	11.83	31.07	30.65	37.38	**	+
	NT2RP4001274	46.98	48.98	34.12	11.26	8.82	9.09	7.45	6.66	5.77	**	**	-
	NT2RP4001276	24.77	28.67	28.03	20.15	20.05	19.84	15.05	9.27	8.86	**	**	-
	NT2RP4001283	274.25	154.44	255.86	208.49	145.59	283.17	127.22	121.38	88.24	*		-
	NT2RP4001299	70.57	64.2	62.96	46.39	43.31	37.19	12.59	32.14	14.83	**	**	-
	NT2RP4001313	1.97	3.19	11.08	5.06	1.72	1.96	1.4	3.15	1.49			
15	NT2RP4001315	13.31	15.88	15.77	13.24	9.24	10.09	4.21	7.24	8.5	*	**	-
	NT2RP4001320	57.94	46.23	43.52	51.85	61.21	49.26	36.69	35.49	37.13	*		-
	NT2RP4001325	218.13	214.83	355	324.95	260.73	208.15	240.45	201.7	209.88			
	NT2RP4001336	66.24	37.07	61.11	58.79	61.6	67.7	54.66	37.6	43.21			
	NT2RP4001339	6.71	9.24	9.26	9.34	4.49	4.79	2.82	4.96	4.68	*		-
20	NT2RP4001343	117.66	66.55	122.62	134.91	97.85	136.86	58.06	81.43	87.93			
	NT2RP4001344	93.3	59.49	108.06	106.25	89.38	122.67	65.91	65.77	78.19			
	NT2RP4001345	8.99	7.64	17.74	11.99	4.82	6.81	4.98	6.9	5.71			
	NT2RP4001351	19.43	14.61	27.02	22.21	10.47	17.51	14.3	12.05	12.26			
	NT2RP4001353	3.32	5.15	8.01	5.72	0.75	1.22	1.09	1.47	0.82	*		-
	NT2RP4001355	4.79	4.23	4.91	4.97	2.19	1.13	2.63	2	2.13	**		-
	NT2RP4001367	14.2	16.94	22.96	11.42	11.61	7.99	7.87	8	4.49	*		-
25	NT2RP4001372	4.19	2.77	5.41	7.79	3.55	1.91	2.83	1.62	2.32			
	NT2RP4001373	51.47	33.24	43.9	16.16	26.86	13.77	10.57	24.44	16.81	*	*	-
	NT2RP4001375	4.45	4.59	11.77	7.62	2.36	2.63	2.14	3.81	2.97			
	NT2RP4001379	5.44	4.91	12.41	7.76	2.24	3.26	2.93	5.12	3.63			
	NT2RP4001381	28.02	25.15	21.15	23.38	16.12	13.96	17.03	26.57	24.23			
30	NT2RP4001386	29.66	19.44	36.04	29.56	18.78	18.25	18.75	24.44	26.66			
	NT2RP4001389	11.24	11.58	9.67	9.26	6.9	5.34	3.69	2.72	3.74	*	**	-
	NT2RP4001396	5.21	4.67	8.34	6.72	2.25	1.78	3.47	3.22	1.99			
	NT2RP4001407	5.66	5.49	6.51	7.81	4.54	1.79	3.65	1.8	5.23			
	NT2RP4001409	8.48	7.57	16.74	7.93	2.96	5.53	4.77	6.78	4.46			
	NT2RP4001410	76.31	89.86	99.62	25.06	52.86	47.85	42.92	82.06	57.7	*		-
35	NT2RP4001414	30.84	57.5	63.9	31.08	20.37	24.44	13.71	23.74	21.51	*		-
	NT2RP4001424	11.24	11.55	15.27	11.2	4.99	6.97	6.22	6.82	6.88	**		-
	NT2RP4001433	19.8	14.14	16.87	12.54	11.03	6.56	10.55	8.89	6.43	*	*	-
	NT2RP4001438	69.21	52.84	81.07	58.91	49.01	54.6	39.37	44.33	43.61	*		-
	NT2RP4001442	7.93	5.58	7.34	6.34	2.77	3.09	4.34	2.59	3.24	*		-
	NT2RP4001447	7.95	6.53	5.53	6.92	3.73	3.72	3.38	1.74	2	**		-
40	NT2RP4001466	26.98	30.25	30.96	13.22	11.9	17.04	5.41	8.17	9.81	**	**	-
	NT2RP4001467	56.03	66.43	78.02	42.37	52.35	39.87	17.7	35.75	26.38	*	**	-
	NT2RP4001472	23.78	41.35	30	13.57	13.9	13.93	11.58	12.27	10.38	*	*	-
	NT2RP4001474	7.87	8.46	14.35	7.2	5.31	5.23	4.32	3.7	3.69	*		-
	NT2RP4001483	6.68	4.49	11.62	7.08	3.5	3.8	3.02	2.79	3.04			
	NT2RP4001488	25.21	54.85	68.99	28.07	36.56	22.06	36.35	46.46	23.9			
45	NT2RP4001492	10.33	5.85	8.11	7.33	2	4.79	7.35	5.55	5.24			
	NT2RP4001498	7.69	4.58	4.14	7.14	3.13	3.73	4.3	3.05	2.12			
	NT2RP4001502	209.76	206.24	150.31	118.11	105.88	95.3	44.44	56.95	57.25	*	**	-
	NT2RP4001503	7.44	8.32	13.64	9.66	7.22	6.9	4.97	6.76	6.61			
	NT2RP4001507	13.79	9.83	18.56	10.78	5.48	8.77	10.23	16.21	17.48			
	NT2RP4001510	5.75	3.91	6.87	6.33	3.38	4.41	4.72	4.9	4.63			
50	NT2RP4001516	8.14	6.69	9.41	7.53	2.26	3.8	4.88	3.25	3.25	*		-
	NT2RP4001520	131.31	173.55	237.05	131.12	129.89	116.61	94.53	82.4	103.86			
	NT2RP4001523	33.88	38.97	38.29	18.41	8.08	12.46	21.96	12.77	13.03	**	**	-
	NT2RP4001524	21.05	28.36	29.26	13.82	9.16	8	8.02	5.86	9.68	**	**	-
	NT2RP4001529	19.64	17.51	18.7	21.14	10.37	22.92	12.83	17.42	17.09			
	NT2RP4001531	12.2	10.44	17.59	14.87	8.44	10.35	9.15	12.78	10.56			
55	NT2RP4001546	200.55	317.08	217.26	217.42	252.35	233.58	165.76	290.78	247.68			
	NT2RP4001547	50.85	72.72	70.29	50.48	41.66	51.65	70.8	75.31	63.14			
	NT2RP4001551	5.28	7.23	6.07	6.96	2.03	2.81	2.74	2.79	2.73	**		-

Table 457

	NT2RP4001555	5.61	4.66	4.4	6.85	1.41	2.54	5.43	2.64	2.46			
	NT2RP4001567	14.43	18.57	12.18	9.17	4.93	4.07	5.01	3.84	5.68	*	**	-
5	NT2RP4001568	20.92	33.87	32.23	19.47	17.65	14.08	25.04	13.01	8.31			
	NT2RP4001569	38.32	29.49	40	37.57	26.2	39.13	21.18	30.23	30.47			
	NT2RP4001571	15.01	7.71	15.89	14.4	7.44	9.88	7.38	9.18	8.27			
	NT2RP4001574	25.53	25.21	25.8	22.48	16.52	21.02	13.78	20.38	15.43	*	*	-
	NT2RP4001575	5.89	6.11	13.99	11.72	4.86	9.13	5.91	5.72	3.19			
	NT2RP4001578	138.32	156.83	176.17	106.73	98.03	117.94	140.07	117.64	162.41	*		-
10	NT2RP4001592	9.9	23.21	17.14	17.16	3.08	11.08	13.53	10.53	12.39			
	NT2RP4001593	39.07	48.78	46.75	25.68	17.84	15.12	20.23	20.2	20.66	**	**	-
	NT2RP4001605	8.89	11.75	9.28	6.36	2.98	4.4	4.38	3.06	5.09	*	**	-
	NT2RP4001606	18.77	11.14	16.78	12.15	11.21	15.99	4.83	13.12	16.6			
	NT2RP4001607	6.86	5.47	8.59	11.52	4.98	6.05	4.83	4.03	5.51			
	NT2RP4001610	3.61	1.38	4	7.17	1.24	4.9	2.72	3.85	3.06			
15	NT2RP4001614	9.32	7.4	5.36	10.94	2.88	8.46	8.3	5.56	6.1			
	NT2RP4001623	4.1	3.9	7.53	8.2	4.59	6.06	6.02	5.72	5.27			
	NT2RP4001626	25.96	32.39	24.45	30.25	8.64	19.85	8.25	9.34	7.78	**		-
	NT2RP4001634	5.5	5.13	5.73	8.25	3.86	4.21	6.58	3.67	4.85			
	NT2RP4001638	6.66	10.41	10.2	8.73	4.08	5.57	10.07	5.59	6.69			
	NT2RP4001644	54.14	31.27	53.8	60.84	32.15	47.2	22.38	29.74	30.92			
20	NT2RP4001646	19.49	10.73	26.93	21.07	12.28	14.22	11.82	16.28	16.41			
	NT2RP4001656	13.27	8.07	17.13	8.91	6.79	8.31	7.24	7.86	6.43			
	NT2RP4001666	5.12	4.37	7.8	6.14	1.29	4.07	3.21	5.08	2.86			
	NT2RP4001670	3.97	4.22	8.36	10.93	2.63	2.89	3.57	4.05	2.82			
	NT2RP4001677	60.48	67.97	86.27	37.88	33.85	40.42	60.13	40.04	66.44	*		-
	NT2RP4001679	63.4	46.03	74.85	69.08	70.96	72.54	80.35	59.3	58.1			
25	NT2RP4001695	25.41	48.09	50.45	43.83	20.99	24.93	40.69	28.74	39.61			
	NT2RP4001696	10.8	7.02	11.48	9.54	3.39	6.61	2.58	6.02	6.23			
	NT2RP4001699	7.34	4.14	12.45	8.78	2.82	5.44	4.48	5.75	8.17			
	NT2RP4001717	14.1	8.06	13.01	8.07	5.02	5.29	6.3	4.01	4.24	*		-
	NT2RP4001719	12.35	7.72	11.2	8.9	5.51	7.17	4.84	7.79	6.21			
	NT2RP4001725	3.63	2.94	5.27	5.13	1.69	2.36	2.09	2.38	2.12			
30	NT2RP4001726	27.43	19.04	36.39	17.49	15.05	17.67	16.15	9	13.24			
	NT2RP4001730	17.07	14.23	28.12	18.8	22.34	22.39	15.23	16.15	19.5			
	NT2RP4001739	13.08	27.52	18.78	28.99	19.24	16.38	17.13	15.51	14.38			
	NT2RP4001741	36.21	33.9	43.76	24.77	17.24	19.76	19.65	43.11	31.46	**		-
	NT2RP4001753	17.2	14.59	16.48	7.48	4.99	6.73	3.91	7.96	13.47	**		-
	NT2RP4001760	8.36	7.54	12.21	7.55	2.73	5.75	3.77	6.5	5.81			
35	NT2RP4001787	449.13	316.48	382.02	579.25	624.67	556.76	483.34	493.96	418.4	**	+	-
	NT2RP4001790	7.47	3.89	8.52	8.8	3.39	5.62	4.59	3.58	5.07			
	NT2RP4001795	63.42	46.97	73.29	43.26	32.42	28.05	20.69	20.32	20.73	*	**	-
	NT2RP4001803	8.84	7.88	10.54	9.34	4	5.93	4.96	3.55	3.59		**	-
	NT2RP4001805	5.95	5.69	10.38	8.15	3.79	5.46	9.95	6.17	7.95			
	NT2RP4001809	55.79	43.66	54.44	43.11	38.36	44.76	37.5	36.54	53.86			
40	NT2RP4001817	34.65	23.28	22.77	22.82	15.26	16.99	9.01	16.13	16.73	*		-
	NT2RP4001822	6.52	3.81	10.26	6.23	2.19	2.7	2.67	9.77	2.8			
	NT2RP4001823	3.6	2.46	7.23	4.29	1.65	1.68	0.91	2.7	2.37			
	NT2RP4001827	92.63	82.49	90.1	26.32	25.71	23.6	20.01	17.73	25.06	**	**	-
	NT2RP4001828	61.47	38.75	56.29	48.73	53.93	46.7	40.24	45.94	36.84			
	NT2RP4001836	44.8	31.89	48.09	43.58	41.3	52.3	39.14	27.95	48.98			
45	NT2RP4001838	6.15	7.83	5.55	9.67	6.83	6.27	7.38	14.64	4.59			
	NT2RP4001841	120.68	83.99	187.16	139.43	130.99	191.28	92.44	82.4	82.84			
	NT2RP4001849	5.44	4.67	11.88	5.66	3.18	2.21	2.03	4.71	2.38			
	NT2RP4001861	120.57	86.96	121.65	102.03	95.48	118.7	109.17	140.23	134.58			
	NT2RP4001877	47.77	41.26	29.9	28.86	24.84	22.31	17.4	14.34	21.88	*		-
	NT2RP4001879	28.67	26.1	20.85	19.88	15.94	14.99	7.59	15.66	4.85	*	*	-
50	NT2RP4001889	38.95	24.39	36.19	23.27	20.66	27.73	35.61	41.13	33.21			
	NT2RP4001893	6.77	9.6	11.58	7.5	6.4	5.73	3.91	4.94	4.11	*		-
	NT2RP4001896	20.14	21.68	20.53	23.47	19.99	18.99	15.61	11.88	13.51	**		-
	NT2RP4001898	54.69	54.01	78.1	65.64	57.05	63.77	28.3	45.74	52.57			
	NT2RP4001901	17.19	14.63	24	14.51	10.05	13.25	15.49	18.92	20.72			
55	NT2RP4001910	121.38	105.48	128.54	129.33	152.14	104.65	69.31	116.85	87.82			
	NT2RP4001925	17.35	19.33	26.78	14.34	7.91	7.52	5.99	7.67	6.41	*	**	-
	NT2RP4001926	13.94	13.08	14.09	14.02	5.92	2.48	4.72	6.01	4.66	**		-

Table 458

	NT2RP4001927	22.95	20.54	20.03	14.02	11.73	7.04	7.86	6.56	6.03	*	**	-	-
	NT2RP4001931	31.71	30.66	39.53	15.12	11.86	11.1	6.42	8.14	7.84	**	**	-	-
5	NT2RP4001933	124.92	135.92	123.56	117.23	83.52	79.43	61.4	54.06	63.46		**	-	-
	NT2RP4001938	21.23	9.61	28.3	17.33	8.99	14.74	12.02	19.38	17.02			-	-
	NT2RP4001942	40.71	46.99	41.11	32.73	26.67	27.19	19.11	35.23	32.36	**		-	-
	NT2RP4001945	3.45	3.93	9.62	6.08	1.55	2.05	2.15	2.81	1.6			-	-
	NT2RP4001946	10.3	8.04	13.38	10.29	3.79	3.79	3.46	4.08	3.41	*	*	-	-
	NT2RP4001947	16.45	15.77	21.11	11.34	9.6	7.02	4.68	3.24	4.94	*	**	-	-
10	NT2RP4001950	5.04	4.87	6.27	6.87	2.41	1.7	3	2.63	1.3	*	*	-	-
	NT2RP4001953	26.47	19.18	22.05	22.48	9.35	15.94	17.83	14.03	17.8			-	-
	NT2RP4001966	6.74	6.56	3.55	6.86	3.2	2.07	1.97	1.5	1.8	*		-	-
	NT2RP4001970	7.84	6.46	14.19	9.16	3.49	5.37	2.96	4.43	3.21			-	-
	NT2RP4001975	16.36	22.03	28.3	17.31	12	7.09	9.7	16.29	13.08			-	-
	NT2RP4001988	38	36.95	48.12	29.2	31.09	30.9	21.07	21.03	23.16	*	**	-	-
15	NT2RP4001996	24.73	23.55	24.27	15.39	14.66	5.03	8.32	9.1	9.68	*	**	-	-
	NT2RP4002014	11.39	15.95	16.62	10.15	7.55	6.98	8.4	7.61	5.52	*	*	-	-
	NT2RP4002018	16.73	14.11	11.76	12.16	9.31	11.09	15.09	12.65	8.98			-	-
	NT2RP4002035	5.82	5.03	4.44	7.72	3.9	4.37	5.69	2.8	2.78			-	-
	NT2RP4002043	18.95	25.2	14.18	17.22	10	14.87	15.39	7.04	10.89			-	-
	NT2RP4002046	24.11	28.29	25.84	19.27	12.78	20.33	11.41	17.55	17.78	*	*	-	-
20	NT2RP4002052	12	15.65	20.88	9.3	9.08	6.85	4.02	3.61	4.24	*	**	-	-
	NT2RP4002056	153.48	150.03	95.32	64.65	34.92	59.97	51.1	38.55	53.86	*	*	-	-
	NT2RP4002057	40.68	39.2	39.83	19.31	30.56	26.73	27.83	37.55	52.18	*		-	-
	NT2RP4002058	17.65	14.46	13.17	10.87	3.28	4.52	5.26	2.89	2.9	*	**	-	-
	NT2RP4002064	5.15	7.64	7.19	5.68	1.88	1.94	2.82	1.16	2.09	**		-	-
	NT2RP4002071	19.67	23.04	16.87	12.91	7.48	6.56	8.07	4.85	9.75	*	**	-	-
25	NT2RP4002075	4.49	2.91	8.1	6.42	3.43	5.27	3.76	2.11	2.28			-	-
	NT2RP4002078	19.28	11.77	21.52	11.04	6.62	7.49	7.2	13.73	14.2	*		-	-
	NT2RP4002081	26.93	23.83	24.19	19.25	16.65	23.73	20.7	21.48	20.63	*	*	-	-
	NT2RP4002083	12.48	9.47	12.44	9.18	6.34	7.57	7.79	10.15	9.98	*		-	-
	NT2RP4002099	4.69	4.27	5.09	6.55	1.89	1.66	2.86	2.04	1.79	**		-	-
	NT2RP4002106	48.22	85.51	111.5	22.9	29.06	16.21	28.91	8.21	26.28	*	*	-	-
30	NT2RP4002111	21.8	28.93	25.95	13.09	13.73	11.32	21.21	10.01	16.62	**		-	-
	NT2RP4002112	18.8	22.05	20.04	17.73	8.26	13.72	15.37	6.12	8.09	*		-	-
	NT2RP4002116	131.42	129.9	145.31	124.89	86.8	130.87	116.59	193.03	130.26			-	-
	NT2RP4002122	9.21	7.05	12.08	10.75	5.68	5.1	3.65	7.4	5.23			-	-
	NT2RP4002126	16.25	10.45	26.23	9.01	12.04	10.44	10.14	17.51	8.7			-	-
35	NT2RP4002133	59.92	73.72	76.92	61.59	43.1	56.16	80.78	84.66	86.01			-	-
	NT2RP4002136	12.24	16.73	29.34	16.04	8.23	7.86	20.93	16.43	17.62			-	-
	NT2RP4002139	65.39	168.51	135.79	98.21	29.79	27.09	86.97	65.15	29.84			-	-
	NT2RP4002174	10.15	13.02	11.19	12.5	4.36	7.32	8.88	11.55	11.53			-	-
	NT2RP4002185	23.38	25.82	19.72	13.23	6.3	10.39	10.9	7.33	11.09	**	**	-	-
	NT2RP4002186	16.88	7.65	12.65	11.9	7.3	14.74	12.63	14.19	17.64			-	-
40	NT2RP4002187	28.59	22.57	36.35	26.74	19.36	12.02	11	23.37	23.58			-	-
	NT2RP4002188	5.08	7.53	8.31	11.66	6.59	7.86	4.55	4.87	6.3			-	-
	NT2RP4002199	5.25	3.74	5.62	11.93	2.92	3.8	2.79	4.05	2.9			-	-
	NT2RP4002206	3.81	1.86	2.83	8.57	1.99	1.73	3.4	4.64	3.09			-	-
	NT2RP4002210	5.45	3.2	5.65	5.42	1.97	2.98	3.71	3.22	3.36			-	-
	NT2RP4002222	6.38	6.14	7.04	6.83	3.57	3.25	6.5	5.55	8.67			-	-
45	NT2RP4002241	19.38	17.71	14.08	18.19	11.3	8.8	22.47	17.63	22.91			-	-
	NT2RP4002248	35.82	21.31	27.47	30.46	20.08	26.03	19.35	24.1	27.06			-	-
	NT2RP4002250	1.58	1.78	7.25	3.8	1.3	0.25	0.61	0.65	1.92			-	-
	NT2RP4002259	5.84	5.18	13.48	7.69	2.79	5.42	4.19	2.88	3.6			-	-
	NT2RP4002268	35.43	25.77	32.22	22.21	30.41	16.71	15.9	32.72	23.26			-	-
	NT2RP4002288	22.95	20.57	22.28	19.59	16.95	19.16	16.63	15.69	17.98	*	**	-	-
50	NT2RP4002290	13.7	13.76	25.96	11.44	11.61	14.66	7.05	8.48	10.18			-	-
	NT2RP4002298	10.23	12.39	16.74	11.6	8.3	6.18	9.56	4.97	3.02			-	-
	NT2RP4002306	15.16	15.97	20.14	18.18	10.48	11.51	13.4	11.06	13.62			-	-
	NT2RP4002308	8.45	5.65	13.02	8.55	4	9.83	3.47	4.84	5.83			-	-
	NT2RP4002336	36.27	19.86	28.94	13.28	11.25	15.46	7.56	12.49	16.8	*	*	-	-
	NT2RP4002340	2.84	2.81	9.7	4.27	0.88	0.87	1.22	1.79	3.04			-	-
55	NT2RP4002361	9.6	7.94	13.29	10.99	5.46	5.57	5.78	8.11	5.48			-	-
	NT2RP4002367	2.79	2.98	7.18	5.28	1.95	2.56	3.24	1.85	1.33			-	-
	NT2RP4002368	24.08	18.92	33.22	37.33	27.57	13.68	19.74	22.15	15.46			-	-

Table 459

	NT2RP4002377	39.07	34.91	52.74	47.19	54.21	38.25	54.01	36.88	39.01			
	NT2RP4002408	8.23	10.17	7.33	8.55	4.11	5.54	5.29	2.67	3.53	*		-
	NT2RP4002425	16.72	9.87	22.95	18.36	10.72	16.61	14.74	22.3	29.56			
5	NT2RP4002432	134.52	97.55	162.62	149.32	142.05	170.39	110.43	102.21	77.71			
	NT2RP4002447	15.99	16.51	16.61	15.14	7.55	8.09	7.58	13.4	16.29			
	NT2RP4002451	15.11	13.46	19.12	12.6	10.1	7.99	7.15	14.07	11.51			
	NT2RP4002461	94.61	109.24	116.21	78.57	91.21	74.75	80.34	65.93	74.08	*	*	-
	NT2RP4002486	16.89	12.32	16.5	14.11	11.37	5.17	6.32	4.06	4.53	**		-
10	NT2RP4002517	13.38	14.55	13.22	12.72	9.03	11.46	10.8	6.18	8.61	*		-
	NT2RP4002556	14.42	18.7	14.04	18.8	13.59	13.31	16.09	6.06	5.52			
	NT2RP4002569	16.26	11.41	27.18	13.33	6.98	10.11	3.13	6.78	11.56			
	NT2RP4002587	4.28	5.9	13.49	5.9	21.35	3.55	2.37	3.48	4.03			
	NT2RP4002591	11.21	8.73	16.61	10.63	3.25	5.39	2.62	6.98	4.42	*		-
	NT2RP4002607	7.19	4.54	8.62	7.82	4.54	6.78	3.93	3.64	3.85			
15	NT2RP4002627	129.04	84.31	131.91	123.08	121.1	113.29	100.69	103.33	117.09			
	NT2RP4002628	23.42	19.42	25.54	15.3	10.07	9.36	10.28	14.93	5.74	*	*	-
	NT2RP4002630	34.52	45.14	38.61	24.65	19.47	21.97	38.2	24.12	21.41	**		-
	NT2RP4002639	69.58	58.92	77.5	92.97	83.89	82.67	76.62	44.55	74.09	*		+
	NT2RP4002641	10.87	7.59	20.93	9.6	5.64	6.42	5.77	9.03	8.9			
	NT2RP4002658	167.82	202.75	171.29	210.71	275.39	155.29	113.71	313.1	177.93			
20	NT2RP4002669	11.89	14.59	18.31	13.81	8.54	6.37	6.6	13.8	11.32			
	NT2RP4002677	38.73	39.84	49.87	21.84	19.97	14	8.4	12.92	7.79	**	**	-
	NT2RP4002715	60.14	28.66	66.85	78.28	49.48	49.64	41.22	48.79	51.15			
	NT2RP4002750	5.11	4.54	6.02	5.02	2.86	2.29	1.61	2.5	1.93	**		-
	NT2RP4002784	13.9	15.39	21.97	16.43	16.29	10.56	10.51	11.54	8.19			
	NT2RP4002791	19.14	16.24	15.43	15.81	11.98	5.79	6.28	6.12	6.25	**		-
25	NT2RP4002811	7.07	4.03	15.62	8.02	4.02	6.88	1.73	4.87	5.66			
	NT2RP4002830	22.24	23	26.1	14.14	12.81	9.89	5.49	12.55	7.49	**	**	-
	NT2RP4002832	6.62	7.2	10.83	9.33	4.27	5.54	7.23	5.78	6.45			
	NT2RP4002850	120.6	112.69	112.51	87.95	73.32	75.57	95.07	111.13	108.7	**		-
	NT2RP4002874	8.25	8.24	13.89	8.67	2.89	3.54	1.21	3.45	2.95	*		-
	NT2RP4002884	89.55	83.99	93.99	87.7	70.28	83.78	63.11	54.66	68.06	**		-
30	NT2RP4002888	6.66	8.16	10.03	7.45	4.69	3.72	4.86	3.64	2.94	*		-
	NT2RP4002891	19	20.18	21.15	16.8	8.39	11.91	12.08	8.99	11.53	*	**	-
	NT2RP4002894	39.86	38.92	34.99	21.18	29.78	22.86	11.88	16.42	39.6	*		-
	NT2RP4002896	7.81	11.66	17.8	10.13	3.4	6.5	5.01	4.37	5.08			
	NT2RP4002905	5.89	3.63	14.35	7.98	3.09	2.98	3	5.21	1.93			
	NT2RP4002907	14.82	12.9	19.78	10.14	7.04	6.74	11.86	12.75	9.47	*		-
35	NT2RP5003459	437.62	468.29	451.9	449.8	544.78	414.46	466.17	464	478.98			
	NT2RP5003461	21.93	17.54	18.05	12	9.18	10.65	7.44	6.63	4.58	**	**	-
	NT2RP5003471	52.72	62.97	42.21	31.11	21.1	25.12	46.83	20.37	35.04	*		-
	NT2RP5003477	5.7	3.4	3.74	5.93	3.44	2.66	3.17	2.23	2.28			
	NT2RP5003487	1749.6	1957.3	1778.8	1241.4	1573.1	1807.7	1562.4	2343.9	2243.6			
	NT2RP5003492	6.08	6.5	15.88	6.67	3.98	3.96	2.59	3.25	1.92			
40	NT2RP5003500	4.26	2.52	9.75	6.65	2.34	2.66	2.29	2.53	3.57			
	NT2RP5003506	10.49	9.24	16.38	12.74	9.52	9.22	9.69	9.29	9.27			
	NT2RP5003512	6.99	7.06	8.63	5.95	2.46	3.36	2.76	2.88	3.49	*	**	-
	NT2RP5003522	10.07	9.26	8.55	5.18	3.12	3	5.35	1.85	3.07	**	**	-
	NT2RP5003524	6.44	9.05	5.63	7.13	1.41	1.72	4.66	2.23	3	*		-
	NT2RP5003527	117.46	141.32	115.3	136.41	95.19	117.09	134.61	57.44	67			
45	NT2RP5003531	24.59	24.67	34.31	22.85	17.67	26.56	12.06	25.82	35.99			
	NT2RP5003534	6.96	7.88	13.1	6.91	5.36	2.92	2.47	4.02	3.38	*		-
	NT2RP6000020	19.43	27.72	47.01	19.42	30.65	12.46	29.24	22.48	15.27			
	NT2RP6000022	13.58	7.81	13.25	8.64	4.5	5.83	7.1	5.5	4.05	*		-
	NT2RP6000050	5.27	8.58	7.67	6.81	3.59	4.26	5.19	3.06	5.18			
	NT2RP6000063	5.9	4.93	5.56	6.03	1.07	1.6	2.56	2.13	3.15	**		-
50	NT2RP6000074	10.12	8.88	7.2	8.89	3.35	3.32	4.76	3.03	4.96	*		-
	NT2RP6000083	36.48	50.53	36.06	34.94	19.9	25.84	29	16.57	36.99			
	NT2RP6000100	9.33	8.85	11.79	8.7	3.93	5.47	3.33	5.54	5.88	*		-
	NT2RP6000123	7.59	5.31	8.35	10.56	5.66	4.44	3.17	5.91	3.98			
	NT2RP6000129	4.7	6.51	7.04	5.86	2.6	3.34	4.3	7.17	3.53			
	NT2RP6000147	23.98	19.21	18.37	28.9	18.17	21.68	18.73	17.92	16.85			
55	NT2RP6000163	6.02	5.5	6.17	6.66	2.33	2.81	2.76	2.24	3.12	**		-
	NT2RP6000181	31.82	37.36	38.55	11.76	5.01	6.27	13.35	6.28	18.64	**	**	-



Table 460

	NT2RP6000182	11.67	12.98	10.81	11.27	4.67	4.19	7.63	8.13	8.65	**	-
	OVARC1000001	10.18	10.98	7.82	10.48	3.67	5.27	8.05	6.3	4.32	*	+
5	OVARC1000003	19.46	16.04	21.53	24.56	18.39	28.35	24.31	27.93	25.27	*	+
	OVARC1000004	154.65	161.68	111.37	257.56	204.62	269.89	148.7	142.43	153.8	*	+
	OVARC1000006	8.96	9.17	13.23	12.36	9.89	7.09	8.46	11.94	16.91	*	-
	OVARC1000013	12.84	15.42	21.83	13.5	7.52	11.75	8.01	7.31	7.45	*	-
	OVARC1000014	9.51	5.51	9.75	8.67	3	2.57	4.2	4.5	5.23		
	OVARC1000017	7.8	10.89	11.1	9.23	5.72	5.56	7.08	8.83	7.59		
10	OVARC1000026	39.97	98.56	58.17	35.12	21.04	21.52	23	21.16	19.52	*	-
	OVARC1000035	53.62	63.74	56.85	49.18	30.89	52.6	44.01	25.83	35.4	*	-
	OVARC1000037	44.18	27.1	33.64	21.27	17.7	36.96	22.76	28.28	23.56		
	OVARC1000058	21.2	16.03	18.93	19.43	6.93	18.25	18.85	19.08	20.93		
	OVARC1000060	8.69	7.53	9.42	11.74	4.69	15.1	7.86	12.81	10.28		
	OVARC1000068	11.63	6.29	9.06	11.58	8.06	9.18	6.71	8.97	7.36		
15	OVARC1000069	130.28	91.82	110.55	138.44	48.02	81.99	34.87	114.87	91.52		
	OVARC1000071	4.7	2.59	5.56	6.14	1.28	3.78	7.5	3.79	3.09		
	OVARC1000075	608.15	715.16	979.97	596.89	401.8	521.41	1505.9	1295.8	1454	**	+
	OVARC1000083	31.41	22.53	32.47	28.89	10.2	12.73	23.7	17.6	16.65		
	OVARC1000085	150.84	132.35	115.14	65.66	79.36	104.26	57.87	55.95	46.39	*	-
	OVARC1000086	21.41	22.84	29.16	11.19	16.67	9.71	14.87	19.23	16.21	*	-
20	OVARC1000087	5.75	4.1	5.37	4.05	5.46	2.99	2.78	3.2	3.4	*	-
	OVARC1000090	32.43	34.99	39.46	22.05	34.29	19.79	30.39	42.7	35.58		
	OVARC1000091	19.21	16.58	18.4	9.39	12.78	9.69	3.97	5.82	3.09	**	-
	OVARC1000092	12.38	12.28	20.09	9.9	9.89	8.91	11.14	12.55	9.97		
	OVARC1000105	143.72	148.63	164.07	88.33	70.71	97.62	141.54	139.36	177.6	**	-
	OVARC1000106	56.13	50.31	43.64	33.71	26.64	28.64	25.97	22.43	26.91	**	-
25	OVARC1000109	41.67	37.23	42.5	18.44	22.06	21.86	20.05	26.41	16.1	**	-
	OVARC1000113	24.72	16.19	25.29	12.07	22.86	8.51	9.56	13.5	7.9	*	-
	OVARC1000114	20.78	17.23	18.89	9.6	15.6	9.38	19.16	20.46	17.77	*	-
	OVARC1000133	17.57	29.71	58.68	7.88	21.62	13.9	11.06	7.62	51.45		
	OVARC1000137	26.29	21.24	32.71	19.41	23.84	21.06	17.64	15.76	21.29		
30	OVARC1000139	159.47	147.34	170.25	146.09	161.46	121.94	114.2	86.17	91.75	**	-
	OVARC1000145	5.46	5.11	5.9	4.05	7.97	2.4	2.98	4.01	3.61	**	-
	OVARC1000148	26.75	26.35	26.82	10.67	7.97	11.29	11.04	13.8	10.7	**	-
	OVARC1000151	10.96	7.69	7.49	4.61	6.76	7.44	5.23	9.46	5.82		
	OVARC1000157	131.87	72.71	159.16	28.64	46	29.09	32.55	30.3	35.03	*	-
	OVARC1000162	5.48	6.74	10.66	5.09	8.45	3.6	3.17	7.57	4.35		
35	OVARC1000168	20.5	23.24	26.19	11.56	15.79	12.79	11.3	16.45	13.91	**	-
	OVARC1000169	67.7	69.5	69.91	59.55	32.42	51.67	35.89	25.97	33.69	**	-
	OVARC1000178	7.01	7.74	9.93	3.35	8.16	5.02	5.67	3.4	4.49	*	-
	OVARC1000182	6.26	2.63	4.45	2.72	4.87	3.13	2.7	3.24	3.81		
	OVARC1000186	14.26	11.19	12.68	6.9	8.25	3.97	5.99	5.56	7.72	*	-
	OVARC1000188	19.42	11.08	15.15	6.26	7.14	4.44	6.66	6.47	9.02	*	-
40	OVARC1000191	10.3	6.61	7.55	5.45	7.49	3.47	4.08	6.65	4.21		
	OVARC1000198	22.01	20.32	21.51	13.28	15.24	8.22	13.24	17.04	19.28	*	-
	OVARC1000208	131.85	125.05	141.2	106.48	130.32	109.42	107.54	141.64	112.43		
	OVARC1000209	37.5	42.42	46.9	35.76	48.15	33.79	26.69	26.98	20.75	**	-
	OVARC1000212	14.17	16.96	15.84	10.34	14.11	8.11	6.32	5.07	5.47	**	-
	OVARC1000216	7.5	5.29	9.53	2.31	4.11	1.95	4.22	3.32	1.67	*	-
45	OVARC1000240	30.72	25.44	20.48	13.87	16.01	11.11	15.84	21.45	17.35	*	-
	OVARC1000241	8.83	9.47	8.6	4.52	5.75	4.08	4.87	6.55	6.44	**	-
	OVARC1000249	12.5	10.38	14.17	6.99	8.18	4.94	7.53	30.07	10.99	*	-
	OVARC1000254	211.04	164.08	171.72	162.84	218.18	173	104.59	109.93	114.49	**	-
	OVARC1000255	8.62	6.5	15.01	2.8	3.3	2.22	1.58	8.88	3.88	*	-
	OVARC1000267	41.48	57.68	54.05	22.69	31.39	23.55	19.25	29.77	21.42	*	-
50	OVARC1000275	6.58	9.72	13.14	1.2	3.21	1.15	3.78	4.58	2.47	*	-
	OVARC1000287	20.12	19.59	19.09	8.41	13.5	9.21	9.7	16.66	9.51	**	-
	OVARC1000288	34.41	32.21	34.44	10.93	20.1	12.59	9.34	11.6	15.85	**	-
	OVARC1000298	37.89	35.05	40.4	26.93	41.61	26.19	16.03	19.69	20.76	**	-
	OVARC1000302	10.27	8.52	8.63	3.64	6.33	2.17	4.38	8.26	6.64	*	-
	OVARC1000304	13.52	8.67	11.83	6.89	9.55	6.81	7.04	9.75	5.89		
55	OVARC1000307	9.2	9.65	13.33	4.99	7.9	7.07	7.34	4.85	4.2	*	-
	OVARC1000309	10.77	7.81	10.14	3.65	4.52	3.3	3.45	4.14	3.51	**	-
	OVARC1000312	38.52	63.36	48.96	16.29	39.99	22.16	11.44	23.2	11.33	*	-

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	OVARC1000313	31.08	25.28	22.97	16.65	33.34	16.32	7.95	14.64	16.92	*	-
	OVARC1000321	95.57	70.17	108.42	49.21	78.85	36.91	71.72	84.76	66.41		
5	OVARC1000326	9.36	7.55	9.19	5.69	4.73	3.83	2.8	4.95	2.81	**	**
	OVARC1000327	9.64	6.54	7.7	4.58	5.69	4.67	3.24	3.34	3.39	*	**
	OVARC1000331	31.51	26.56	17.69	20.2	32.18	25.32	7.77	12.73	9.94	*	*
	OVARC1000335	10.5	10.92	9.98	3.56	6.12	5.55	3.62	2.51	3.12	**	**
	OVARC1000347	22.28	19.59	19.77	14.38	17.51	15.31	11.64	10.94	10.7	*	**
	OVARC1000348	9.03	9.66	11.56	3.27	3.92	2.72	2.5	3.43	2.51	**	**
10	OVARC1000363	17.67	18.03	15.99	8.09	14.09	9.86	7.93	4.93	7.38	*	**
	OVARC1000377	9.05	5.89	9.25	3.23	6.62	3.71	2.88	2.47	4.83	*	*
	OVARC1000382	11.38	10.29	10.44	4.87	5.92	3.1	5	4.78	5.93	**	**
	OVARC1000384	15.04	16.77	12.96	3.9	4.19	3.88	3.11	4.29	3.9	**	**
	OVARC1000401	12.88	8.81	11.8	7.36	8.78	6.88	5.26	4.94	4.67	**	**
	OVARC1000406	452.57	396.91	414.58	242.32	241.63	222.43	202.53	242.65	184.03	**	**
15	OVARC1000407	11.18	13.52	12.76	4.82	6.15	3.43	3.77	3.81	3.74	**	**
	OVARC1000408	143.25	152.71	130.24	110.8	163.58	95.03	87.98	95.98	86.83	**	*
	OVARC1000410	12.11	11.07	15.74	6.71	11.27	6.87	6.11	5.6	3.42	**	*
	OVARC1000411	11.28	8.14	7.71	4.73	4.82	3.45	4.09	4.41	4.68	*	*
	OVARC1000414	15.72	17.28	11.48	7.59	8.9	10.02	14.36	14.47	14.88	*	*
	OVARC1000420	11.3	11.1	10.67	5.43	7.49	5.25	8.15	6.28	6.64	**	**
20	OVARC1000421	21.51	18.12	14.96	8.46	10.6	6.1	8.22	6.83	7.06	*	**
	OVARC1000427	255.84	237.66	229.09	230.15	286.16	201.09	155.75	128.13	139.78	**	*
	OVARC1000431	86.97	107.76	104.05	53.83	76.2	48.18	31.1	18.06	18.56	*	**
	OVARC1000437	18.7	18.85	16.29	10.2	15.26	9.01	9.96	5.69	8.45	*	**
	OVARC1000439	14.55	21.25	13.48	9.92	17.37	9.21	5.86	5.66	4.06	*	*
25	OVARC1000440	37.93	36.45	33.24	14.99	19.86	14.94	10.14	8.93	10.09	**	**
	OVARC1000442	47.65	39.77	34.86	17.92	25.44	19.14	36.52	26.4	37.91	*	*
	OVARC1000443	9.63	12.52	9.02	8.56	33.14	5.66	16.38	5.13	9.47		
	OVARC1000461	8.43	5.22	4.46	4.04	5.64	3.64	3.41	4.7	3.49		
	OVARC1000465	13.05	12.4	8.82	5.16	5.82	3.89	4.59	3.18	2.41	*	**
	OVARC1000466	22.78	19.36	18.72	10.66	17.86	12.45	11.65	7.24	8.12	**	*
30	OVARC1000467	8.03	5.77	8.99	2.45	3.8	2.2	3.29	2.29	3.38	*	*
	OVARC1000470	15.96	13.65	10.41	7.96	9.91	7.26	9.53	10.16	10.25		
	OVARC1000473	12.49	10.05	10.69	6.2	7.49	6.37	10.6	7.2	9.15	**	*
	OVARC1000479	24.56	30.78	25.75	8.77	13.76	7.96	8.07	9.81	9.07	**	**
	OVARC1000484	41.23	29.61	25.62	15.32	17.14	13.32	29.7	26.23	34.72	*	*
	OVARC1000486	15.8	17.22	17.4	11.06	13.85	9.12	14.13	11.53	12.18	*	*
35	OVARC1000496	6.74	8.5	5.88	2.96	8.22	5.46	2.84	3.93	3.9	*	*
	OVARC1000520	8.86	5.17	6.53	2.16	5.01	3.05	4.06	3.97	5.92		
	OVARC1000522	35.51	29.95	29.3	26.12	30.21	22.71	22.42	16.55	18.06	**	*
	OVARC1000526	25.75	25.79	19.89	12.38	14.14	8.6	32.78	19.39	27.42	**	*
	OVARC1000529	17.7	16.61	13.49	7.72	9.26	6.61	12.03	7.5	12.39	**	*
	OVARC1000533	31.08	27.41	22.88	25.25	24.54	12.97	18.02	13.21	18.14	*	*
40	OVARC1000543	11.04	5.87	5.45	4.07	4.48	2.25	3.68	3.22	4.84		
	OVARC1000550	9.45	7.02	5.98	3.29	4.46	2.66	4.35	2.47	4.43	*	*
	OVARC1000553	34.95	36.44	34.04	16.33	24.77	21.97	31.22	31.95	33.2	**	*
	OVARC1000556	22.37	23.81	26.15	14.72	11.54	9.38	19.99	16.63	22.58	**	*
	OVARC1000557	11.61	9.78	7.49	2.51	3.89	2.24	6.45	4.03	5.39	**	*
	OVARC1000561	67.36	70.57	52.24	30.14	35.45	26.39	87.82	47.67	77.14	**	*
45	OVARC1000564	79.74	89.59	94.8	35.3	37.73	54.01	49.59	52.84	37.26	**	**
	OVARC1000573	11.41	12.83	14.29	6.97	10.13	6.51	5.93	10.17	8.55	*	*
	OVARC1000576	235.06	210.51	199.48	203.8	258.47	200.46	142.26	126.19	115.56	**	*
	OVARC1000578	15.29	13.44	14.45	8.15	12.93	8.56	9.81	12.76	11.9	*	*
	OVARC1000581	5.46	3.63	4.65	3.12	3.25	1.85	1.84	1.64	2.35	**	*
	OVARC1000586	99.11	90.08	96.7	58.86	53.54	48.9	78.17	82.33	62.01	**	*
50	OVARC1000588	5.04	6.16	5.9	2.73	4.3	3.79	4.96	4.69	3.2	*	*
	OVARC1000605	11.72	9.54	8.96	6.4	6.63	6.02	4.7	4.72	5.55	*	**
	OVARC1000622	86.95	79.96	78.79	29.56	66.79	40.9	71.63	93.74	75.18	*	*
	OVARC1000636	9.18	7.82	11.99	5.56	6.68	4.67	5.37	6.74	3.7	*	*
	OVARC1000640	9.32	12.02	12.8	8.63	10.33	8.57	6.08	8.89	7.4	*	*
	OVARC1000649	137.37	159.82	123.65	116.33	170.6	128.38	91.38	85.12	81.65	**	*
55	OVARC1000661	14.89	15.01	20.86	11.94	15.89	11.61	9.31	9.27	13.9		
	OVARC1000677	42.34	38.62	28.23	30.67	34.02	28.61	19.25	22.35	28.93		
	OVARC1000678	18.66	21.84	18.64	9.55	15.51	8.53	9.3	11.98	8.4	*	**

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	OVARC1000679	17.17	15.32	16.17	8.84	11.11	9.5	8.07	11.07	12.27	**	*	-	-
	OVARC1000681	8.2	7.24	6.7	4.69	3.61	5.03	3.58	6.1	3.97	**	*	-	-
	OVARC1000682	113.12	97.53	93.09	104.53	135.81	99.85	59.24	48.57	73.95		*	-	-
5	OVARC1000689	57.01	42.21	46.96	44.44	54.09	47.18	30.34	27.71	26.26		*	-	-
	OVARC1000700	15.99	15.69	20.71	10.16	14.93	8.67	10.07	14.65	13.84			-	-
	OVARC1000703	26.78	29.43	35.22	14.83	20.62	12.69	19.45	19.63	21.91	*	*	-	-
	OVARC1000722	101.86	85.68	116.52	89.03	99.63	84.39	90.99	59.44	79.26		*	-	-
	OVARC1000726	14.33	9.39	12.54	8.8	8.89	8.63	5.72	6.56	7.04		*	-	-
	OVARC1000727	10.18	7.75	13.09	5.79	7.58	4.18	6.38	6.81	6.67			-	-
10	OVARC1000730	29.15	29.95	31.68	12.76	10.82	12.92	11.85	21.92	19.46	**	*	-	-
	OVARC1000741	29.33	29.17	34.55	13.03	37.4	9.12	12.19	21.98	17.49		*	-	-
	OVARC1000746	7.78	5.19	7.05	4.39	4.32	3.45	2.05	2.62	3.13	*	**	-	-
	OVARC1000764	38.05	40.13	44.9	31.76	33.36	24.43	25.99	25.42	30.04	*	**	-	-
	OVARC1000769	15.32	19.03	26.3	6.54	8.47	6.17	10.92	9.44	11.01	*	*	-	-
15	OVARC1000771	12.14	10.36	12.36	5.65	9.59	2.99	5.56	6.75	5.39	**		-	-
	OVARC1000773	208.54	178.97	168.4	156.38	229.88	197.98	120.99	98.51	115.59	**		-	-
	OVARC1000775	34.96	28.91	27.77	13.91	16.38	12.88	14.63	18.43	17.02	**	**	-	-
	OVARC1000778	16.25	14.26	17.29	7.71	11.77	9.22	9.21	13.13	13.25	*		-	-
	OVARC1000779	5.51	4.08	7.92	1.14	3.76	1.42	1.72	21.49	16.55			-	-
	OVARC1000781	14.72	11.11	14.65	7.53	10.61	4.88	3.59	7.19	4.56	*	**	-	-
20	OVARC1000787	16.08	11.69	22.35	5.66	7.21	5.45	9	11.11	9.91	*		-	-
	OVARC1000789	23.78	29.78	21.78	12.72	20.51	12.99	10.1	11.61	10.12	**		-	-
	OVARC1000800	37.24	52.19	47.92	15.44	23.62	15.47	18.1	25.22	22.47	**	**	-	-
	OVARC1000802	10.69	12.79	19.22	5.61	8.97	4.92	12.57	10.26	7.88			-	-
	OVARC1000810	41.47	36.61	45.9	14.82	21.04	14.45	26.69	32.64	43.34	**		-	-
	OVARC1000811	19.55	15.32	20.3	9.11	11.03	10.04	5.82	8.76	8.16	**	**	-	-
25	OVARC1000814	47.61	40.61	47.27	21.78	30.43	20.51	28.06	40.57	35.2	**		-	-
	OVARC1000816	30.44	36.85	45.82	25.26	35.06	20.13	15.73	10.27	23.79	*		-	-
	OVARC1000817	7.44	5.99	13.01	2.4	3.28	3.96	1.6	3.36	1.57	*		-	-
	OVARC1000834	9.2	11.08	10.6	3.33	5.92	2.58	4.12	4.4	2.95	**	**	-	-
	OVARC1000846	33.2	36.76	34.02	15.54	20.84	16.18	25.4	21.7	22.13	**	**	-	-
	OVARC1000850	10.1	9.46	13.94	3.02	6.63	4.93	5.97	6.78	5.46	*	*	-	-
30	OVARC1000853	124.13	83.82	117.1	50.7	94.43	66.32	58.07	66.46	64.96	*		-	-
	OVARC1000862	9.56	7.61	8.86	6.22	4.52	5.06	2.49	2.85	3.78	*	**	-	-
	OVARC1000873	22.12	9.86	11.25	3.95	10.2	7.01	4.33	4	5.56			-	-
	OVARC1000875	25.32	18.88	20.49	9.43	11.13	12.13	10.43	9.71	12.19	**	**	-	-
	OVARC1000876	14.43	11.76	13.8	4.33	8.64	6.48	3.87	5.38	3.7	**	**	-	-
	OVARC1000883	16.65	14.83	22.63	10.71	10.46	10.25	4.07	3.52	3.44	*	**	-	-
35	OVARC1000885	14.94	15.72	15.2	7.47	13.49	6.08	8.84	6.87	4.31	**		-	-
	OVARC1000886	13.43	12.39	14.55	7.87	12.43	7.38	15.33	6.54	7.36			-	-
	OVARC1000890	238.12	222.49	244.97	168.11	248.06	165.63	120.4	102.6	108.39	**		-	-
	OVARC1000891	14.84	13	11.09	4.07	5.36	4.55	3.08	4.38	3.01	**	**	-	-
	OVARC1000897	5.52	4.78	5.55	2.64	2.48	2.49	2.14	2.77	2.38	**	**	-	-
	OVARC1000912	18.82	12.83	16.34	8.16	8.42	8.22	8.21	8.74	10.52	*	*	-	-
40	OVARC1000914	14.59	8.15	9.14	3.85	5.26	5.95	4.68	5.3	4.1	*		-	-
	OVARC1000915	17.53	15.34	14.44	6.42	7.74	4.39	7.85	11.07	8.04	**	**	-	-
	OVARC1000916	15.19	18.72	21.06	9.85	20.11	11.22	12.02	12.35	10.4	*		-	-
	OVARC1000924	11.12	12.86	14.01	5.55	9.51	4.44	3.13	4.61	3.65	*	**	-	-
	OVARC1000928	46.27	37.28	34.31	5.2	8.81	6.65	4.93	6.15	5.85	**	**	-	-
	OVARC1000936	10.09	10.55	9.33	5.2	9.07	4.74	3.02	5.31	5.15	**		-	-
45	OVARC1000937	7.99	8.04	6.58	4.25	5.19	2.94	3.85	3.95	5.45	*	*	-	-
	OVARC1000945	15	14.98	13.39	5.71	5.62	7.78	3.1	4.11	2.76	**	**	-	-
	OVARC1000948	7.88	5.06	4.83	2.65	3.28	2.79	2.69	2.39	2.47	*	*	-	-
	OVARC1000956	14.88	11.07	13.93	5.15	8.05	6.51	8.38	4.46	6.46	**	*	-	-
	OVARC1000959	16.85	16.96	14.18	9.84	10.41	6.42	15.3	9.78	14.01	**		-	-
	OVARC1000960	47.32	52.37	41.49	22.16	32.89	19.82	46.28	34.15	44.56	*		-	-
50	OVARC1000964	306.84	272.77	304.89	274.01	264.01	211.54	160.52	108.2	102.39	**		-	-
	OVARC1000971	7.74	6.08	3.76	3.85	7.47	4.63	2.45	4.82	2.32			-	-
	OVARC1000975	109.05	95.15	91.82	89.45	126.14	83.84	54.44	48.09	54.61	**		-	-
	OVARC1000976	6.41	7.34	5.63	3.4	4.98	2.89	5.48	3.56	2.85	*		-	-
	OVARC1000981	24.82	24.19	24.61	14.13	15.11	11.79	18.79	11.54	16.77	**	*	-	-
55	OVARC1000982	21.37	12.18	12.3	7.66	16.73	9.68	5.67	4.54	5.45	*		-	-
	OVARC1000984	10.44	9.85	10.17	2.64	4.79	2.24	2.88	2.32	3.54	**	**	-	-
	OVARC1000995	27.57	24.28	19.39	14.42	17.35	10.4	23.31	17.65	22.26	*		-	-

Table 463

	OVARC1000996	12.75	15.42	13.22	7.58	7.82	4.86	10.5	9.45	10.8	**	*	-	-
	OVARC1000999	77.92	64.11	52.33	34.61	41.57	26.78	51.13	38.47	53.84	*		-	-
5	OVARC1001000	34.25	25.88	23.55	13.32	17.72	11.08	24.85	23.48	28.11	*		-	-
	OVARC1001004	4.45	4.47	4.74	3.56	4.7	2.11	3.94	2.09	3.24			-	-
	OVARC1001010	7.8	4.93	6.92	2.94	3.81	2.97	3.34	2.1	2.69	*	*	-	-
	OVARC1001011	10.56	5.96	7.28	2.55	4.47	3.01	5.82	4.52	6.66	*		-	-
	OVARC1001030	135.15	261.75	227.94	119.93	118.81	67.28	114.11	94.32	117.34			-	-
	OVARC1001032	10.53	7.53	10.42	4.6	4.01	3.78	8.13	6.94	7.33	**		-	-
10	OVARC1001034	10.83	11.24	8.27	5.28	4.2	4.55	7.53	5.89	7.35	**	*	-	-
	OVARC1001038	36.07	37.32	30.24	14.88	24.71	11.8	14.41	10.88	16.24	*	**	-	-
	OVARC1001040	40.95	33.02	36.27	20.4	24.74	15.2	38.11	31.08	34.73	**		-	-
	OVARC1001041	28.88	24.51	24.41	14.12	19.17	10.91	20.98	17.34	23.83	*		-	-
	OVARC1001044	8.66	8.02	6.34	3.74	2.76	3.79	6.52	3.05	4.17	**		-	-
	OVARC1001049	23.67	22.64	22.97	8.16	12.73	9.28	19.46	22.57	21.53	**		-	-
15	OVARC1001051	381.08	484.89	350.06	354.62	546.22	323.29	741.7	383.07	703.22			-	-
	OVARC1001054	6.6	5.59	5.17	3.06	5.01	2.19	3.89	3.27	2.79		**	-	-
	OVARC1001055	14.4	14.98	14.95	7.9	10.31	6.02	5.76	7.98	6.8	**	**	-	-
	OVARC1001062	17.06	13.11	19.77	9.47	7.02	5.92	5.47	7.54	3.76	*	**	-	-
	OVARC1001065	58.8	47.67	46.94	41.39	58.25	31.45	28.27	24.21	23.74	**		-	-
20	OVARC1001068	12.24	9.85	10	9.05	10.45	10.03	4.46	8.42	5.6	*		-	-
	OVARC1001072	5.2	5.85	5.86	2.66	7.45	1.74	3.96	4.57	2.54	*		-	-
	OVARC1001073	7.5	8.58	12.65	4.76	6.4	4.65	5.22	6.96	5.47			-	-
	OVARC1001074	4.7	5.22	6.88	3.02	6.61	3.48	7.1	3.06	2.4			-	-
	OVARC1001078	12.05	11.95	9	4.67	9.88	3.56	7.61	7.71	7.4	*		-	-
	OVARC1001085	11.18	10.66	13.33	5.34	5.76	6.26	7.62	7.57	5.14	**	*	-	-
	OVARC1001086	9.39	8.11	10.75	4.2	10	3.47	6.76	8.44	4.74			-	-
25	OVARC1001091	241.22	186.8	193.81	163.03	271.86	178.86	140.22	106.42	112.84		*	-	-
	OVARC1001092	18.15	15.63	18.59	22.78	28.04	21.17	13.63	16.45	14.87	*		-	-
	OVARC1001104	8.1	6.77	10.2	3.75	7.44	6.44	3.73	7.33	6.12			-	-
	OVARC1001107	107.49	92.87	112.02	98.9	125.4	90.42	58.37	49.66	59.61	**		-	-
	OVARC1001113	4.26	4.3	6.18	3.48	7.31	2.59	2.8	2.95	2.48	*		-	-
30	OVARC1001117	14	17.53	15.78	9.22	10.42	7.27	18.6	16.88	12.72	**		-	-
	OVARC1001118	28.39	26.32	27.08	13.26	13.63	13.64	14.58	18.84	21.16	**	*	-	-
	OVARC1001125	15.09	9.24	18.28	5.27	6.72	6.56	3.81	6.47	3.35	*	*	-	-
	OVARC1001129	8.66	7.06	12.46	3.03	6.25	3.24	5.49	10.45	5.05			-	-
	OVARC1001132	9.08	13.23	15.1	8.86	15.2	9.07	5.57	13.13	8.52			-	-
	OVARC1001138	155.24	193.79	160.3	115.39	149.38	101.68	122.48	164.58	137.03			-	-
35	OVARC1001141	12.99	10.8	12.94	7	9.03	7.57	7.48	10.75	7.3	**	*	-	-
	OVARC1001154	128.63	107.01	106.33	119.46	158.63	83.66	81.42	78.16	83.39		*	-	-
	OVARC1001161	17.68	27.92	21.1	11.55	22.82	12.42	16.84	15.27	15.42			-	-
	OVARC1001162	21.74	16.75	19.82	10.26	11.33	9.72	10.1	12.69	11.14	**	**	-	-
	OVARC1001163	10.91	8.03	10.73	4.37	5.95	4.38	3.95	7.35	4.62	**	*	-	-
	OVARC1001167	38.47	38	43.81	17.29	22.87	18.91	28.74	29.72	36.08	**	*	-	-
40	OVARC1001169	11.94	7.48	10.4	5.85	13.24	4.72	3.88	5.51	4.65	*		-	-
	OVARC1001170	26.22	26.34	31.69	14.46	15.02	12.36	12.5	14.3	11.17	**	**	-	-
	OVARC1001171	143.81	236.48	129.81	114.4	117.18	158.91	77.44	54.36	128.19			-	-
	OVARC1001173	24.91	33.6	36.93	11.93	16.26	13.53	26.95	27.14	25.91	**		-	-
	OVARC1001176	209.32	244.43	234.51	205.75	340.26	228.89	167.09	179.74	200.74	*		-	-
	OVARC1001180	67.2	61.17	66.56	30.38	32.42	26.76	42.84	47.13	54.33	**	*	-	-
45	OVARC1001188	18.84	14.15	17.06	4.37	15.93	5.9	10.16	39.68	8.56			-	-
	OVARC1001200	14.51	7.89	14.82	6.11	7.72	3.65	4.16	15.56	6.11			-	-
	OVARC1001202	37.46	21.56	29.17	10.06	10.43	13.25	17.78	23.14	18.29	*		-	-
	OVARC1001206	6.83	6.97	11.31	3.06	5.96	2.9	2.03	8.52	4.3			-	-
	OVARC1001209	56.31	51.58	60.2	57.91	69.04	54.41	36.32	29.24	28.87	**		-	-
	OVARC1001219	14.82	14.11	12.95	3.65	7.48	4.86	4.34	7.98	3.54	**	**	-	-
50	OVARC1001222	17.11	17.29	18.38	6.61	16.42	9.64	6.56	7.21	5.56	**	**	-	-
	OVARC1001232	34.23	34.49	36.17	16.43	23.42	19.3	24.37	27.16	28.45	**	**	-	-
	OVARC1001240	22.68	22.79	23.45	11.83	13.49	10.07	14	20.54	14.23	**	*	-	-
	OVARC1001243	8.41	5.82	7.86	3.1	7.95	3.99	3.48	18.25	1.41			-	-
	OVARC1001244	43.29	22.42	33.3	20.02	23.25	15.87	15.69	21.46	15.18			-	-
	OVARC1001246	191.8	262.18	216.69	139.76	292.92	181.43	261.49	147.46	197.54			-	-
55	OVARC1001247	33.18	25.43	26.03	8.87	21.81	17.23	8.61	11	7	**		-	-
	OVARC1001260	10.58	9.81	13.5	4.35	12.46	3.56	7.06	8.38	13.07			-	-
	OVARC1001261	10.86	9.17	11.3	5.17	7	3.2	4.94	4.19	3.51	*	**	-	-

Table 464

	OVARC1001268	91.7	87.42	103.18	50.09	61.38	43.24	78.98	90.56	56.28	**	-	-
	OVARC1001270	7.04	6.65	7.37	4.89	4.4	3.37	2.36	3.78	2.58	**	**	-
5	OVARC1001271	19.59	14.31	19.8	9.15	12.99	7.59	10.4	9.45	13.28	*	*	-
	OVARC1001282	9.08	5.35	8.29	3.47	3.89	2.86	2.79	2.02	1.62	*	*	-
	OVARC1001296	8.37	7.88	7.76	3.73	3.83	3.51	3.2	2.52	1.42	**	**	-
	OVARC1001306	8.13	8.36	10.06	2.51	4.13	1.61	1.91	3.24	2.11	**	**	-
	OVARC1001314	6.35	7.88	10.42	5.15	6.88	5.6	5.8	2.73	3.16	*	*	-
	OVARC1001316	9.21	9.19	7.4	3.28	5.15	2.41	2.09	2	2.6	**	**	-
10	OVARC1001329	66.76	60.97	62.75	30.71	36.83	28.85	49.5	54.71	56.06	**	*	-
	OVARC1001330	6.94	7.09	6.08	3.83	3.92	2.72	1.52	3.71	2.62	**	**	-
	OVARC1001336	20.53	13.52	17.21	8.37	10.93	7.02	7.67	13.22	12.66	*	*	-
	OVARC1001338	9.67	3.35	7.39	3.31	2.87	2.49	3.22	2.79	2.03	*	*	-
	OVARC1001339	93.84	87.95	84.06	45.91	66.98	50.22	43.37	46.73	40	**	**	-
	OVARC1001340	6.83	5.17	8.34	3.19	3.73	1.7	2.64	3.21	3.16	*	*	-
15	OVARC1001341	30.38	40.21	33.21	15.81	17.56	16.77	23.98	16.89	14.16	**	*	-
	OVARC1001342	319.96	384.64	298.02	528.73	514.44	449.66	353.76	251.2	152.62	*	+	-
	OVARC1001344	24.05	19.69	20.03	8.91	10.1	7.96	16.66	12.81	15.35	**	*	-
	OVARC1001357	6.41	18.75	6.59	4.08	6.56	3.73	3.75	4.14	3.16	*	*	-
	OVARC1001359	59.32	54.06	31.23	23.17	43.75	45.21	51.59	26.81	37.78	*	*	-
20	OVARC1001360	5.67	4	3.9	1.82	2.67	1.87	1.59	2.07	1.71	*	**	-
	OVARC1001369	7.6	9.8	9.35	5.24	6.16	2.48	5.5	3.41	1.68	*	*	-
	OVARC1001372	9.97	8.14	5.06	1.49	5.79	2.2	2.9	3.07	0.96	*	*	-
	OVARC1001376	27	25.34	21.25	12.73	15.31	10.9	17.23	14.16	15.91	**	*	-
	OVARC1001381	39.84	52.86	35.2	18.78	31.21	17.84	39.83	32.09	35.47	*	*	-
	OVARC1001391	4.35	4.74	4.59	3.41	5.61	3.07	2.93	3.15	1.97	*	**	-
	OVARC1001392	11.01	13.87	11.26	7.11	8.72	6.36	4.32	4.97	3.08	*	**	-
25	OVARC1001399	7.11	9.27	5.73	3.62	4.78	3.62	4.04	3.29	4.7	*	*	-
	OVARC1001417	8.65	8.11	7.05	3.69	5.18	3.15	2.59	2.11	3.11	**	**	-
	OVARC1001419	9.55	7.34	7.59	3.69	5.75	3.4	4.52	2.92	1.58	*	**	-
	OVARC1001425	13.5	5.66	6.59	3.04	5.54	5.43	3.66	1.31	1.7	*	*	-
	OVARC1001436	14.91	13.09	11.35	5.12	5.94	3.89	4.56	3.69	3.48	**	**	-
30	OVARC1001442	5.57	6.26	6.22	3.11	6.56	2.54	5.62	2.71	2.72	*	*	-
	OVARC1001451	30.68	20.35	20.93	10.57	21.04	10.84	19.07	21.71	23.53	*	*	-
	OVARC1001452	16.95	14.67	11.44	7.52	6.15	5.24	7.7	11.36	6.64	**	*	-
	OVARC1001453	7.86	6.06	6.61	4.22	6.52	4.39	4.72	4.86	4.79	*	*	-
	OVARC1001476	20.63	24.57	30.44	15.92	22.32	7.34	11.05	12.16	16.07	*	*	-
	OVARC1001480	7.35	4.8	7.98	3.71	4.84	5.16	2.87	2.08	3.16	*	*	-
35	OVARC1001489	11.25	5.88	6.53	8.16	19.5	4.38	4.69	2.8	2.81	*	*	-
	OVARC1001493	15.28	11.36	13.67	4.88	4.94	2.76	9.11	6.21	8.31	**	*	-
	OVARC1001496	32.05	27.24	23.8	12.75	20.64	11	9.38	5.04	10.85	*	**	-
	OVARC1001499	5.67	6.05	4.7	2.72	3.78	1.85	2.85	4.6	2.57	*	*	-
	OVARC1001506	31.76	25.87	22.22	8.57	18.43	9.44	18.79	15.06	20.59	*	*	-
	OVARC1001509	17.78	13.64	12.09	7.06	8.79	5.76	15.13	14.75	21.14	*	*	-
40	OVARC1001510	8.59	5.24	6.08	3.07	5.95	3.22	7.27	7.67	4.5	*	*	-
	OVARC1001516	10.81	12.88	13.12	5.8	9.08	6.34	8.79	7.64	9.61	*	*	-
	OVARC1001525	7.75	5.51	6.34	3.13	4.32	3.66	4.26	3.77	3.8	*	*	-
	OVARC1001542	30.12	29.23	28.39	14.89	25.03	14.49	18.26	13.2	26.28	*	*	-
	OVARC1001544	27.99	28.47	20.46	12.55	18.48	10.77	36.56	24.05	33.39	*	*	-
	OVARC1001546	6.07	8.98	10.22	3.38	5.35	8.68	3.38	3.45	4.28	*	*	-
45	OVARC1001547	4.36	6.21	6.19	3.96	3.95	1.63	2.77	2.7	2.24	**	*	-
	OVARC1001555	137.04	110.5	136.25	120.36	174.1	119.31	90.66	69.83	70.87	*	*	-
	OVARC1001560	10.54	9.21	9.05	6.2	10.38	4.19	4.33	6.13	2.34	*	*	-
	OVARC1001569	28.34	25.69	28.31	17.71	19.82	21.58	15.15	17.9	15.82	**	**	-
	OVARC1001570	9.57	12.59	13.54	7.21	9.92	6.14	6.01	6.08	8.45	*	*	-
	OVARC1001577	10.2	13.78	13.09	13.59	16.75	9.11	10.56	8.87	5.25	*	*	-
50	OVARC1001578	0	0.27	1.12	0.09	2	0.48	1.37	0.77	0	*	*	-
	OVARC1001596	18.44	38.66	31.49	14.48	23.49	16.88	13.34	13.82	12.27	*	*	-
	OVARC1001600	12.84	12.05	12.79	8.39	9.83	7.52	7.16	10.38	7.31	**	*	-
	OVARC1001607	17.69	15.72	17.94	10.9	18.71	12.05	10.18	16.33	11.6	*	*	-
	OVARC1001610	7.42	7.24	11.17	5.09	7.94	4.34	2.78	4.22	3.55	*	*	-
	OVARC1001611	3.52	5.78	9.33	2.82	5.44	3.47	2.68	4.9	2.76	*	*	-
55	OVARC1001615	7.22	4.15	9.71	3.66	4.51	3.88	4.88	4.91	5.78	*	*	-
	OVARC1001636	5.13	4.74	6.26	4.34	6.6	4.17	6.58	6.24	9.12	*	*	-
	OVARC1001668	40.93	55.07	40.85	20.99	33.29	18.89	40.58	43.41	37.28	*	*	-

Table 465

	OVARC1001702	9.4	5.63	9.29	4.18	2.13	4.1	3.32	3.32	2.46	*	*	-	-
	OVARC1001703	7.15	7.4	12.31	4.47	5.7	4.5	5.85	8.24	3.65				
5	OVARC1001710	18.66	12.34	27.68	8.37	10.17	11.06	8.89	17.12	13.23				
	OVARC1001711	18.7	15.2	21.81	10.78	18.26	9.63	7.19	14.6	8.6	*		-	
	OVARC1001713	106.12	95.89	110.84	111.33	127.16	96.1	59.14	62.39	67.07	**		-	
	OVARC1001725	7.41	8.41	15.02	6.01	22.46	3.17	4.32	4.47	6.9				
	OVARC1001726	9.14	11.76	13.16	5.3	10.91	4.63	7.72	5.13	7.08	*		-	
	OVARC1001727	6.13	4.36	5.44	2.42	3.92	3.64	2.37	4.79	3.09	*		-	
10	OVARC1001731	326.35	314.92	333.21	240.06	116.88	168.02	275.41	235.36	284.79	*	*	-	-
	OVARC1001735	10.45	7.4	10.3	3.26	6.6	5.16	2.85	50.48	3.58	*		-	
	OVARC1001741	51.89	35.06	44.69	30.3	40.05	30.18	29.82	27.49	31.74	*		-	
	OVARC1001745	48.03	48.42	50.14	20.26	24.89	18.25	35.38	41.14	42.19	**	*	-	-
	OVARC1001759	8.58	9.79	14.25	4.9	9.68	2.54	3.21	5.87	3.66	*		-	
	OVARC1001762	15.44	18.76	16.88	4.99	8.2	5.87	5.45	4.57	3.61	**	**	-	-
15	OVARC1001766	83.39	85.91	87.93	59.55	79.17	53.32	53.78	49.12	57.96	**		-	
	OVARC1001767	7.04	5.21	8.42	2.96	5.88	2.78	2.97	1.63	2.74	*		-	
	OVARC1001768	14.52	13.49	18.22	6.31	12.6	7.55	3.97	6.24	6.88	**		-	
	OVARC1001770	26.33	28.28	29.2	13.86	20.54	11.13	6.52	15.1	8.61	*	**	-	-
	OVARC1001776	7.09	4.63	7.55	4.18	5.49	2.76	2.6	3.29	2.71	*		-	
	OVARC1001791	10.39	7.82	10.63	6.37	4.38	3.31	3.58	4.2	5.4	*	**	-	-
20	OVARC1001795	7.98	5.23	12.47	1.59	4.12	3.1	3.31	4.76	7.14			-	-
	OVARC1001798	40.84	44.26	46	20.27	29.31	16.26	30.23	32.18	29.44	**	**	-	-
	OVARC1001802	21.47	24.32	21.73	9.56	17	10.13	13.8	16.34	14.18	*	**	-	-
	OVARC1001805	21.41	25.19	22.93	13.01	23.64	11.53	6.55	5.13	2.96	**		-	-
	OVARC1001807	9.03	4.95	8.69	4.35	5.41	3.66	4.23	6.47	5.73			-	-
25	OVARC1001809	149.46	129.89	172.57	133.13	197.68	130.62	61.18	73.6	73.85	**		-	-
	OVARC1001812	14.81	11.9	18.98	7.06	7.79	6.77	7.18	8.19	7.69	*	*	-	-
	OVARC1001813	16.16	13.4	12.96	5.79	9.88	6.64	9.17	11.83	7.83	*	*	-	-
	OVARC1001820	13.24	13.12	21.66	6.46	7.84	7.81	9.43	11.92	8.26	*		-	-
	OVARC1001828	7.36	8.18	15.13	2.53	4.46	3.16	2.97	2.27	1.93	*		-	-
	OVARC1001833	7.55	8	10.4	3.73	5.88	2.72	2.14	3.67	2.55	*	**	-	-
	OVARC1001839	9.51	8.23	9.47	3.48	6.12	2.44	2.33	1.23	3.33	*	**	-	-
30	OVARC1001846	10.75	6.47	12.96	4.44	5.49	4.43	2.19	5.18	4.87	*		-	-
	OVARC1001849	21.23	22.64	18.18	12.84	14.77	8.26	9.88	17.09	10.17	*	*	-	-
	OVARC1001861	14.15	12.35	14.96	7.86	9.2	6.06	6.33	6.39	8.07	**	**	-	-
	OVARC1001873	10.37	9.13	10.41	3.08	3.81	3.28	3.75	2.72	3.55	**	**	-	-
	OVARC1001879	12.35	13.47	14.5	4.79	6.62	4.85	9.81	8.26	4.82	**	*	-	-
	OVARC1001880	17.95	16.04	17.13	6.7	12.3	6.25	9.7	7.19	8.89	*	**	-	-
35	OVARC1001883	10.68	7.64	9.62	5.66	5.31	4.96	4.5	5.37	3.66	*	**	-	-
	OVARC1001900	21.57	23.04	21.79	9.35	13.16	8.64	4.93	5.9	5.98	**	**	-	-
	OVARC1001901	6.1	3.23	6.27	3.76	3.35	2.44	2	2.36	2.55	*		-	-
	OVARC1001911	5.85	6.08	5.24	3.87	3.1	3.23	3.29	4.37	2.41	**	*	-	-
	OVARC1001916	15.55	14.04	13.05	10.21	8.26	9.44	6.7	7.73	11.27	**	*	-	-
40	OVARC1001928	4.28	4.17	5.98	2.82	2.37	1.14	3.65	1.6	1.43	*	*	-	-
	OVARC1001937	25.6	15.71	13.44	9.48	11.18	11.27	11.49	12.97	7.51			-	-
	OVARC1001940	8.76	8.78	8.37	2.83	3.28	2.84	2.16	2.96	2.02	**	**	-	-
	OVARC1001942	20.24	15.16	17.14	7.55	9.31	5.48	5.3	6.71	7.34	**	**	-	-
	OVARC1001943	29.68	32.41	20.55	12.97	22.62	15.27	4.34	4.72	5.72	**		-	-
	OVARC1001949	14.19	11.75	10.33	3.19	5.85	4.46	2.89	6.47	5.47	**	**	-	-
45	OVARC1001950	13.94	15.9	10.94	6.19	9.29	6.75	8.04	7.58	9.81	*	*	-	-
	OVARC1001952	122.9	130.05	103.73	90.55	135.58	102.89	79.11	70.36	72.15	**	**	-	-
	OVARC1001954	7.45	6.81	6.15	3.11	3.63	2.91	2.32	2.33	2.18	**	**	-	-
	OVARC1001963	12.44	11.79	17.61	6.04	6.32	5.28	6.38	9.47	7.04	*	*	-	-
	OVARC1001983	25.71	30.08	25.81	12.15	15.68	10.47	16.02	11.31	11.87	**	**	-	-
	OVARC1001987	13.81	15.75	12.25	6.15	7.8	4.37	5.37	6.61	4.93	**	**	-	-
50	OVARC1001989	18.41	16.89	13.96	7.74	13.38	8.71	14.94	11.39	11.29	*		-	-
	OVARC1001991	12.31	10.21	10.74	6.47	8.3	7.41	6.69	6.19	5.31	*	**	-	-
	OVARC1002005	33.83	38.39	35.62	17.89	27.06	20.01	28.16	23.73	27.11	**	**	-	-
	OVARC1002044	25.13	24.53	23.58	14.08	17.38	11.27	23.29	17.04	24.49	**		-	-
	OVARC1002046	79.06	107.27	86.51	49.53	77.97	65.8	68.65	65.46	67.43	*		-	-
	OVARC1002050	9.22	6.62	10.19	4.05	4.76	4.15	4.13	2.81	4.5	*	*	-	-
55	OVARC1002058	18.18	16.91	17.55	13.19	18.87	6.99	24.17	22.71	28.4	*	*	-	-
	OVARC1002066	67.02	72.72	47.65	37.79	39.59	35.74	62.17	50.77	51.33	*		-	-
	OVARC1002082	34.4	33.12	24.78	17.13	27.63	15.59	48.32	29.05	33.16			-	-

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	OVARC1002091	18.78	19.82	15.43	10.02	4.76	6.56	9.66	6.62	10.94	**	**	-	-
	OVARC1002092	11.35	7.73	4.3	3.87	5.5	2.76	3.85	4.56	3.79			-	-
	OVARC1002093	11.71	8.5	20.66	4.96	14.44	7.82	5.85	5.4	7.08			-	-
5	OVARC1002094	6.29	6.49	6.65	2.69	4.04	2.24	4.34	3.07	3.08	**	**	-	-
	OVARC1002107	13.48	8.34	12.83	6.06	7.84	6.33	9.41	7.18	12.5	*	*	-	-
	OVARC1002112	26.38	33.01	27.23	12.79	21.35	12.35	12.54	9.82	14.29	*	**	-	-
	OVARC1002126	65.16	69.33	51.38	44.56	51.62	38.84	65.71	52.52	60.89			-	-
	OVARC1002127	6.15	6.37	5.32	1.95	4.41	3.09	5.22	3.46	3.37	*	*	-	-
10	OVARC1002138	5.22	5.32	3.68	5.16	3.08	2.95	2.56	2.26	2.94	*	*	-	-
	OVARC1002143	7.3	4.6	3.7	3.29	5.14	1.8	3.79	3.64	5.8			-	-
	OVARC1002156	14.33	13.86	13.02	10.03	12.28	6.78	8.59	6.29	5.67	**	**	-	-
	OVARC1002158	9.15	5.03	4.65	3.18	3.11	2.41	3.88	2.86	4.37			-	-
	OVARC1002165	67.03	61.86	54.25	23.78	36.97	31.97	46.19	44.24	42.15	**	*	-	-
	OVARC1002176	10.61	13.89	9.02	5.22	6.29	4.46	9.03	7.11	8.09	*	*	-	-
15	OVARC1002178	11.02	11.22	6.01	3.16	5.47	2.82	6.17	3.48	3.57	*	*	-	-
	OVARC1002182	6.32	5.52	5.4	2.92	5.92	3.91	6.46	4.29	5.82			-	-
	OVARC1002185	13.32	14.59	15.01	5.81	10.11	6.86	7.78	7.13	8.82	**	**	-	-
	PLACE1000004	9.74	9.21	11.61	4.85	7.73	5.01	4.83	8.27	4.93	*	*	-	-
	PLACE1000005	27.12	18.01	21.46	13.29	16.54	9.78	14.01	13.75	13.04	*	*	-	-
	PLACE1000006	91.12	57.04	55.23	34.88	52.28	43.96	6.98	11.96	13.8	**	**	-	-
20	PLACE1000007	7.26	8.75	8.28	8.37	10.72	8.06	3.04	5.48	2.7	*	*	-	-
	PLACE1000014	2.23	2.04	4.15	1.42	4	3.02	1.88	2.43	1.7			-	-
	PLACE1000031	25.49	34.88	32.13	13.67	27.22	11.3	27.49	25.37	24.47			-	-
	PLACE1000033	18.11	15.97	17.95	12.01	14.01	16.72	14.29	10.78	15.77			-	-
	PLACE1000040	8.82	8.21	10.8	5.78	10.45	6.53	3.91	7.12	4.69	*	*	-	-
	PLACE1000048	20.38	17.3	18.51	15.36	23.63	12.54	8.78	9.57	6.66	**	**	-	-
25	PLACE1000050	5.4	7.04	6.5	2.42	4.86	4.46	3.72	6.27	1.7			-	-
	PLACE1000061	9.33	8.61	17.26	5.67	11.39	8.55	3.23	9.76	4.54			-	-
	PLACE1000066	6.66	5.77	17.49	7.42	6.83	5.75	5.92	4.2	3.99			-	-
	PLACE1000075	12.56	13.3	14.47	10.46	23.06	11.81	12.58	8.36	7.76			-	-
	PLACE1000078	16.43	18.48	16.12	10.89	9.95	8.28	13.59	13.8	12.7	**	*	-	-
	PLACE1000081	10.24	9.79	10.46	3.99	5.51	5	3.34	5.78	6.89	**	*	-	-
30	PLACE1000086	24.93	18.79	23.44	11.66	12.45	12.8	14.85	17.83	16.54	**	*	-	-
	PLACE1000094	9.77	8.35	20.14	5.83	7.13	8.45	9.11	6.86	4.47			-	-
	PLACE1000101	13.24	13.69	14.14	7.47	11.68	8.08	3.54	8.15	5.57	*	**	-	-
	PLACE1000121	13.12	18.46	20.42	15.19	20.27	14.52	7.88	10.58	8.77	*	*	-	-
	PLACE1000133	9.91	9.72	12.83	7.9	8.22	8.5	5.09	6.11	8.25	*	*	-	-
	PLACE1000142	9.88	8.89	10.42	4.19	7.46	3.72	7.05	4.74	5.82	*	**	-	-
35	PLACE1000146	26.84	30.96	24.74	12.94	22.4	10.59	30.36	28.2	29.92	*	*	-	-
	PLACE1000163	7.41	5.19	10.36	3.1	5	4.08	3.16	3.43	3.29	*	*	-	-
	PLACE1000172	27.22	20.45	29.16	10.4	14.2	9.22	8.64	12.45	11.02	**	**	-	-
	PLACE1000181	113.9	71.51	73.22	49.28	64.78	42.83	38.76	53.7	55.02			-	-
	PLACE1000184	17.72	15.27	19.8	11.79	14.01	13.85	9.11	9.87	10.76	*	**	-	-
	PLACE1000185	16.19	14.48	17.72	7.66	7.1	6.34	4.1	6.59	4.27	**	**	-	-
40	PLACE1000198	9.65	11.81	15.71	11.09	11.55	8.4	6.38	19.65	7.03			-	-
	PLACE1000213	6.26	6.05	11.46	4.09	6.36	3.94	3.17	3.29	3.78			-	-
	PLACE1000214	9.15	11.17	11.68	8.73	8.08	4.64	3.79	6.02	5.34	**	**	-	-
	PLACE1000220	25.57	22.54	23.7	11.03	13.14	7.79	10.18	10.81	12.09	**	**	-	-
	PLACE1000231	14.42	18.43	23.26	5.64	9.79	6.68	7.36	7.88	9.82	*	*	-	-
45	PLACE1000236	7.58	6.02	8.68	1.98	6.24	5.31	3.56	10.92	5.78			-	-
	PLACE1000245	26.52	25.91	22.56	9.19	16.74	15.36	8.75	9.5	10.2	*	**	-	-
	PLACE1000246	45.69	36.58	50.55	14.83	17.16	15.14	8.9	11.47	10.62	**	**	-	-
	PLACE1000258	9.85	11.52	11.33	3.16	7.83	3.08	2.46	5.51	4.37	*	**	-	-
	PLACE1000288	14.3	14.29	20.76	4.5	8.13	8.1	4.73	7.76	5.77	*	*	-	-
	PLACE1000292	22.65	21.9	21.53	9.54	18.93	11.23	12.98	16.24	12.38	*	**	-	-
50	PLACE1000302	24.34	18.15	25.79	8.82	16.47	8.9	10.89	16.25	19.37	*	*	-	-
	PLACE1000304	9.25	6.15	7.74	5.54	8.18	3.68	3.39	11.18	2.7			-	-
	PLACE1000308	15.07	8.66	14.03	6.88	10.38	7.58	8.62	8.08	9.22			-	-
	PLACE1000309	50.33	32.12	45.32	24.2	31.82	23.11	35.7	38.12	29.88			-	-
	PLACE1000312	7.8	7.45	13.99	4.65	6.15	3.95	7.1	6.14	4.22			-	-
	PLACE1000330	37.2	43.13	26.2	23.56	30.84	17.96	20.8	28.35	14.01			-	-
55	PLACE1000332	19.72	22.93	22.77	9.1	18.25	13.71	15.08	10.86	13.37	*	**	-	-
	PLACE1000347	18.65	20.7	25.21	9.08	28.96	11.34	16.06	14.13	12.46	*	*	-	-
	PLACE1000351	4.55	3.12	7.2	2.8	3.17	2.14	6.68	4.21	4.87			-	-

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	PLACE1000374	4.36	4.25	6.34	4.3	3.67	2.84	1.94	3.1	1.77	*	-
	PLACE1000380	16.1	6.91	17.82	9.8	10.53	4.49	5.18	5.02	6.92		
5	PLACE1000383	6.36	4	6.16	2.37	2.92	2.52	2.89	0.95	0.87	*	-
	PLACE1000397	11.59	7.26	11.9	2.79	5.06	5.01	6.09	6.59	6.48	*	-
	PLACE1000401	9.04	6.59	7.42	3.23	3.26	3.54	3.28	2.6	2.94	**	-
	PLACE1000406	13.08	8.33	14.95	2.59	5.95	3.66	6.86	10.26	6.27	*	-
	PLACE1000412	8.51	7.48	7.35	3.42	4.96	3.44	3.84	4.02	2.52	**	-
	PLACE1000420	18.93	23.33	27.28	7.24	14.78	9.32	4.07	6.78	6.75	*	-
10	PLACE1000421	17.83	12.09	14.21	5.67	5.38	4.01	4.24	5.77	6.73	**	-
	PLACE1000423	9.91	10.66	9.25	5.17	5.46	3.16	3.23	3.33	2.82	**	-
	PLACE1000424	6.41	4.46	8.86	3.52	3.38	1.84	2.63	2.91	2.34	*	-
	PLACE1000430	9.9	7.48	10.47	5.49	5	3.45	3.57	3.09	3.55	*	-
	PLACE1000433	8.1	6.1	7.11	1.95	4.44	2.14	2.34	1.88	2.11	*	-
	PLACE1000435	28.95	26.53	24.32	14.09	14.79	9.09	16.84	11.65	12.23	**	-
15	PLACE1000437	13.7	9.76	13.69	6.32	11.96	9.08	8.69	6.76	4.42	*	-
	PLACE1000442	4.21	4.33	5.54	1.97	3.93	1.28	2.62	4.3	2.3		-
	PLACE1000444	8.39	8.02	5.47	3.23	8.73	7.32	3.64	5.13	5.23		-
	PLACE1000453	8.24	8.08	7.4	2.64	6.34	3.96	5.87	6.05	5.1	*	-
	PLACE1000456	9.14	8.93	7.88	4.6	6.83	3.55	4.93	5.65	3.15	*	-
	PLACE1000465	29.59	27.02	24.71	10.66	16.38	9.53	7.25	7.03	4.61	**	-
20	PLACE1000481	10.19	8.45	9.18	6.24	5.2	4.46	5.55	2.41	2.95	**	-
	PLACE1000492	14.54	13.99	15.18	6.98	17.38	5.81	5.24	4	6.05	**	-
	PLACE1000508	8.74	6.29	6.02	2.46	6.75	1.48	4.68	3.01	3.04	*	-
	PLACE1000512	4.85	3.74	3.65	2.37	3	3.01	2.27	2.44	1.75	*	-
	PLACE1000540	12.96	8.47	7.79	4.5	9.85	7.03	5.75	9.5	3.54		-
	PLACE1000541	10.16	15.98	11.44	6.25	17.26	10.37	7.65	6.38	9.85		-
25	PLACE1000546	13.1	11.96	11.32	7.18	10.25	10.48	6.08	5.2	6.25	**	-
	PLACE1000547	8.49	5.52	7.86	5.49	10.6	14.98	5.43	2.62	3.64	*	-
	PLACE1000560	22.37	15.31	18.14	8.36	10.85	7.86	6.26	3.35	3.9	*	-
	PLACE1000562	8.22	7.18	9	4.62	4.33	3.02	4.18	2.13	2.7	**	-
	PLACE1000564	17.41	14.24	11.35	10.42	10.44	10.34	8.72	6.17	6.09	*	-
	PLACE1000583	11.44	8.04	7.49	4.72	4.9	3.91	5.24	5.95	5.26	*	-
30	PLACE1000587	7.15	6.59	3.7	3.14	3.88	4.15	3.78	3.64	4.07		-
	PLACE1000588	18.91	11.92	9.8	5.65	7.81	8.36	8.6	5.83	6.87		-
	PLACE1000596	11.7	13.56	11.65	8.47	13.84	9.08	10.58	5.53	9.44		-
	PLACE1000599	9.76	11.08	9.94	6.95	10.5	6.09	4.81	2.43	3.16	**	-
	PLACE1000605	16.65	12.34	15.55	9.49	9.68	6.14	6.32	3.07	5.49	*	-
	PLACE1000610	13.13	11.57	11.01	8.74	7.05	4.41	9.69	6.2	4.65	*	-
35	PLACE1000611	44.34	42.43	32.52	26.13	31.67	19.73	63.56	39.23	50.7		-
	PLACE1000626	7.16	6.36	6.63	3.54	3.14	2.93	5.25	5.57	5.32	**	-
	PLACE1000633	7.75	6.07	5.61	4.09	5.95	4.33	4.51	3.72	5.54		-
	PLACE1000636	9.18	4.57	3.73	3.4	5.99	3.07	2.89	4.22	5.33		-
	PLACE1000653	13.52	15.36	9.28	7.56	11.63	7.5	6.22	4.09	7.58	*	-
	PLACE1000656	16.45	24.27	20.78	6.6	13.98	8.95	13.7	10.63	9.13	*	-
40	PLACE1000663	17.59	14.23	11.72	6.71	8	7.43	15.75	11.07	16.5	*	-
	PLACE1000706	22.58	27.08	16.29	14.32	16.15	9.77	10.6	7.13	11.87	*	-
	PLACE1000712	15.91	18.32	12.16	10.41	18.03	9.89	15.21	13.33	14.12		-
	PLACE1000716	9.51	6.38	10.32	4.38	8.28	5.91	5.52	6.18	6.28		-
	PLACE1000740	62.65	63.87	75.82	66.13	88.56	67.41	54.02	47.28	39.42	*	-
	PLACE1000748	21.69	20.13	21.77	15.61	19.67	14.26	16.35	17.23	19.62	*	-
45	PLACE1000749	8.09	6.77	9.49	5.21	7.14	4.97	2.01	3.41	3.49	**	-
	PLACE1000751	5.85	6.89	7.76	3.42	4.79	3.39	2.03	3.31	2.82	*	-
	PLACE1000755	17.27	23.58	23.84	13.28	21.64	9.25	15.55	10.98	9.19	*	-
	PLACE1000769	3.3	5.09	3.02	3.66	5.56	3.4	3.76	2.68	2.93		-
	PLACE1000778	43.25	43.09	44.83	22.77	18.03	27.54	20.87	24.08	21.65	**	-
	PLACE1000785	31.35	17.11	31.03	9.35	9.07	8.25	11.86	8.82	7.46	*	-
50	PLACE1000786	5.99	3.18	7.12	2.4	4.01	1.88	2.45	4.94	6.92		-
	PLACE1000793	62.95	70.84	86.12	74.56	80.1	68.58	59.03	72.61	48.69		-
	PLACE1000795	170.82	165.32	165.81	123.39	175.42	137.1	104.41	82.02	95.27	**	-
	PLACE1000798	34.34	30.96	28.31	19.04	23.22	14.81	22.05	22.97	28.25	*	-
	PLACE1000812	16.41	17.23	19.15	11.98	12.41	10.24	15.41	13.57	12.8	**	-
	PLACE1000823	25.51	22.51	19.45	15.2	17.94	10.61	13.45	15.88	12.99	*	-
55	PLACE1000825	9.78	4.9	7.94	5.02	3.89	3.86	4.94	3.55	4.1		-
	PLACE1000838	37.15	32.03	40.12	17.98	18.59	17.35	19.92	15.21	15.97	**	-



Table 468

	PLACE1000841	7.87	7.94	8.8	7.6	12.23	10.86	5.33	4.89	4.56	**	-
	PLACE1000843	16.04	20.1	24.44	8.07	13.38	10.99	7.02	9.18	7.59	* **	-
	PLACE1000849	5.43	7.23	9.29	4.99	5.8	4.19	3.26	3.96	2.16	*	-
5	PLACE1000856	209.98	229.07	253.03	209.39	256.66	183.75	147.93	119.29	119.6	**	-
	PLACE1000863	16.12	16.52	27.27	10.41	12.7	10.18	13.62	16.56	12.54		-
	PLACE1000876	16.98	21.81	24.49	11.69	18.7	12.24	19.45	15.76	20.21		-
	PLACE1000899	225.37	148.25	253.61	106.96	112.25	68.21	130.08	130.64	120.26	*	-
	PLACE1000907	11.9	9.88	11.62	4.52	6.53	6.56	4.58	7.2	4.58	** **	-
10	PLACE1000909	219.81	187.78	224.87	129.92	144.43	97.69	209.39	207.09	231	**	-
	PLACE1000912	4.53	4.31	6.11	1.98	4.16	2.65	2.79	1.25	1.4	*	-
	PLACE1000914	13.65	11.52	16.16	6.76	9.53	7.59	5.22	5.53	2.91	* **	-
	PLACE1000918	13.18	11.98	16.82	5.88	9.64	8.52	8.09	14.67	8.16	*	-
	PLACE1000927	6.93	7.22	10.54	4.38	6.32	3.11	4.55	3.47	4.34	*	-
	PLACE1000931	9.5	7.15	10.84	7.43	6.57	4.4	3.12	4.27	3.39	**	-
15	PLACE1000944	12.44	7.29	10.38	5.9	6.11	4.93	5.15	6.79	5.9	*	-
	PLACE1000948	15.03	15	16.76	7.56	11.29	7.62	5.5	9.31	6.83	** **	-
	PLACE1000958	5.27	4.99	7.38	2.51	5.7	3.99	1.85	6.23	4.43	.	-
	PLACE1000972	8.38	5.92	10.49	3.65	7.53	4.25	3.77	5.86	4.19		-
	PLACE1000977	11.29	8.32	15.95	5.04	5.25	7.02	2.5	10.48	3.14		-
	PLACE1000979	13.89	7.86	9.86	3.34	7.43	5.36	4.42	5.93	8.8		-
20	PLACE1000986	30.12	30.53	34.37	25.05	28	23.07	15.94	15.63	18.52	* **	-
	PLACE1000987	19.26	23.97	21.74	13.41	21.5	10.91	16.26	13.02	12.47	*	-
	PLACE1001000	4.37	7.15	10.87	3.42	3.04	2.14	2.69	2.93	3.43		-
	PLACE1001007	6.61	2.96	5.44	2.81	6.06	3.04	2.78	3.89	2.07		-
	PLACE1001010	9.46	6.18	10.43	5.02	5.52	3.2	5.18	3.73	3.91	* *	-
	PLACE1001015	7.99	5.3	8.03	6.19	7.65	4.6	3.26	3.31	2.3	*	-
25	PLACE1001016	17.51	11.26	16.44	6.61	7.04	6.42	3.95	3.27	2.38	* **	-
	PLACE1001022	14.42	12.9	14.76	4.97	7.37	5.56	7.11	8.21	7.4	** **	-
	PLACE1001024	11.18	12.76	12	5.14	10.39	4.2	4.43	3.88	2.99	**	-
	PLACE1001036	105.59	109.4	58.51	52.8	114.22	89.89	113.54	86.02	137.21		-
	PLACE1001038	9.63	8.86	10.53	4.68	5.51	5.33	2.98	5.92	7.98	**	-
	PLACE1001048	7.22	3.94	6.41	5.19	5.21	3.49	3.25	3.01	2.83	*	-
30	PLACE1001054	17.12	18.15	23	21.95	14.11	11.96	6.57	6.82	6.81	**	-
	PLACE1001062	7.69	5.86	7.49	3.03	6.18	4.98	5.6	1.77	1.91	*	-
	PLACE1001063	11.82	13.23	13.09	8.34	8.29	7.45	3.15	3.88	2.78	** **	-
	PLACE1001076	17.46	15.27	22.58	9.61	12.22	10.09	9.5	6.93	10.2	* *	-
	PLACE1001081	8.04	6.12	10.01	3.34	3.8	3.43	2.11	2.93	3.84	* *	-
35	PLACE1001088	1077.5	1434.9	897.35	706.08	898.84	874	835.46	1189	1173.1		-
	PLACE1001092	41.3	35.7	38.59	14.58	20.22	12.39	28.15	30.94	33.71	** *	-
	PLACE1001098	27.39	22.29	18.87	5.94	11.11	13.11	8.05	8.36	7.66	* **	-
	PLACE1001100	12.04	12.72	14.57	7.69	8.66	8.94	7.95	8.39	9.98	** *	-
	PLACE1001104	10.26	8.03	11.29	7.1	4.81	4.72	5.84	4.16	5.12	* *	-
	PLACE1001114	19.87	21.11	13.11	5.44	7.05	8.22	2.52	3.44	2.49	* **	-
	PLACE1001118	16.04	15.17	13.54	9.49	13.49	10.14	5.69	6.26	3.99	**	-
40	PLACE1001123	11.13	9.28	10.37	3.01	8.71	7.98	2.59	2.22	5.96	**	-
	PLACE1001136	9.63	8.36	10.4	4.16	7.83	10.1	11.4	6.43	4.95		-
	PLACE1001144	22.24	18.89	18.24	5.11	10.59	8.11	16.88	14.03	17.77	**	-
	PLACE1001147	9.73	14.79	11.54	7.5	5.73	6.98	3.33	4.01	4.07	* **	-
	PLACE1001148	16.26	12.46	13.41	8.25	12.02	6.54	11.91	10.71	11.91		-
45	PLACE1001159	5.83	2.18	9.14	5.55	4.85	2.75	3.37	5.16	1.28		-
	PLACE1001168	6.64	5.38	5	2.78	4.75	2.95	4.38	2.12	2.36	*	-
	PLACE1001171	17.87	14.63	16.06	9.77	9.8	9.82	9.4	7.26	9.58	** **	-
	PLACE1001183	24.74	23.48	20.67	15.23	15.9	11.49	12.71	7.91	11.36	** **	-
	PLACE1001185	8.91	7.62	8.02	4.21	7.14	4.11	5.56	3.21	2.94	* **	-
	PLACE1001201	16.85	15.12	18.88	10.04	10.01	9	9.33	10.2	8.94	** **	-
	PLACE1001229	15.21	12.61	13.94	9.57	11.26	12.86	8.81	8.47	8.63	**	-
50	PLACE1001231	13.31	19.61	12.2	8.58	26.11	14.91	13.39	13.43	8.59		-
	PLACE1001238	6.16	6.8	5.78	3.46	6.45	5.07	3.57	1.84	3.63	**	-
	PLACE1001241	7.81	12.55	8.77	4.56	8.8	2.29	6.75	1.69	5.45		-
	PLACE1001242	15.15	9.43	9.57	6.93	8.62	5.05	5.42	2.86	4.67	*	-
	PLACE1001247	18.19	25.95	17.43	7.95	13.13	8.09	9.19	7.53	8.42	* *	-
55	PLACE1001250	27.19	16.6	15.62	14.1	21.99	16.23	13.87	8.35	7.98		-
	PLACE1001257	5.07	4.07	3.3	6.21	3.6	2.05	3.64	3.01	2.62		-
	PLACE1001272	11.61	5.34	6.33	4.73	5.73	6.35	5.18	6.02	6.39		-

Table 469

	PLACE1001279	20.66	18.57	13.78	9.04	11.1	8.58	6.47	4.72	6	*	**	-	-
	PLACE1001280	13.73	13.22	15.63	11.44	10.47	6.22	11.2	7.22	13.37				
5	PLACE1001294	6.1	5.02	7.03	2.98	5.24	4.37	4.18	2.25	4.36				
	PLACE1001295	9.52	6.34	5.73	4.11	5.38	4.8	4.66	3.72	5.16				
	PLACE1001300	110.16	136.11	96.73	55.88	77.8	69.78	127.86	93.28	123.22	*		-	-
	PLACE1001304	22.83	23.36	19.82	13.09	11.18	12.56	8.64	8.3	14.22	**	**	-	-
	PLACE1001311	22.93	29.08	18.33	13.63	11.98	8.91	18.15	14.72	19.17	*		-	-
	PLACE1001323	5.15	4.73	4.73	2.24	3.77	2.07	2.58	2.19	2.91	*	**	-	-
10	PLACE1001325	6.51	4.36	2.66	3.73	4.01	0.79	3.09	1.19	1.69				
	PLACE1001340	12.71	9.9	7.91	5.93	10.17	3.62	8.49	5.49	7.3				
	PLACE1001344	7.26	5.61	6.3	3.22	4.87	2.35	5.26	3.25	5.47	*		-	-
	PLACE1001351	10.82	9.34	9.06	4.54	4.04	2.83	5.68	5.94	6.17	**	**	-	-
	PLACE1001366	16.46	16.32	12.21	7.96	10.61	8	10.02	6.25	6.08	*	*	-	-
	PLACE1001377	10.72	11.21	8.12	8.14	11.01	6.18	7.03	5.07	5.96	*	*	-	-
15	PLACE1001383	8.47	7.74	7.34	7.01	7.31	9.16	4.38	4.51	5.67	**		-	-
	PLACE1001384	5.51	3.13	4.87	2.26	4.64	2.12	1.25	1.77	2.28	*		-	-
	PLACE1001387	3.71	2.66	5.28	2.18	4.13	3.15	1.31	2.35	1.76				
	PLACE1001395	2.97	1.83	2.95	0.9	3.39	0.94	2.26	2.27	0.93				
	PLACE1001399	43.48	36.95	39.47	25.54	39.02	28.91	11.4	22.35	12.37	**		-	-
	PLACE1001401	8.85	12.13	13.82	4.1	7.84	5.28	5.15	5.58	4.43	*	*	-	-
20	PLACE1001407	6.42	8.95	6.88	3.19	5.6	3.04	3.23	2.38	2.93	*	**	-	-
	PLACE1001412	4.65	3.97	3.56	2.52	8.46	2.63	3.1	2.07	4.54				
	PLACE1001414	10.05	7.04	8.23	5.26	7.99	5.53	4.37	7.32	4.41				
	PLACE1001416	18.05	14.76	21.75	8.21	15.69	7.54	12.66	14.94	10.13				
	PLACE1001433	10.35	9.53	10.38	6.47	9.26	5.35	4.33	6.8	5.78	**		-	-
	PLACE1001440	15.78	8.2	12.06	9.97	10.51	7.97	4.11	5.02	3.17	*		-	-
25	PLACE1001456	5.95	5.2	7.6	4.32	4.51	3.68	3.46	6.83	4.09				
	PLACE1001464	7.17	7.13	12.08	4.46	13.26	4.47	2.92	3.59	4.74	*		-	-
	PLACE1001468	5.87	5.89	7.51	4.49	7.19	3.15	4.98	3.89	5.45				
	PLACE1001484	1.93	2.72	3.26	3.17	5.24	2.3	3.27	1.7	4.61				
	PLACE1001500	5.55	5.43	7.47	3.4	4.88	4.91	3.43	5.41	4.22				
30	PLACE1001502	10.13	6.73	10.36	4.95	5.09	3.9	4.24	7.4	4.55	*		-	-
	PLACE1001503	18.94	15.22	23.11	6.62	14.6	9.42	9.19	12.06	11.69	*	*	-	-
	PLACE1001505	14.33	11.5	15.08	6.94	9.91	8.35	5.05	5.21	4.29	*	**	-	-
	PLACE1001513	9.76	7.84	14.27	4.51	12.01	5.72	4.02	6.18	4.23	*	*	-	-
	PLACE1001516	12.33	10.13	14.29	6.5	8.85	7.91	5.4	6.92	5.78	*	*	-	-
	PLACE1001517	22.78	28.63	26.65	15.6	22.43	12.49	25.55	23.34	19.3				
	PLACE1001523	4.85	4.2	4.25	1.46	3.64	2.44	3.61	4.37	5.02	*		-	-
35	PLACE1001526	15.63	6.8	12.63	5.9	5.99	8.7	6.38	8.18	11.68				
	PLACE1001534	13.26	10.83	12.93	4.83	7.66	4.05	5.45	22.34	4.41	**		-	-
	PLACE1001536	12.35	10.07	11.17	5.95	10.51	7.42	7.47	10.57	7.69				
	PLACE1001545	7.78	9.31	13.04	5.48	7.28	3.94	2.6	3.19	3.02	*		-	-
	PLACE1001551	11.64	13.9	20.49	7.15	9.98	9.21	7.74	8.57	7.76				
40	PLACE1001564	5.33	7.01	11.33	5.64	6.02	6.32	3.9	3.45	6.93				
	PLACE1001570	8.81	7.17	13.9	5.61	7.77	3.89	5.34	9.04	4.82				
	PLACE1001571	30.16	29.44	29.76	18.26	25.49	9.78	12.94	16.78	20.12	**		-	-
	PLACE1001595	49.16	53.02	65.48	26.84	29.86	29.28	20.63	17.19	22.48	**	**	-	-
	PLACE1001602	17.93	20.86	26.59	9.8	15.66	12.03	25.23	43.22	27.97	*		-	-
	PLACE1001603	16	11.85	13.84	6.26	7.5	5.17	10.37	25.06	14.43	**		-	-
45	PLACE1001608	313.79	262.26	299.49	248.62	194.58	212.51	255.55	259.42	224.33	*		-	-
	PLACE1001610	34.83	33.4	50.14	21.2	19.91	21.09	16.25	16.43	15.58	*	*	-	-
	PLACE1001611	16.58	14.57	13.52	8.27	15.57	6.53	5.96	3.97	4.4	**		-	-
	PLACE1001629	15.86	14.27	16.52	6.92	12.73	5.97	9.05	9.4	8.15	*	**	-	-
	PLACE1001632	15.6	14.68	11.95	5.15	11.43	6.76	4.77	3.59	2.95	*	**	-	-
	PLACE1001634	10.26	9.24	12.21	4.71	7.41	4.15	3.93	4.97	4.63	*	**	-	-
50	PLACE1001637	29.75	28.67	36.48	16.79	19.46	16.75	23.41	26.79	22.84	**		-	-
	PLACE1001640	28.95	18.03	24.89	16.93	21.97	12.71	8.91	11.62	9.32	*	*	-	-
	PLACE1001655	8.24	5.56	6.83	4.09	4.25	2.93	2.13	3.7	1.34	*	*	-	-
	PLACE1001672	8.94	18.15	13.66	4.81	11.29	4.01	5.1	4.86	14.47				
	PLACE1001676	39.58	47.75	47.96	23.16	26.28	21.98	31.5	32.99	28.58	**	**	-	-
	PLACE1001683	7.54	6.2	11.62	2.16	4.9	3.68	2.93	3.43	3.72	*		-	-
55	PLACE1001691	10.4	6.5	11.03	4.05	13.34	5.07	4.28	5.31	2.34	*		-	-
	PLACE1001692	3.74	6.24	4.95	3.58	3.97	3.4	3.88	3.22	2.42				
	PLACE1001705	11.04	7.84	13.66	10.64	5.83	6.51	5.2	5.34	3.62	*		-	-

Table 470

	PLACE1001716	13.89	6.26	12.85	5.68	7.61	3.53	6.17	4.09	5.84				
	PLACE1001720	20.23	23.86	21.86	17.41	19.42	17.41	10.68	9.34	8.72	*	**	-	-
	PLACE1001728	21.97	14.68	15.36	7.87	10.67	10.96	10.39	5.46	5.25	*	*	-	-
5	PLACE1001729	7.28	8.78	9.32	4.24	3.8	3.29	3.96	2.03	2.64	**	**	-	-
	PLACE1001739	18.08	18.75	18.08	11.34	16.38	11.72	10.55	8.26	8.75	*	**	-	-
	PLACE1001740	60.6	61.56	51.85	52.21	47.26	48.39	41.09	28.81	37.51	**	**	-	-
	PLACE1001745	155.43	121.46	146.04	80.69	92.15	78.37	106.17	102.99	100.25	**	*	-	-
	PLACE1001746	12.07	9.53	11.89	5.08	6.32	6.38	6.4	7.42	7.33	**	**	-	-
10	PLACE1001748	20.09	15.85	13.57	8.98	10.94	8.77	6.58	3.28	8.51	*	*	-	-
	PLACE1001753	8	5.61	7.17	2.42	2.42	2.08	3.13	1.99	2.1	**	**	-	-
	PLACE1001760	16.81	13.89	14.09	5.89	6.99	11.7	8.68	6.91	7.81	*	**	-	-
	PLACE1001767	7.75	5.83	9.04	3.14	5.58	2.6	2.92	2.72	1.2	*	**	-	-
	PLACE1001771	6.86	8.78	6.5	5.1	22.6	7.92	6.68	3.61	1.79				
	PLACE1001775	10.25	8.72	8.89	5.62	4.98	4.94	5.79	4.51	5.33	**	**	-	-
15	PLACE1001777	55.87	33.24	46.38	19.69	26.37	22.71	26.45	22.89	29.83	*	*	-	-
	PLACE1001781	7.62	4.99	5.26	2.61	3.65	3.27	2.46	2.47	3	*	*	-	-
	PLACE1001783	8.67	3.54	4.17	1.75	1.71	2.1	2.79	1.87	2.94				
	PLACE1001786	10.13	7.03	6.19	5.28	7.53	4.48	4.3	2.57	2.1	*	*	-	-
	PLACE1001788	9.62	8.2	7.79	2.13	3.02	3.67	3.87	1.93	2.04	**	**	-	-
	PLACE1001795	12.86	13.57	11.91	3.76	6.82	4.77	2.63	4.68	2.65	**	**	-	-
20	PLACE1001799	15.19	12.46	11.73	6.44	10.22	5.84	11.66	9.72	12.14	*	*	-	-
	PLACE1001810	19.9	17.99	15.3	8.61	16.81	15.9	19.42	15.41	19.52				
	PLACE1001817	9.2	10.03	10.24	5.73	12.6	6.09	4.49	4.6	5.41	**	**	-	-
	PLACE1001821	8.12	9.65	9.24	5.34	5.81	5.22	5.09	4.7	3.49	**	**	-	-
	PLACE1001836	14.74	10.74	8.7	7.59	8.81	4.93	6.55	5.02	5	*	*	-	-
	PLACE1001844	8.12	5.11	7.16	1.96	5.82	2.85	3.18	2.67	1.5	*	*	-	-
25	PLACE1001845	13.24	11.82	8.77	7.59	7.48	3.74	4.84	2.2	2.42	**	**	-	-
	PLACE1001858	9.06	7.62	7.23	4.16	3.93	3.22	7.66	3.49	3.91	**	**	-	-
	PLACE1001869	5.88	6.08	4.84	3.37	6.33	2.79	3.14	2.33	2.54	**	**	-	-
	PLACE1001890	14.71	9.13	7.02	7.27	10.27	7.92	6.48	7.41	7.57				
	PLACE1001897	21.63	13.66	12.13	7	10.58	7.47	6.17	7.42	7.81	*	*	-	-
	PLACE1001902	25.9	24.36	23.51	11.89	19.02	13.01	23.32	19.87	28.51	*	*	-	-
30	PLACE1001904	4.8	4.58	4.71	4.2	4.02	2.48	4	1.2	3.18				
	PLACE1001907	11.99	11.09	12.77	4.36	7.42	4.55	5.4	2.81	6.4	**	**	-	-
	PLACE1001910	17.55	13	11.78	10.79	10.86	3.78	8.75	3.34	6.51	*	*	-	-
	PLACE1001912	16.99	20.76	18.01	10.56	10.89	7.91	12.99	8.39	12.1	**	*	-	-
	PLACE1001918	10.35	11.16	9.4	5.64	8.81	4.76	8.14	4.97	7.28	*	*	-	-
35	PLACE1001920	3.62	1.84	1.09	2.06	2.78	2.12	0.89	2.37	2.67				
	PLACE1001928	33.91	29.31	26.67	16.07	24.12	10.81	21.1	17.01	25.49	*	*	-	-
	PLACE1001930	13.35	8.41	9.7	5.16	9.65	8.14	5.7	4.65	9.73				
	PLACE1001949	83.24	64.21	68.63	50.5	75.89	66.37	92.93	85.41	92.12	*	*	-	+
	PLACE1001959	8.04	5.93	10.64	4.56	6.1	3.95	4.33	5.06	5.07				
	PLACE1001969	8.52	5.51	4.9	2.62	4.36	2.04	3.84	2.43	3.2				
40	PLACE1001974	16.8	19.43	17.28	9.77	10.54	5.8	6.98	5.43	6.49	**	**	-	-
	PLACE1001981	11.42	11.82	8.18	7.19	8.78	5.34	7.9	5.15	5.59	*	*	-	-
	PLACE1001983	9.22	8.71	12.62	5.54	7.95	6.32	7.39	5.63	6.5				
	PLACE1001989	27.47	22.77	28.46	13.3	18.78	12.49	12.35	16.17	10.35	*	**	-	-
	PLACE1002004	8.73	7.48	9.33	6.79	9.77	5.49	6.57	6.13	4.33	*	*	-	-
	PLACE1002008	10.54	8.97	12.2	6.77	11.46	10.25	3.74	7.33	3.11	*	*	-	-
45	PLACE1002015	12.37	10.1	13.36	6.64	10.58	8.15	7.89	14.69	9.22				
	PLACE1002044	18.51	15.04	21.28	6.21	11.74	9.02	6.6	10.2	12.21	*	*	-	-
	PLACE1002046	3.16	4.19	5.33	2.46	6.56	3.13	3.41	1.95	2.73				
	PLACE1002052	4.29	2.34	2.47	1.89	4.94	1.55	4.09	3.83	3.62				
	PLACE1002066	4.5	3.49	6.01	2.29	3.79	2.93	3.54	3.65	2.92				
	PLACE1002072	6.4	5.54	6.91	3.66	5.16	4.7	3.95	6.12	2.07	*	*	-	-
50	PLACE1002073	12.89	11.8	16.36	10.66	11.47	7.97	5.88	5.64	4.74	**	**	-	-
	PLACE1002080	18.63	22.97	23.1	12.21	18.28	13.9	13.6	15	15.2	*	*	-	-
	PLACE1002081	23.13	27.18	27.3	14.91	18.06	14.86	16.14	20.45	20.82	**	*	-	-
	PLACE1002090	11.49	14.13	12.79	4.54	7.24	4.65	4.29	3.51	5.75	**	**	-	-
	PLACE1002095	5.46	5.54	4.46	5.08	11.47	7.41	4.99	5.27	7.8				
	PLACE1002102	8.22	13.54	14.09	8.11	14.1	7.74	9.04	16.2	14.08				
55	PLACE1002109	17.45	10.93	19.35	12.82	7.15	7.61	9.22	12.81	9.47				
	PLACE1002115	6.48	5.79	9.09	2.86	4.39	3.56	3.32	3.75	3.44	*	*	-	-
	PLACE1002119	3.98	5.58	7.03	2.87	6.47	3.2	3.72	4.12	4.62				

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	PLACE1002140	8.54	9.5	15.02	4.83	8.98	6.88	2.91	6.38	4.28	*	-
	PLACE1002150	27.18	33.61	30.05	18.28	25.09	23.98	12.7	14.95	15.29	* **	-
5	PLACE1002153	173.25	217.95	284.37	422.44	424.65	291.99	262.39	242.27	220.74	*	+
	PLACE1002157	7.42	5.99	8.84	3.16	6.59	2.52	3.59	2.5	5.34	*	-
	PLACE1002163	9.5	10.33	17.51	4.81	9.35	4.71	6.61	8.07	8.46		-
	PLACE1002168	406.19	407.62	562.52	187.65	80.86	161.78	377.56	231.11	429.49	**	-
	PLACE1002170	23.07	18.68	22.02	9.58	14.95	10.12	4.39	9.86	5.14	* **	-
	PLACE1002171	118.3	86.27	82.5	107.58	135.49	96.73	60.2	59.88	56.63	*	-
10	PLACE1002180	12.53	12.02	17.4	11.66	15.77	12.8	11.61	13.11	10.84		-
	PLACE1002184	76.94	90.34	67.89	42.12	70.86	43.23	20.87	27.8	29.07	**	-
	PLACE1002200	5.64	6.44	11.56	2.73	4.37	3.29	2.8	2.86	3.48		-
	PLACE1002205	5.47	5.6	9.09	2.28	6.05	2.28	3.51	2.6	1.9	*	-
	PLACE1002213	11	9.68	7.88	3.37	8.5	3.33	5.73	2.26	4.33	*	-
	PLACE1002219	30.67	24.88	33.1	11.7	18.03	17.11	5.85	10.58	12.01	* **	-
15	PLACE1002227	5.38	6.1	6.51	3.19	5.95	3.48	3.48	8.52	2.37		-
	PLACE1002253	7.93	4.46	10.74	3.51	5.52	2.84	4.18	3.76	3.24		-
	PLACE1002256	10.19	4.49	11.42	3.66	5.44	3.17	1.81	4.48	5.21		-
	PLACE1002259	6.68	9.14	16.04	2.32	8.56	3.26	2.76	5.45	13.61		-
	PLACE1002285	15.21	20.2	16.69	10.84	18.4	10.19	8.14	7.95	6.12	**	-
	PLACE1002301	11.84	7.92	13.87	3.5	5.75	4.91	3.98	8.04	4.04	*	-
20	PLACE1002310	9.3	8.21	7.36	1.56	5.25	3.56	3.57	2.81	3.34	* **	-
	PLACE1002311	6.47	4.93	7.42	3.5	5.65	2.75	2.49	2.97	1.32	*	-
	PLACE1002319	23.43	17.43	19.83	7.96	14.77	10.74	10.78	13.23	11.96	* *	-
	PLACE1002329	7	4.89	6.25	3.06	3.73	2.65	1.68	2.85	1.64	* **	-
	PLACE1002333	16.35	14.3	13.78	9.29	11.1	10.53	8.49	6.32	5.51	** **	-
	PLACE1002342	14.18	15.16	20.35	5.96	11.78	6.24	4.58	8.15	6.84	* **	-
25	PLACE1002343	9.54	8.56	16.64	3.45	4.23	3.21	2.86	1.85	3.18	*	-
	PLACE1002355	8.47	11.34	12.23	4.32	8.27	5.65	2.98	2.78	4.19	* **	-
	PLACE1002358	6.25	5.01	7.85	2.33	4.09	1.66	2.63	1.27	2.04	* **	-
	PLACE1002359	94.59	64.3	78.26	42.47	26.68	29.68	51.17	53.76	59.14	**	-
	PLACE1002374	11.64	7.08	11.73	4.84	7	4.57	3.23	3.62	3.66	*	-
30	PLACE1002376	10.84	6.42	7.57	6.56	6.2	4.93	8.79	6.04	6.62		-
	PLACE1002379	14.26	10.82	12.17	6.95	8.14	6.98	5.34	4.44	3.6	** **	-
	PLACE1002386	7.89	3.52	7.76	1.91	2.26	2.95	2.4	2.03	2.94		-
	PLACE1002395	17.68	20.65	22.77	6.45	9.6	7.04	4.3	2.63	2.39	** **	-
	PLACE1002399	9.59	8.59	10	4	5.08	4.5	2.83	2.8	3.46	** **	-
	PLACE1002407	14.84	17.54	12.15	4.78	9.29	6.64	5.32	3.95	6.87	* **	-
35	PLACE1002433	18.89	14.68	17.11	8	12.47	6.81	12.74	12.61	16.41	*	-
	PLACE1002437	6.94	5.04	7.88	4.77	3.72	3.8	1.97	3.5	4.81	*	-
	PLACE1002438	8.47	9.76	8.93	6.11	6.03	2.52	3.69	3.74	4.55	* **	-
	PLACE1002446	61.22	60.91	53.35	35.08	40.23	34.18	52.04	54.81	48.63	**	-
	PLACE1002447	50.06	38.25	48.75	30.92	38.93	28.36	26.38	23.5	18.47	**	-
	PLACE1002450	8.68	4.18	8.14	2.56	3.07	3.06	3.45	3.27	1.66	*	-
40	PLACE1002462	20.62	21.36	20.69	8.83	13.93	7.63	14.57	11.43	17.67	** *	-
	PLACE1002465	6.3	10.21	4.45	2.37	6.62	4.25	3.41	1.81	3.99		-
	PLACE1002474	8.9	10.86	8.01	5.33	8.28	3.73	2.36	3.29	4.22	**	-
	PLACE1002477	10.23	12.91	13.31	8.45	8.55	11.89	12.5	6.6	14.96		-
	PLACE1002493	5.44	5.3	4.56	4.99	2.63	4.56	5.81	1.5	1.86		-
	PLACE1002497	9.23	6.42	6.03	5.54	3.94	3.18	4.77	3.01	2.42	*	-
45	PLACE1002499	28.78	23.91	22.93	13.59	10.19	9.79	16.45	7.7	12.71	** *	-
	PLACE1002500	9.83	6.14	9.08	4.34	6.18	2.49	5.4	1.41	3.42	*	-
	PLACE1002514	57.39	61.96	51.39	31.16	36.96	26.56	53.37	39.47	40.85	**	-
	PLACE1002518	7.97	7.12	4.14	3.92	5.36	3.52	3.58	1.82	2.65	*	-
	PLACE1002529	14.35	10.84	8.84	6.09	12.13	6.95	3.37	3.6	3.7	**	-
	PLACE1002532	6.92	6.97	5.35	4.94	5.47	4.76	4.62	5.36	3.19		-
50	PLACE1002536	9.3	12.32	10.38	5.35	4.64	5.41	7.12	5.91	4.59	** *	-
	PLACE1002537	7.11	8.85	6.37	5.99	5.45	6.3	4.25	3	3.53	**	-
	PLACE1002539	7.92	6.45	7.28	2.97	5.46	7.97	2.07	2.63	4.82	*	-
	PLACE1002547	14.65	14.48	12.7	9.78	11.89	6.33	5.01	4.47	6.38	**	-
	PLACE1002571	27.85	40.71	17.49	16.84	14.71	12.01	13.72	7.48	9.31		-
	PLACE1002578	11.7	10.9	10.03	8.42	11.59	6.31	11.22	5.24	9.68		-
55	PLACE1002583	12.45	8.98	8.93	4.7	6.58	5.37	8.92	7.31	10.13	*	-
	PLACE1002591	14.95	9.64	30.65	14.99	14.6	1.99	10.65	10.99	7.37		-
	PLACE1002598	134.77	135.3	115.7	105.05	127.67	81.8	77.51	75.71	89.77	**	-

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	PLACE1002604	8.27	3.87	5.87	4.56	4.62	4.03	4.08	2.97	4.32				
	PLACE1002612	7.74	6.07	5.48	4.79	5.04	4.26	2.87	1.84	4.68	*		-	
5	PLACE1002625	8.98	7.38	5.26	3.91	6.23	4.29	4.63	2.42	5.37				
	PLACE1002638	10.71	6.82	9.31	4.39	4.89	3.67	4.86	2.91	4.12	*	*	-	-
	PLACE1002655	20.05	17.22	10.12	8.15	9.62	8.61	4.45	4.4	4.69	*			
	PLACE1002665	2.85	2.11	1.16	1.34	3.18	0.77	1.36	1.74	1.47				
	PLACE1002685	40.11	36.95	37.09	21.27	32.67	18.25	35	28.12	33.61	*		-	
	PLACE1002692	10.4	8.99	7.49	3.22	6.32	3.77	7.61	3.76	6.83	*		-	
10	PLACE1002714	16.77	11.38	9.27	6.42	9.93	4.45	11.48	11.6	13.87				
	PLACE1002721	75.97	53.95	40.28	41.2	57.12	33.39	36.52	34.39	33.55				
	PLACE1002722	22.13	17.93	14.21	5.69	15.15	8.22	22.92	15.1	22.19				
	PLACE1002726	7.85	7.95	6.76	3.03	4.47	1.55	5.1	2.92	3.72	**	**	-	-
	PLACE1002756	11.64	12.77	9.75	6.41	12.37	7.42	9.89	7.27	9.98				
	PLACE1002768	14.14	13.66	17.41	6.96	8.91	8.35	8.23	12.96	13.43	**		-	
15	PLACE1002772	11.58	12.05	13.28	5.34	9.18	5.42	7.04	6.7	6.74	*	**	-	-
	PLACE1002775	3.87	3.22	3.82	4.05	3.19	0.98	1.6	5	2.48				
	PLACE1002780	8.73	8.1	8.81	2.91	6.16	2.92	3.15	6.37	4.26	*	*	-	-
	PLACE1002782	15.09	16.8	18.22	6.13	9.37	3.95	11.73	13.03	12.96	**	*	-	-
	PLACE1002794	41.39	43.8	46.4	31.76	35.79	20.44	25	22.44	21	*	**	-	-
	PLACE1002795	26.08	25.22	25.57	11.54	12.89	13.19	17.32	17.1	14.49	**	**	-	-
20	PLACE1002811	45.78	45.63	45.46	25.72	32.56	23.15	17.78	22.39	22.66	**	**	-	-
	PLACE1002815	15.82	13.42	19.22	7.58	7.46	5.69	11.61	7.34	8.29	**	*	-	-
	PLACE1002816	4.86	2.68	5.34	8.68	10.83	8.75	3.44	3.56	2.71	**		+	
	PLACE1002822	12.2	11.93	11.07	6.15	11.75	10.16	7.41	12.24	8.12				
	PLACE1002833	9.14	11.66	12.33	5.57	7.46	7.07	4.75	8.35	4.08	*	*	-	-
	PLACE1002834	6.07	5.81	8.84	3.09	3.53	4.27	1.8	2.98	2.41	*	*	-	-
25	PLACE1002835	58.22	46.91	63.08	49.95	62.63	44.56	42.91	35.34	35.49	*		-	-
	PLACE1002839	20.38	22.46	21.91	8.31	11	7.79	15.07	14.42	13.25	**	**	-	-
	PLACE1002851	24.75	15.11	15.09	7.91	14.09	8.63	20.69	22.56	25.92				
	PLACE1002853	17.64	15.34	22.8	5.52	6.45	6.1	6.28	8.18	4.17	**	**	-	-
	PLACE1002881	24.86	14.92	26.75	13.38	16.28	13.04	14.2	20.46	17.04				
	PLACE1002901	14.25	14.06	17.74	6.8	8.96	8.66	8.78	4.53	4.12	**	**	-	-
30	PLACE1002904	18.88	26.12	22.33	14.53	22.41	13.83	9.21	13.95	10.54	*		-	-
	PLACE1002905	4.41	8.93	12	2.54	8.87	4.07	3.83	5.83	4.18				
	PLACE1002908	13.22	16.1	15.63	15.4	12.99	11.14	8.47	5.63	8.35	**		-	-
	PLACE1002911	10.97	9.2	9.02	6.7	11.96	7.89	5.04	4.71	5.5	**		-	-
	PLACE1002941	15.88	10.4	17.73	6.14	8.22	5.77	14.58	18	12.89	*		-	-
	PLACE1002950	23.65	20.5	17.79	16.96	17.44	5.49	24.31	14.61	17.93				
35	PLACE1002955	5	5.58	7.97	3.29	6.71	3.61	3.06	3.96	2.19	*		-	-
	PLACE1002958	88.1	92.98	103.56	90.74	91.81	78.41	59.31	53.18	47.63	**		-	-
	PLACE1002962	3.13	4.33	9.15	0.9	4.01	2.47	0.8	0.76	1.87				
	PLACE1002967	35.4	50.14	51.41	21.55	34.48	29.97	31.98	26.21	37.19				
	PLACE1002968	4.93	4.01	6.65	3.18	3.05	1.93	2.74	2.46	2.95	*	*	-	-
	PLACE1002976	59.32	76.52	110.97	52.57	103.04	77.15	42.49	35.2	48.8				
40	PLACE1002991	6.98	4.41	7.57	2.11	5.56	3.18	2.77	5.13	6.66				
	PLACE1002993	13.31	16.98	19.44	6.54	17.73	10.56	9.53	20.73	7.89				
	PLACE1002996	33.54	26.83	25.33	24.84	36.88	25.62	15.5	28.74	20.59				
	PLACE1003010	5.97	5.37	8.7	4.68	3.28	4.88	3.8	4.41	3.12				
	PLACE1003025	19.13	20.65	29.6	10.42	22.81	11.62	14.02	22.04	12.57				
	PLACE1003027	4.81	4.57	8.94	2.3	4.47	0.55	3.14	5.14	2.31				
45	PLACE1003044	13.45	13	13.59	5.33	7.16	6.74	3.17	4.52	2.59	**	**	-	-
	PLACE1003045	16.2	13.12	16.27	11.21	14.83	10.08	8.58	7.66	5.73	**		-	-
	PLACE1003052	15.26	13.65	16.48	5.57	12.75	6.74	15.39	12.34	13.31	*		-	-
	PLACE1003083	26.86	32.06	29.46	16.75	26.42	15.92	23.57	20.32	20.14	*		-	-
	PLACE1003085	11.46	7.5	13.4	5.76	9.36	4.66	6.66	6.58	5.57				
	PLACE1003092	13.44	11.78	13.5	8.16	11.43	7.08	8.07	7.87	6.9	*	**	-	-
50	PLACE1003097	6.17	6.46	16.32	3.05	5.89	3.08	3.13	5.88	4.77				
	PLACE1003100	36.23	40.39	38.56	32.04	32.87	28.75	26.62	23.05	18.02	*	**	-	-
	PLACE1003108	11.34	8.75	20.83	7.36	13.72	5.15	3.96	4.75	4.82				
	PLACE1003115	7.34	6.75	7.41	3.32	6.32	2.75	1.65	0.73	1.92	**		-	-
	PLACE1003120	12.49	11.78	16.03	7.63	9.21	4.76	11.87	11.32	7.77	*		-	-
	PLACE1003135	7.09	5.05	7.89	3.8	2.81	2.79	2.64	3.42	1.44	*	*	-	-
55	PLACE1003136	68.81	77.15	81.76	65.96	72.38	60.39	44.74	39.52	47.1	**		-	-
	PLACE1003141	9.02	4.98	11.12	4.59	4.76	5.17	4.62	5.32	3.84				

Table 473

	PLACE1003145	12.65	9.94	12.43	3.74	5.65	4.53	6.94	8.05	4.35	**	*	-	-
	PLACE1003147	26.48	26.41	26.84	11.9	16.38	12.11	16.22	18.19	14.71	**	**	-	-
5	PLACE1003153	10.51	10.55	11.78	2.97	6.22	4.35	5.52	7.01	3.61	**	**	-	-
	PLACE1003163	8.08	7.83	4.23	1.17	6.16	2.64	1.92	2.39	2.29		*	-	-
	PLACE1003172	11.82	10	15.87	6.77	13.23	9.45	7.97	8.79	7.46			-	-
	PLACE1003174	15.37	9.05	12.28	9.12	4.76	2.9	4.07	4.06	4.97		*	-	-
	PLACE1003176	5.18	3.89	6.16	2.81	3.31	2.68	2.96	3.04	2.06	*	*	-	-
	PLACE1003181	9.36	6.29	8.52	1.78	2.48	3.42	2.28	1.97	1.19	**	**	-	-
10	PLACE1003184	23.08	18.89	20.23	9.3	11.84	12.17	13.78	13.13	10.63	**	**	-	-
	PLACE1003190	8.27	8.79	9.4	3.25	4.54	3.59	4.27	2.82	4.68	**	**	-	-
	PLACE1003200	9.79	7.56	9.39	2.41	6.08	2.83	2.42	1.72	3.3	*	**	-	-
	PLACE1003205	126.72	130.26	137.95	113.01	122.92	109.79	99.16	86	89.92	*	**	-	-
	PLACE1003209	2.16	16.18	2.48	0.47	10.18	0.97	2.71	3.36	3.16			-	-
	PLACE1003214	22.58	19.76	20.17	11.54	15.74	15.47	11.96	12.4	14.5	*	**	-	-
15	PLACE1003229	11.83	11.81	10.65	4.92	4.84	3.94	7.34	5.53	5.38	**	**	-	-
	PLACE1003238	8.67	6.17	6.07	3.06	1.84	4.56	1.99	2.39	2.01	*	**	-	-
	PLACE1003249	64.47	55.31	48	33.64	42.61	31.3	33.47	28.86	18.94	*	*	-	-
	PLACE1003256	18.3	25.49	17.26	10.97	13.36	18.51	17.3	11.04	4.08			-	-
	PLACE1003258	49.07	49.35	44.47	34.46	50.32	29.75	23.51	18.19	23.43	**		-	-
	PLACE1003279	10.3	14.58	7.71	5.42	10.68	4.9	6.28	3.11	11.78			-	-
20	PLACE1003294	21.78	16.35	23.18	6.69	11.5	6.25	12.62	8.7	9.35	*	*	-	-
	PLACE1003296	42.17	40.86	35.97	38.78	41.16	32.25	23.79	17.48	17.34	**		-	-
	PLACE1003297	49.69	50.94	40.2	15.98	31.29	21.96	19.68	11.27	24.02	*	**	-	-
	PLACE1003302	25.32	31.25	29.06	9.93	15.98	12.55	24.23	16.15	20.93	**	*	-	-
	PLACE1003334	185.2	152.92	141.49	146.89	154.17	125.41	110.94	69.78	76.19	*		-	-
	PLACE1003337	48.98	43.27	41.6	31.2	33.91	22.01	17.95	11.14	16.35	*	**	-	-
25	PLACE1003342	33.19	37.72	34.03	17.42	45.69	20.1	23.58	17.03	23.28	**		-	-
	PLACE1003343	6.84	5.22	10.11	7.16	4.99	3.86	5.46	2.81	3.26			-	-
	PLACE1003344	11.02	7.76	2.99	1.99	8.29	3.43	7.57	2.34	3.75			-	-
	PLACE1003353	19.54	21.69	17.69	8.25	8.74	5.2	10.76	10.8	13.5	**	**	-	-
	PLACE1003361	44.83	37.64	33.66	33.83	37.42	32.13	26.59	20.73	23.72	*		-	-
	PLACE1003366	12	18.42	15.82	7.6	12.12	4.37	10.36	5.92	5.45	*		-	-
30	PLACE1003369	4.81	3.43	3.93	0.94	3.73	1.31	1.63	1.07	0.84	**		-	-
	PLACE1003372	13.64	7.8	10.54	3.88	10.47	3.36	4.52	1.77	3.52	*		-	-
	PLACE1003373	8.88	8.18	9.38	3.94	3.76	0.99	4.29	2.31	3.38	**	**	-	-
	PLACE1003375	22.91	23.46	16.65	11.55	17.67	11.28	29.27	13.77	19.27			-	-
	PLACE1003378	1.92	0.43	0.47	1.45	0.86	1.22	0.77	0.97	0.76			-	-
	PLACE1003383	15.75	12.58	10.55	7.3	8.49	3.81	2.43	7.46	2.15	*	*	-	-
35	PLACE1003394	19.46	13.29	10.26	6.3	12.66	5.09	11.98	10.6	17.14			-	-
	PLACE1003401	8.87	6	5.04	3.66	4.75	2.93	5.66	3.3	5.47			-	-
	PLACE1003405	7.6	8.07	5.91	3.39	5.27	4.58	4.12	1.47	2.3	*	*	-	-
	PLACE1003407	10.24	7.49	7.79	2.43	3.28	2.12	4.16	2.37	3.5	**	**	-	-
	PLACE1003420	7.71	5.57	6.39	3.78	6.36	2.21	2.89	1.88	2.26	**		-	-
40	PLACE1003428	6.55	5.9	4.45	2.19	4.16	0.9	3.49	2.31	8.87	*		-	-
	PLACE1003432	51.6	69.55	75.77	36.76	44.92	44.22	42.27	64.14	52.55	*		-	-
	PLACE1003438	1.98	2.35	1.48	2.21	4.73	1.43	4.08	0.93	0.7			-	-
	PLACE1003452	3.01	3.41	4.3	1.8	3.84	2.08	2.34	2.25	1.64	*		-	-
	PLACE1003454	3.87	4.87	5.58	2.54	4.5	3.92	2.57	2.43	1.33	*		-	-
	PLACE1003455	2.92	2.41	4.04	1.6	1.9	1.64	1.75	0.8	1.88	*	*	-	-
	PLACE1003456	2.36	4.17	3.63	2.06	10.37	2.22	2.4	1.94	0.64			-	-
45	PLACE1003460	4.76	5.09	4.73	4.08	6	2.64	6.38	3.46	2.92			-	-
	PLACE1003478	6.15	2.11	2.66	1.92	3.96	2	5.39	1.91	4.04			-	-
	PLACE1003484	6.84	8.17	8.98	4.36	6.73	3.1	4.12	4.68	4.63	**		-	-
	PLACE1003493	83.14	41.9	88.74	60.01	72.45	45.07	64.55	71.53	53.96			-	-
	PLACE1003503	7.36	5.03	5.29	1.12	3.91	3.51	2.36	3.64	2.4	*		-	-
50	PLACE1003505	32.2	45.22	38.51	20.24	36.17	23.66	24.44	34.5	27.01			-	-
	PLACE1003516	7.02	7.8	7.71	2.88	5.85	3.76	2.24	2.98	3.86	*	**	-	-
	PLACE1003519	4.06	1.81	5.55	3.83	3.85	1.91	2.58	1.64	0.34			-	-
	PLACE1003520	12.72	16.96	9.15	8.71	16.58	8.45	4.85	6.39	5.22	*	*	-	-
	PLACE1003521	14.95	10.13	14.17	6.02	7.53	5.56	6.77	8.38	4.75	*	*	-	-
	PLACE1003525	20.17	19.13	25.59	15.85	14.55	12.63	20.97	18.71	22.36	*		-	-
55	PLACE1003528	35.65	25.12	43.38	21.63	30.38	28.64	16.02	24.64	18.65			-	-
	PLACE1003529	11.19	16.69	21.6	20.8	16.66	31.76	18.24	15.7	15.44			-	-
	PLACE1003537	3.15	4.02	8.21	3.24	3.64	3.89	1.76	2.65	2.32			-	-

Table 474

	PLACE1003549	16.21	19.52	27.74	11.72	18.71	13.09	12.65	15.02	13.74			
	PLACE1003553	12.63	20.69	18.89	10.17	18.28	8.51	8.12	9.44	8.9	*	-	
	PLACE1003566	9.49	12.35	9.77	7.53	10.49	7.08	3.77	4.66	6.9	*	-	
5	PLACE1003568	5.3	4.9	19.78	3.8	7.59	3.87	5.3	6.3	4.21			
	PLACE1003573	32	27.25	37.46	17.52	23.28	16.23	15	18.28	19.13	* **	-	-
	PLACE1003575	66.07	60.03	70.99	42.8	62.9	38.6	75.17	59.46	62.58			
	PLACE1003583	8.33	4.65	6.88	3.47	6.26	5.07	2.38	3.4	4.1	*	-	
	PLACE1003584	12.09	10.66	18.02	7.17	8.48	19.2	8.54	7.15	2.79			
10	PLACE1003592	29.77	33.55	28.89	21.34	26.31	15.85	12.59	8.49	12.12	* **	-	-
	PLACE1003593	7.15	3.54	8.27	3.34	2.24	1.83	3.11	5.19	5.45			
	PLACE1003594	7.18	8.49	9.31	5.03	6.61	3.38	4.99	3.18	2.37	* **	-	-
	PLACE1003596	5.11	3.13	4.25	2.82	5	3.14	3.75	4.1	3.76			
	PLACE1003598	31.57	29.75	31.55	14.81	20.6	17.31	5.31	17.81	7.34	** **	-	-
	PLACE1003602	6.51	2.47	7.47	1.84	4.91	0.98	2.4	4.6	2.56			
15	PLACE1003605	10	6.14	7.29	5.28	8.85	3.75	6.45	5.07	2.93			
	PLACE1003611	15.94	16.54	24.25	11	9.1	12.46	10.14	10.62	12.83	*	-	
	PLACE1003618	7.78	7.74	12.1	3.49	6.12	2.68	4.58	5.29	6.93	*	-	
	PLACE1003625	14.19	21.53	18.27	11.53	22.81	17.82	13.8	9.54	11.86			
	PLACE1003626	11.55	14.38	14.6	5.94	11.97	7.26	4.57	4.49	2.04	**	-	
	PLACE1003630	3.86	4.65	3	4.62	4.58	3.02	3.68	3.68	1.66			
20	PLACE1003635	8.33	7.29	10.19	5.35	5.59	4.6	3.51	4.48	4.17	* **	-	-
	PLACE1003638	4.33	3.09	4.93	3.86	6.02	2.38	2.01	3.6	1.35			
	PLACE1003644	35.03	24.77	24.25	19.14	20.11	17.95	8.77	10.6	6.97	**	-	
	PLACE1003654	75.56	74.57	74.52	77.61	72.17	67	35.39	33.92	31.06	**	-	
	PLACE1003656	7.81	5.19	8.37	3.06	4.32	3.8	1.16	1.63	2.96	* **	-	-
	PLACE1003660	16.25	21.8	21.11	12.32	17.1	13.06	14.44	12.72	12.99	*	-	
25	PLACE1003669	12.05	8.79	12.65	4.93	9.33	7.48	3.9	4.69	4.41	**	-	
	PLACE1003670	110.15	83.05	76.99	55.55	52.05	50.36	48.6	63.39	52.6	* *	-	-
	PLACE1003671	11.47	3.49	4.69	7.13	4.59	4.35	3.71	2.69	2.22			
	PLACE1003697	9.65	10.83	16.05	9.21	10.08	8.25	6.51	4.97	6.76	*	-	
	PLACE1003704	10.59	7.92	10.14	6.15	6.81	6.51	4.22	3.63	3.86	* **	-	-
	PLACE1003709	9.06	8.99	10.78	5.34	6.7	5.47	3.53	3.36	1.83	** **	-	-
30	PLACE1003711	28.05	31.28	32.33	21.12	31.77	27.07	16.12	16.73	14.21	**	-	
	PLACE1003723	27.32	34.97	28.91	18.16	26.8	21.24	17.63	17.4	10.81	**	-	
	PLACE1003724	29.33	36.12	25.65	19.94	34.26	21.71	26.66	13.83	15.71			
	PLACE1003737	8.24	6.31	9.31	2.89	4.06	2.72	3.31	2.56	3.28	** **	-	-
	PLACE1003738	5.02	4.71	5.03	8.76	2.78	9.43	1.8	2.2	2.93	**	-	
	PLACE1003742	17.85	18.69	20.82	14.24	7.57	8.14	10.49	8.98	8.16	* **	-	-
35	PLACE1003744	5.48	2.82	3.4	0.66	1.04	1.08	1.74	1.94	0.38	*	-	
	PLACE1003758	23.32	22.73	21.79	9.9	15.26	16.38	15.29	14.75	13.36	* **	-	-
	PLACE1003760	40.1	57.96	44.54	28.85	37.15	22.14	11.09	14.54	11.41	**	-	
	PLACE1003762	65.35	58.09	77.98	35.3	88.27	46.92	46.48	32.75	38.3	*	-	
	PLACE1003765	93.01	107	70.69	55.75	97.14	46.35	33.33	44.53	44.51	*	-	
40	PLACE1003768	34.07	21.23	23.34	10.87	13.6	6.67	25.2	17.43	28.3	*	-	
	PLACE1003771	5.38	5.57	5.27	3.47	7.27	2.71	1.77	1.77	2.44	**	-	
	PLACE1003772	5.63	7.96	4.89	1.17	7.74	2.12	3.12	2.24	2.28	*	-	
	PLACE1003783	5.15	3.84	3.95	2.36	3.83	1.92	1.65	1.17	0.84	**	-	
	PLACE1003784	5.59	6.96	5.68	2.81	4.01	2.73	3.1	2.42	1.88	** **	-	-
	PLACE1003788	34.98	33.59	27.31	19.49	15.1	21.27	12.2	5.92	10.73	* **	-	-
	PLACE1003795	26.48	33.02	23.72	12.5	28.84	12.28	23.33	16.94	16.45			
45	PLACE1003827	9.74	8.51	10.55	21.41	16.48	10.33	5.7	3.14	1.91	**	-	
	PLACE1003833	14.14	10.78	12.27	5.74	8.62	5.66	5.59	6.29	7.37	* **	-	-
	PLACE1003839	259.31	241.18	222.89	217.52	173.45	205.17	163.55	139.4	151.61	**	-	
	PLACE1003845	69.72	60.2	118.04	40.89	28.14	26.89	48.08	43.86	45.73			
	PLACE1003850	9.53	11.45	9.42	3.3	8.43	5.88	6.51	3.87	5.97	*	-	
50	PLACE1003852	32.49	28.32	26.73	21.76	30.69	26.63	18.45	14.12	17.92	**	-	
	PLACE1003858	19.9	13.83	13.86	8.03	12.82	5.24	7.08	4.19	7.71	*	-	
	PLACE1003861	40.22	66.3	33.51	12.47	57.37	18.72	33.23	18.67	19.13			
	PLACE1003864	34.51	84.76	122.59	61.83	70.16	55.03	69.32	56.31	42.37			
	PLACE1003870	9.43	6.5	5.9	2.94	3.32	3.4	5.69	3.86	5.74	*	-	
	PLACE1003885	10.07	6.76	3.91	3.5	6.22	3.91	3.49	3.72	6.33			
55	PLACE1003886	12.66	12.76	10.57	6.28	9.54	3.51	13.66	8.88	12.28	*	-	
	PLACE1003888	15.48	13.6	17.45	7.94	12.36	6.23	14.56	8.73	9.07	*	-	
	PLACE1003892	6.59	4.85	8.21	5.64	7.14	2.75	3.77	2.15	4.24			

Table 475

	PLACE1003900	9.05	5.59	5.53	3.41	9.33	4.49	4.41	6.87	4.79				
	PLACE1003902	9.43	6.06	7.46	2.35	3.67	1.76	3.96	1.76	3.05	*	*	-	-
	PLACE1003903	17.33	19.36	14.55	9.42	10.87	10.03	9.08	6.56	7.77	**	**	-	-
5	PLACE1003915	14.67	18	11.19	12.64	10.36	9.98	8.5	5.29	8.8		*	-	-
	PLACE1003918	10.58	6.62	8.73	7.34	5.29	3.45	7.05	5.69	4.94				
	PLACE1003923	11.24	8.95	4.47	2.95	4.6	4.65	4.65	3.26	3.87				
	PLACE1003932	9.02	5.88	4.39	2.18	9.39	4.8	6.3	4.31	5.14				
	PLACE1003936	11.92	7.46	8.85	2.47	4.23	4.36	9.51	9.11	10.65	*		-	-
10	PLACE1003966	11.6	10.3	9.01	5.2	6.1	4.37	6.77	5.83	6.22	**	**	-	-
	PLACE1003968	4.88	5.07	4.71	0.66	3.28	0.8	3.51	1.87	0.72	*	*	-	-
	PLACE1004018	4.89	2.45	2.55	4.7	8.1	2.19	2.99	1.85	1.89				
	PLACE1004020	12.24	14.87	17.86	7.54	8.19	5.65	7.35	9.99	10.06	*	*	-	-
	PLACE1004028	2.49	1.88	2.35	1.78	7.14	2.28	1.01	1.49	0.82		*	-	-
	PLACE1004034	6.5	4.91	7.64	2.7	5.45	2.86	3.71	3.07	1.75		*	-	-
15	PLACE1004042	5.94	2.98	4.53	2.04	4.08	3.55	3.58	3.9	2.95				
	PLACE1004078	6.26	4	5.13	2.35	3.57	1.92	1.94	3.66	4.31	*		-	-
	PLACE1004103	4.16	6.73	8.68	2.05	3.45	2.36	1.89	0.91	3.01	*	*	-	-
	PLACE1004104	0.6	1.12	3	1.89	7.2	1.01	1.88	2.79	1.52				
	PLACE1004113	0.85	1	0.69	0.62	4.18	1	1.54	0.77	1.59				
20	PLACE1004114	12.27	11.63	12.84	9.04	6.13	6.15	17.17	8.3	11.59	**		-	-
	PLACE1004118	25.56	29.6	34.14	10.69	22.13	12.84	16.2	19.15	19.4	*	*	-	-
	PLACE1004128	6.77	8.44	8.16	3.47	7.23	7.78	2.81	3.08	3.14		**	-	-
	PLACE1004130	9.36	4.88	10.96	8.2	7.53	9.87	4.28	6.71	6.1				
	PLACE1004149	2.51	2.43	6.21	2.78	5.35	2.6	3.3	3.26	2.01				
	PLACE1004156	13.06	9.08	13.29	7.39	11.05	6.74	9.05	9.4	10.62				
25	PLACE1004160	20.97	19.94	23.27	14.03	30.3	7.33	16.97	16.65	14.66	*		-	-
	PLACE1004161	7.06	8.18	8.06	5.83	7.98	4.77	4.77	4.44	4.99		**	-	-
	PLACE1004166	41.1	39.11	42.06	19.36	22.19	21.87	24.56	28.32	30.02	**	**	-	-
	PLACE1004168	32.92	30.07	31.55	16.2	15.66	13.35	21.23	25.32	27.11	**	*	-	-
	PLACE1004170	14.53	21.92	19.94	10.32	12.85	10.61	11.03	18.31	8.2	*		-	-
	PLACE1004178	2.75	3.62	3.97	2.55	6.19	3.35	0.34	1.55	0.72		**	-	-
30	PLACE1004183	36.95	43.53	45.99	27.78	51.84	25.82	21.25	25.43	23.92		**	-	-
	PLACE1004197	5.75	5.24	7.84	2.14	4.97	3.74	3.04	2.49	3.28		*	-	-
	PLACE1004199	21.75	27.66	12.12	12.42	24.13	11.64	10.47	10.88	12.46				
	PLACE1004203	11	13.62	10.81	4.23	10.81	6.59	10.74	11.32	12.32				
	PLACE1004242	20.49	16.48	21.11	6.81	6.93	13.71	6.23	11.27	9.24	*	**	-	-
	PLACE1004249	6.73	11	11.25	4.47	10.26	6.2	5.79	8.22	6.09				
35	PLACE1004255	32.98	36.35	38.9	17.52	26.48	21.84	27.95	27.86	29.02	*	*	-	-
	PLACE1004256	12.54	10.51	15.03	5.99	5.51	6.23	3.84	5.04	3.23	**	**	-	-
	PLACE1004257	3.25	14.27	11.31	3.36	8.12	8.15	2.7	9.49	4.03				
	PLACE1004258	11.89	26.37	21.62	8.76	18.18	12.25	12.69	13.44	9.66				
	PLACE1004270	8.17	8.34	11.88	6.47	6.77	11.76	8.27	3.74	6.39				
	PLACE1004272	1.52	1.56	3.17	1.04	3.51	0.46	1.56	1.06	1.78				
40	PLACE1004273	23.31	38.14	20.87	17.38	14.34	7.01	17.2	17.07	20.56				
	PLACE1004274	12.13	13.19	15.06	6.12	12.19	6.04	6.47	11.78	6.75				
	PLACE1004277	18.65	17.3	16.15	12.2	21.29	13	13.46	15.12	20.1				
	PLACE1004279	20.99	17.87	19.27	8.96	30.05	13	8.21	11.3	11.19		**	-	-
	PLACE1004282	12.55	12.53	16.59	4.95	9.12	5.25	6.7	6.34	5.89	*	**	-	-
	PLACE1004284	9.58	14.66	15.53	8.95	7.35	5.65	6.2	6.82	3.1	*	*	-	-
45	PLACE1004289	11.29	10.79	11.74	3.16	5.71	3.35	2.35	6.14	2.14	**	**	-	-
	PLACE1004299	19.52	18.15	16.36	8.87	22.44	9.43	11.73	9.62	8.57		**	-	-
	PLACE1004302	6.5	4.57	6.26	4.18	7	3.55	1.56	4.16	0.55		*	-	-
	PLACE1004305	7.16	4.88	7.78	4.02	11.98	4.38	3.44	4.62	2.94		*	-	-
	PLACE1004316	21.08	20.32	25.43	14.83	15.07	12.7	13.59	13.17	12.8	*	**	-	-
	PLACE1004322	9.54	3.44	10.02	13.05	22.34	1.36	2.52	7.35	3.43				
50	PLACE1004325	13.79	15.32	21.15	8.25	8.41	6.63	10.63	11.11	9.78	*		-	-
	PLACE1004332	13.76	26.81	27.83	10.52	16.97	4.86	9.28	8.37	7.2		*	-	-
	PLACE1004336	9.25	9.04	10.31	3.17	5.77	3.05	2.53	4.29	2.93	**	**	-	-
	PLACE1004346	11.14	15.86	16.19	8.6	6.7	8.17	14.67	2.81	3.65	*		-	-
	PLACE1004358	4.9	6.6	5.3	4.66	3.48	2.52	2.87	2.07	1.85		**	-	-
	PLACE1004376	4.37	7.66	6.28	3.82	16.23	3.24	18.46	3.42	3.06				
55	PLACE1004384	20.82	15.88	20.1	10.2	14.54	11.76	10.47	11.55	9.77	*	**	-	-
	PLACE1004385	16.21	25.32	29.3	6.24	11.85	7.12	18.49	9.57	9.67	*		-	-
	PLACE1004388	13.03	15.64	14.98	6.25	11.49	8.38	7.85	6.97	4.61	*	**	-	-



Table 476

	PLACE1004405	6.83	7.82	8.42	1.74	2.87	2.17	1.79	1.77	1.06	**	**	-	-
	PLACE1004407	11.75	11.43	14.16	6.35	10.59	6.28	6.13	6.07	6.47	*	**	-	-
5	PLACE1004424	6.94	8.4	8.66	2.02	6.19	2.66	3.43	3.43	2.34	*	**	-	-
	PLACE1004425	15.08	13.72	13.35	6.65	11.37	7.31	11.7	10.39	11.17	*	*	-	-
	PLACE1004427	9.79	7.13	8.53	5.79	4.82	4.58	2.31	1.96	2.72	*	**	-	-
	PLACE1004428	8.46	5.33	5.57	3.25	3.29	3.21	2.85	2.65	3.1	*	*	-	-
	PLACE1004433	6.57	5.12	7.26	2.15	3.61	2.86	2.76	2.36	3.32	*	**	-	-
	PLACE1004435	5.31	5.07	8.8	2.76	3.41	3.61	2.83	0.69	1.36	*		-	-
10	PLACE1004437	123.66	158.84	144.08	116.56	167.95	86.05	49.84	88.42	68.77	**		-	-
	PLACE1004441	10.02	12.73	11.55	5.63	11.08	5.24	5.14	4.56	2.63	**		-	-
	PLACE1004446	4.95	5.73	4.69	2.19	3.83	1.62	2.79	2.61	2.66	*	**	-	-
	PLACE1004450	17.21	13.77	11.35	7.43	9.82	10.35	13.72	15.81	15.38			-	-
	PLACE1004451	21.93	21.83	22.42	14.24	15.13	14.34	10.39	9.42	10.97	**	**	-	-
	PLACE1004456	5.66	3.89	4.79	2.22	5.14	3.7	4.95	1.66	2.31			-	-
15	PLACE1004458	6.57	4.16	7.77	2.1	5.75	2.16	2.41	3.03	1.54	*		-	-
	PLACE1004460	6.93	5.13	4.79	2.01	4.85	1.65	3.61	2.54	1.12	*		-	-
	PLACE1004467	10.11	11.82	9.53	2.74	4.49	5.1	3.12	1.44	1.55	**	**	-	-
	PLACE1004471	14.09	22.14	14.79	8.38	18.33	11.21	5.81	8.78	5.83	*		-	-
	PLACE1004473	8.27	14.31	9.86	3.42	8.92	3.77	4.46	5.47	8.39			-	-
	PLACE1004475	4.2	2.67	2.47	2.6	8.42	6.68	3.42	2.58	2.7			-	-
20	PLACE1004482	42.46	39.9	32.17	18.98	31.24	19.51	41.1	31.66	45.4	*		-	-
	PLACE1004491	3.4	5.37	4.92	2.26	2.87	1.21	3.11	1.77	1.09	*	*	-	-
	PLACE1004492	14.75	10.5	4.26	8.39	16.03	7.27	3.28	2.19	2.31			-	-
	PLACE1004506	18.11	19.82	21.23	12.46	23.49	16.62	17.33	12.61	13.21	*		-	-
	PLACE1004507	14.62	14.01	19.19	12.21	20.75	13.12	5.25	3.93	6.09	**		-	-
25	PLACE1004510	8.27	7.11	7.77	4.2	4.81	1.36	5.06	2.94	3.49	*	**	-	-
	PLACE1004516	5.75	6.67	3.83	4.51	8.48	2.72	4.69	2.56	3.06			-	-
	PLACE1004518	9.64	6.39	6.6	5.58	7.29	2.45	2.45	4.03	4.48	*		-	-
	PLACE1004519	45.05	38.06	29.43	16.22	21.37	17.38	37.02	29.03	42.7	*		-	-
	PLACE1004520	5.65	5.88	4.83	5	23.3	3.26	7.89	2.48	5.32			-	-
	PLACE1004530	8.55	8.01	8.19	4.33	4.87	3.07	5.74	4.33	5.72	**	**	-	-
	PLACE1004545	16.35	9.42	10.89	5.28	6.16	4.82	7.69	5.29	6.88	*		-	-
30	PLACE1004547	8.88	4.99	7.28	3.79	10.69	2.44	2.07	2.03	2.03	*		-	-
	PLACE1004548	8.06	7.34	7.17	1.99	3.55	1.53	3.36	1.74	4.09	**	**	-	-
	PLACE1004550	9.29	4.74	4.57	6.39	7.24	2.64	11.12	3.11	5.12			-	-
	PLACE1004551	28.29	24.92	17.22	13.36	20.97	8.68	22.61	16.23	21.2			-	-
	PLACE1004559	38.64	25.35	19.12	16.44	15.14	16.5	25.43	24.95	33.62			-	-
35	PLACE1004562	50.29	46.32	50.21	54.16	56.41	39.84	35.71	42.24	45.43			-	-
	PLACE1004564	12.01	9.86	9.29	4.62	9.04	5.79	9.27	6.54	10.21			-	-
	PLACE1004604	17.66	17.86	15.11	9.74	9.81	7.66	16.75	11.47	16.51	**		-	-
	PLACE1004611	6.51	3.64	4.04	1.34	7.9	1.38	3.77	0.9	3.89			-	-
	PLACE1004629	7.22	4.23	7.21	2.88	5.64	1.27	4	2.37	6.88			-	-
	PLACE1004630	5.71	5.71	5.05	2.41	3.38	0.92	6.59	3.07	5.19	*		-	-
40	PLACE1004637	15.22	15.19	15.73	4.5	6.73	18.68	5.83	11.18	5.64	*		-	-
	PLACE1004645	16.19	10.08	17.1	10.36	11.57	13.97	10.9	12.36	6.68			-	-
	PLACE1004646	4.97	5.64	4.39	4.13	5.71	3.39	2.58	3.34	2.67	**		-	-
	PLACE1004648	5.49	4.11	3.96	3.64	5.16	4.29	1.91	1.5	0.14	**		-	-
	PLACE1004655	3.31	1.36	2.13	1.15	3.39	0.72	0.74	1.06	1.47			-	-
	PLACE1004658	61.58	67.15	67	38.54	49.97	38.25	52.62	54.12	65.08	**		-	-
45	PLACE1004664	1.19	4.36	2.93	2.86	5.73	2.7	1.85	2.13	1.51			-	-
	PLACE1004672	28.88	30.42	25.6	16.98	20.16	13.59	16.28	11.87	13.82	**	**	-	-
	PLACE1004674	4.27	1.5	4.11	2.41	3.15	1.89	1.56	2.96	3.87			-	-
	PLACE1004681	6.54	6.41	13.08	7.27	21.72	12.91	4.64	4.9	3.36			-	-
	PLACE1004686	4.34	3.3	4.61	2.4	3.38	2.38	2.29	3.63	0.39			-	-
	PLACE1004690	6.4	6.12	8.6	4.32	13.96	8.66	2.73	4.56	2.78	*		-	-
50	PLACE1004691	12.44	14.52	17.78	7.94	13.42	7.13	8.04	12.14	11.56			-	-
	PLACE1004693	8.4	10.27	9.88	5.82	5.16	5.28	2.45	3.25	2.73	**	**	-	-
	PLACE1004701	144.88	198.16	97.68	190.88	167.91	84.32	88.33	73.95	139.9			-	-
	PLACE1004705	3.47	3.01	2.93	2.39	3.96	1.27	1.92	3.49	3.87			-	-
	PLACE1004708	48.88	43.13	45.03	31.98	28.55	23.56	15.06	39.44	11.77	**		-	-
	PLACE1004716	20.04	14.83	24.39	8.19	12.11	8.27	8.37	8.78	9.57	*	*	-	-
55	PLACE1004722	5.57	7.39	10	4.45	6.54	3.93	3.57	3.69	3.48	*	*	-	-
	PLACE1004736	16.71	17.15	24.67	12.34	13.91	6.89	9.19	22.16	13.53			-	-
	PLACE1004737	5.22	7.74	7.78	3.83	6.24	1.98	3.06	3.38	3.05	*		-	-

Table 477

	PLACE1004740	5.7	7.45	13.2	8.48	9.7	6.78	5.51	4.01	4.39			
	PLACE1004743	25.2	29.5	32.11	15.32	29.52	15.01	26.22	23.41	28.91			
5	PLACE1004751	26.3	37.3	36.23	17.86	40.34	16.49	27.84	27.38	23.37			
	PLACE1004757	27.21	29.89	35.01	20.07	11.76	13.22	19.63	14.54	16.78	*	**	-
	PLACE1004761	36.62	28.57	36.7	16.84	22.51	18.17	11.71	16.47	11.41	**	**	-
	PLACE1004773	6.34	3	4.53	3.16	3.36	2.2	2.15	2.55	2.95			
	PLACE1004775	6.98	4.5	11.09	2.47	5.26	2.58	2.74	2.24	1.32			
	PLACE1004777	22.12	29.48	36.12	13.38	18.93	13.39	17.54	20.58	18.98	*		-
10	PLACE1004793	38.61	50.6	39.99	29.77	37.64	25.63	24.47	24.63	21.5	**		-
	PLACE1004796	8.45	9.48	8.63	3.38	9.79	3.2	3.16	2.68	3.41	**		-
	PLACE1004804	5.96	3.66	3.88	1.07	6.07	2.59	2.15	2.35	2.21	*		-
	PLACE1004813	7.54	8.6	8.99	4.2	5.66	4.51	4.87	4.35	4.23	**	**	-
	PLACE1004814	4.13	4.9	5.89	3.27	11.52	2.25	2.11	31.08	4.24			
	PLACE1004815	5.57	3.05	6.31	3.48	4.55	1.54	4.88	2.03	1.26			
15	PLACE1004816	10.65	12.52	15.46	46.15	13.59	7.88	11.01	6.49	24.95			
	PLACE1004824	10.1	10.18	14.93	3.84	7.8	4.37	6.87	4.52	8.59	*		-
	PLACE1004827	6.33	6.31	10.2	1.77	3.73	0.89	1.94	4.36	3.45	*	*	-
	PLACE1004836	18.51	24.59	14.94	5.86	11.83	5.72	3.63	5.6	4.83	*	**	-
	PLACE1004838	32.68	37.85	26.97	17.25	33.96	16.53	18.4	22.65	17.82	*		-
	PLACE1004840	26.67	33.84	24.99	11.9	21.32	10.63	17.68	19.77	20.11	*	*	-
20	PLACE1004842	29.36	29.36	36.71	26.03	17.22	20.39	11.25	16.65	13.58	*	**	-
	PLACE1004850	12.96	12.93	16.16	9.69	10.5	6.77	8.83	9.34	8.77	*	**	-
	PLACE1004868	19.8	16.22	20.8	8.53	16.93	9.03	11.19	11.11	9.47	**		-
	PLACE1004885	7.93	7.22	6.94	1.5	3.78	3.6	1.94	2.3	1.73	**	**	-
	PLACE1004886	8.48	8.07	17.49	4.04	4.63	2.9	4.53	4.47	2.5			
	PLACE1004887	11.79	13.7	11.52	6.38	10.2	7	3.69	4.3	5.52	*	**	-
25	PLACE1004896	6.25	6.09	7.72	0.93	8.2	4.59	2.58	2.25	1.01	**		-
	PLACE1004900	11.28	8.08	8.69	8.58	6.42	4.7	4.96	5.45	3.62	*		-
	PLACE1004902	7.13	7.38	10.7	4.87	6.92	2.81	4.29	4.21	2.64	*		-
	PLACE1004904	23.08	23.38	37.33	15.52	22.71	12.92	16.1	22.74	25.02			
	PLACE1004911	11.74	10.67	12.36	7.47	12.66	7.84	6.28	5.55	4.09	**		-
	PLACE1004913	12.82	12.15	14.37	4.58	7.86	4.67	7.24	7.07	6.68	**	**	-
30	PLACE1004918	17.31	18.68	18.94	7.36	10.01	6.44	8.32	5.56	6.18	**	**	-
	PLACE1004930	6.79	6.06	5.6	1.3	2	3.65	2.19	1.6	1.33	**	**	-
	PLACE1004934	14.99	19.19	12.29	5.42	10.92	8.11	4.61	8.66	7.47	*	*	-
	PLACE1004937	18.93	13.85	13.4	11.81	10.98	11.51	15	13.14	16.45			
	PLACE1004949	5	5.22	6.64	5.79	3.31	3.09	4.44	4.05	3.5	*		-
	PLACE1004969	13.91	13.85	11.55	11.71	12.45	9.25	4.82	9.25	5.58	*		-
35	PLACE1004970	28.75	33.22	29.53	13.51	29.35	23.54	15.11	12.88	14.15	**		-
	PLACE1004972	13.26	11.27	10.14	5.85	6.98	5.82	4.89	3.42	1.54	**	**	-
	PLACE1004974	16.47	29.85	28.89	16.44	23.94	17.53	14.71	17.1	12.72			
	PLACE1004975	12.92	11.66	12.08	5.89	13.8	6.88	5.54	3.55	3.43	**		-
	PLACE1004979	7.78	7.47	6.98	3.07	7.65	3.76	4.2	4.56	6.5	*		-
40	PLACE1004982	30.58	23.61	26.29	14.3	19.23	11.42	16.82	24.16	30.51	*		-
	PLACE1004985	29.66	24.94	25.1	15.66	19.26	12.6	21.78	17.15	20.28	*	*	-
	PLACE1005003	16.43	14.5	16.78	6.69	10.88	11.47	1.79	5.8	6.41	*	**	-
	PLACE1005004	5.26	4.21	4.06	1.44	3.4	2.25	2.76	1.23	1.09	*	*	-
	PLACE1005005	17.79	13.99	18.79	11.99	10.57	8.86	7.49	5.3	5.99	*	**	-
	PLACE1005011	10.94	14.04	9.8	3.35	9.24	6.44	3.46	2.32	0.6	**		-
45	PLACE1005026	31.74	35.88	28.88	14.82	24.65	14.67	35.74	25.33	28.57	*		-
	PLACE1005027	26.29	29.23	15.87	7.97	19.55	9.09	25.84	19.81	24			
	PLACE1005031	38.12	16.05	14.24	9.18	25.55	17.12	7.22	9.47	10.36			
	PLACE1005036	13.86	12.84	17.42	8.68	15.64	10.29	11.23	7.16	6.77	*		-
	PLACE1005041	111.13	87.66	72.07	36.83	51	43.47	99.34	93.97	97.87	*		-
	PLACE1005046	27.6	29	18.07	15.06	19.65	20.68	22.16	13.25	24			
50	PLACE1005047	50.64	34.98	35.58	25.13	37.56	21.77	26.01	15.91	25.77	*		-
	PLACE1005052	10.39	12.55	10.8	4.67	15.46	6.61	10.9	9.05	16			
	PLACE1005055	24.31	33.8	18.61	16.75	10.79	11.1	19.54	11.46	10.17			
	PLACE1005066	7.67	8.41	7	12.21	61.68	20.27	25.44	4.84	8.48			
	PLACE1005077	9.62	6.97	5.62	4.44	4.68	3.2	5.42	5.71	7.8			
	PLACE1005085	10.11	4.46	3.84	3.42	3.7	2.05	2.8	5.01	2.86			
55	PLACE1005086	11.97	11.74	11.67	7.31	18.85	7.84	6.74	6.63	9.62	*		-
	PLACE1005088	86.57	83.56	74.65	79.4	89.3	75.33	56.8	52.44	57.53	**		-
	PLACE1005089	6.31	4.13	4.27	1.8	3.13	4.07	2.18	0.55	2.04	*		-

Table 478

	PLACE1005101	11.5	9.29	11.94	9.18	4.8	5.47	5.22	3.69	6.78	*	**	-	-
	PLACE1005102	22.17	25.98	27.54	6.07	7.69	6.94	7.15	5.65	7.82	**	**	-	-
5	PLACE1005108	10.15	7.73	6.02	2.99	6.05	3.33	4.8	7.23	6.47				
	PLACE1005110	3.97	2.39	3.45	3.59	3.78	1.51	2.14	1.33	2.15				
	PLACE1005111	23.94	21.69	16.98	14.04	21.5	8.57	20.32	16.74	23.71				
	PLACE1005123	16.94	14.46	12.96	5.45	9.5	5	6.89	4.29	5.82	*	**	-	-
	PLACE1005124	9.14	6.62	6.15	2.06	5.47	1.8	6.61	3.46	5.33	*		-	-
	PLACE1005128	6.83	4.81	4.87	1.09	3.42	1.91	3.3	3.63	2.82	*	*	-	-
10	PLACE1005130	12.43	17.68	12.68	4.58	11.05	5.79	12.55	5.44	10.87				
	PLACE1005141	6.07	3.99	5.18	6.23	2.88	1.1	9.65	2.17	2.82				
	PLACE1005146	10.52	9.7	6.88	6.24	10.69	5.88	5.25	8.14	5.49				
	PLACE1005152	91.15	76.64	75.79	51.06	95.95	52.59	42.4	38.1	38.75	**		-	-
	PLACE1005157	5.11	3.75	6.06	2.82	4.86	2.4	1.9	2.79	1.7	*		-	-
	PLACE1005162	24.79	23.25	27.03	17.82	26.77	20.32	10.52	15.51	11.65	**		-	-
15	PLACE1005170	9.55	7.54	6.99	11.08	19.85	14.4	3.82	8.2	5.94				
	PLACE1005176	5.55	5.17	6.85	2.52	4.13	3.01	2.09	2.54	1.26	*	**	-	-
	PLACE1005181	10.56	18.07	15.09	7.46	9.06	8.01	10.91	12.85	10.11	*		-	-
	PLACE1005184	3.64	4.4	5.5	5.28	11.77	4.26	3.84	3.69	3.06				
	PLACE1005186	5.96	5.07	5.66	2.88	2.54	3.26	3.64	4.33	4.72	**	*	-	-
	PLACE1005187	20.53	14.71	18.55	9.5	10.66	10.36	12.23	12.87	7.61	*	*	-	-
20	PLACE1005189	8.28	7.72	11.92	4.24	7.19	3.99	6.84	7.52	5.99				
	PLACE1005193	39.26	44.11	39.59	31.34	38.66	28.91	36.03	40.56	33.69				
	PLACE1005200	1391.4	1317.2	1202.3	1770.3	2457.3	1744.3	1189.8	1397.9	586.38	*		+	
	PLACE1005206	48.27	41.57	88.17	48.38	52.86	50.82	27.19	13.53	58.32				
	PLACE1005216	10.1	9.74	10.26	5.79	10.41	5.95	3.4	3.26	4.05	**		-	-
25	PLACE1005223	36.86	44.94	37.06	23.02	26.39	16.59	23.41	26.05	19.76	*	**	-	-
	PLACE1005225	5.34	5.81	6.83	4.25	3.02	5.27	2.59	3.79	3.7	*		-	-
	PLACE1005232	37.45	31.95	45.29	20.08	17.68	11.81	24.42	25.92	23.95	**	*	-	-
	PLACE1005239	7.93	6.66	12.45	5.29	3.66	4.36	3.81	3.89	4.86				
	PLACE1005243	16.13	27.58	27.13	19.28	15.8	19.25	6.8	13.48	9.67	*		-	-
	PLACE1005250	5.37	6.75	7.77	5.96	4.93	3.55	3.78	5.49	3.24				
30	PLACE1005261	61.12	61.95	56.67	47.53	36.14	42.92	20.88	23.52	21.14	**	**	-	-
	PLACE1005266	7.03	6.91	9.71	5.82	8.14	5.96	4.18	3.69	5.53	*		-	-
	PLACE1005271	8.47	8.61	6.86	4.77	7.74	3.27	3.65	3.57	3.35	**		-	-
	PLACE1005277	20.92	15.1	22.31	9.09	13.8	9.19	14.68	15.64	18.36	*		-	-
	PLACE1005287	15.1	8.12	14.31	5.25	6.44	6.19	5.01	4.78	3.02	*	*	-	-
	PLACE1005299	10.04	6.09	8.79	4.5	5.75	7.77	4.03	4.98	7.58				
35	PLACE1005305	8.97	7.38	9.77	4.47	3.45	4.18	3.14	3.99	3.81	**	**	-	-
	PLACE1005307	12.01	9.78	33.93	6.5	6.01	6.92	5.78	5.91	8.37				
	PLACE1005308	6.72	9.28	13.18	4.37	5.39	4.05	5.69	4.54	7.02				
	PLACE1005313	8.46	6.04	10.79	5.16	6.95	3.74	4.51	3	4	*		-	-
	PLACE1005320	9.29	12.54	14.31	7.32	9.29	5.14	4.92	4.65	5.56	**		-	-
	PLACE1005327	31	25.4	35.29	16.09	17.4	11.88	9.82	14.36	14.83	**	**	-	-
40	PLACE1005331	13.95	13.36	13.69	9.09	7.58	7.27	7.77	10.5	7.36	**	**	-	-
	PLACE1005335	11.38	7.64	13.28	5.94	7.87	3.65	8.18	25.07	9.78				
	PLACE1005336	29.59	23.98	23.59	14.99	18	12.79	23.63	28.14	27.34	*		-	-
	PLACE1005351	11.96	8.58	19.03	4.6	4.51	3.68	3.27	6.24	4.61	*		-	-
	PLACE1005366	73.8	70.81	70.61	45.9	65.72	42.52	55.33	53.05	50.72	*	**	-	-
	PLACE1005373	9.8	6.9	15.51	3.87	3.73	2.69	2.9	3.58	2.99	*	*	-	-
45	PLACE1005374	31.25	37.89	30.27	12.29	20.74	12.12	33.17	26.39	29.29	**		-	-
	PLACE1005383	9.15	7.91	6.27	5.38	5.79	4.82	3.77	5.77	7.02	*		-	-
	PLACE1005388	14.78	7.34	14.13	9.31	7.11	6.02	6.28	5.49	5.89				
	PLACE1005409	11.86	10.31	14.09	4.95	5.84	5.2	5.09	4.29	5.35	**	**	-	-
	PLACE1005410	13.35	9.74	14.55	5.14	6.18	4.53	6.86	5.79	5.13	**	*	-	-
	PLACE1005426	10.65	4.8	11.31	4.23	3.51	3	2.46	6.49	1.78				
50	PLACE1005431	8.27	7.3	10.2	3.04	3.82	2.32	3.59	3.79	5.31	**	*	-	-
	PLACE1005453	7.65	9.23	18.96	3.09	5.38	3.63	2.3	4.42	3.43				
	PLACE1005467	10.75	11.01	23.28	4.33	7.93	7.46	6.29	7.36	5.29				
	PLACE1005471	7.1	9.43	5.6	3.8	6.04	3.15	3.31	6.18	12.95				
	PLACE1005476	29.52	27.39	29.6	15.57	12.74	15.37	14.04	14.17	16.62	**	**	-	-
	PLACE1005477	9.37	7.91	13.74	3.68	6.31	4.63	5	3.74	6.24	*	*	-	-
55	PLACE1005480	7.1	8	8.36	5.61	4.81	4.45	4.92	2.94	2.27	**	**	-	-
	PLACE1005481	10.21	6.44	10.18	3.66	4.76	4.41	5.76	4.63	3.43	*	*	-	-
	PLACE1005494	9.19	9.94	10.69	3.34	4.05	3.41	4.87	3.69	4.02	**	**	-	-

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	PLACE1005495	11.05	11.48	9.86	5.01	5.38	4.26	3.3	3.97	3.58	**	**	-	-
	PLACE1005497	9.89	9.26	8.02	3.87	6.07	3.47	3.99	3.58	2.73	**	**	-	-
5	PLACE1005499	23.46	21.47	29.66	8.65	19.6	10.05	16	19.54	21.59	*	*	-	-
	PLACE1005502	9.18	6.48	6.37	3.45	3.87	4.29	4.21	4.81	4.94	*	*	-	-
	PLACE1005513	33.31	27.28	25.19	10.65	9.46	7.45	5.15	5.68	9.33	**	**	-	-
	PLACE1005515	11.7	9.47	10.48	3.66	3.88	4.7	6	4.7	5.35	**	**	-	-
	PLACE1005519	8.43	6.62	7.72	4.49	2.77	2.81	3.1	2.36	5.05	**	*	-	-
	PLACE1005526	8.8	10.4	11.16	2.78	4.21	2.23	3.21	3.51	3.18	**	**	-	-
10	PLACE1005528	26.91	22.55	23.87	12.32	10.17	9.81	19.08	11.09	17.43	**	*	-	-
	PLACE1005530	20.34	15.73	21.3	12.14	14.27	9.82	8.49	8.49	4.49	*	**	-	-
	PLACE1005536	18.12	14.92	18.89	3.17	4.7	3.13	5.93	4.22	4.19	**	**	-	-
	PLACE1005539	42.25	35.31	35.69	15.02	20.49	15.33	32.11	27.06	37.95	**		-	-
	PLACE1005543	35.86	20.69	14.02	11.25	7.4	11.67	9.96	8.84	11.47			-	-
	PLACE1005544	4.98	5.73	4.38	2.31	2.15	3.58	3.94	2.43	3.09	*	*	-	-
15	PLACE1005550	26.58	26.63	19.78	16.15	16.36	16.32	11.17	10.41	11.67	*	**	-	-
	PLACE1005554	23.49	15.23	16.27	7.02	8.22	4.71	11.04	7.45	10.06	*	*	-	-
	PLACE1005557	10.41	9.97	10.58	3.15	3.37	2.55	4.57	1.9	2.76	**	**	-	-
	PLACE1005563	10.87	11.46	9.72	4.64	6.41	6.88	7.08	5.98	5.9	**	**	-	-
	PLACE1005569	27.85	17.24	16.24	8.47	8.97	6.39	9.6	5.75	9.27	*	*	-	-
20	PLACE1005574	29.21	21.31	10.09	12.87	15.06	14.88	14.12	11.93	13.7			-	-
	PLACE1005584	80.18	66.17	69.3	73.19	89.15	68.42	53.92	40.06	44.96	*		-	-
	PLACE1005590	14.81	9.97	11.59	6.51	9.72	8.47	7.14	6.35	7.74	*		-	-
	PLACE1005595	23.18	18.25	21.16	12.01	10.55	9.94	19.07	11.17	15.91	**		-	-
	PLACE1005601	11.31	7.51	15.39	5.61	6.28	8.37	7.21	9.02	6.01			-	-
	PLACE1005603	18.98	21.86	14.52	8.39	9.87	6.77	12.21	11.52	14.3	*		-	-
25	PLACE1005604	8.92	8.05	5.89	5	4.08	4.67	3.54	2.41	2.72	*	**	-	-
	PLACE1005611	33.68	22.2	29.76	11.8	16.07	9.26	20.54	21.42	26.07	*		-	-
	PLACE1005622	30.69	27.64	23.31	11.83	18.8	12.91	22.33	27.88	24.08	*		-	-
	PLACE1005623	9.95	5.8	5.03	2.69	3.21	2.46	4.37	5.18	4.94			-	-
	PLACE1005630	8.17	9.56	9.09	4.43	7.2	3.43	4.75	3.89	4.7	*	**	-	-
	PLACE1005639	60.6	66.64	49.38	29.59	36.73	29.78	61.43	55.47	68.03	**		-	-
30	PLACE1005646	17.8	13.84	15.64	9.47	9.48	7.41	6.37	4.37	5.79	**	**	-	-
	PLACE1005647	13.8	11.09	12.51	5.66	5.78	5.71	6.46	4.42	5.24	**	**	-	-
	PLACE1005648	28.95	31.24	20.78	11.15	9.99	10.48	23.48	13.79	10.43	**		-	-
	PLACE1005653	16.03	13.03	11.9	5.52	4.03	5.5	8.65	5.02	7.5	**	*	-	-
	PLACE1005656	15.9	11.93	10.98	7.3	8.49	5.09	13.9	11.98	12.97	*		-	-
	PLACE1005659	10.5	8.34	6.31	5.3	4.01	3.82	4.61	3.03	4.74	*	*	-	-
35	PLACE1005660	12.82	10.45	9.32	4.78	5.95	3.56	5.23	2.26	5.04	**	**	-	-
	PLACE1005664	23.43	27.28	25.73	6.86	20.98	19.65	21.23	13.1	15.7	*	*	-	-
	PLACE1005666	12.43	11.64	13.67	7.79	10.52	6.99	11.1	12.9	13.47	*		-	-
	PLACE1005669	14.08	13.16	10.98	6.36	8.32	3.2	8.01	5.64	11	*		-	-
	PLACE1005682	22.57	20.73	18.81	7.71	10.55	7.1	12.18	6.07	11.14	**	**	-	-
	PLACE1005698	7.18	6.68	8.02	7.04	5.88	4.02	4.11	5.29	4.18	**		-	-
40	PLACE1005708	17.69	17.02	22.05	11.44	15.51	9.8	12.59	9.54	8.25	*	*	-	-
	PLACE1005725	9.73	11.27	13.97	7.09	8.31	6.27	4.4	6.46	6.4	*	*	-	-
	PLACE1005727	10.04	8.34	11.08	6.79	10.76	10.55	4.59	6.83	6.56	*	*	-	-
	PLACE1005730	13.44	12.68	11.77	6.36	7.19	8.47	5.04	7.92	8.47	**	**	-	-
	PLACE1005736	5.83	5.5	7.74	3.15	14.38	1.73	4.63	3.09	3.33	*		-	-
	PLACE1005739	7.01	13.06	9.75	7.43	7.8	5.14	2.96	4.16	3.47	*		-	-
45	PLACE1005745	8.04	6.14	6.43	4.26	4.82	5.89	4.13	2.63	4.39	*	*	-	-
	PLACE1005752	128.36	102.07	139.38	89.6	72.86	89.83	103.85	94.56	103.55	*	*	-	-
	PLACE1005755	13.46	9.22	14.54	4.95	6.97	3.84	5.58	5.65	3.87	*	*	-	-
	PLACE1005756	10.54	16.55	18.56	10.11	10.69	10.1	6.71	10.57	12.53			-	-
	PLACE1005760	5.35	5.71	8.64	9.33	6.58	7.47	2.74	8.03	2.74			-	-
	PLACE1005763	18.11	17.1	15.35	9.45	11.68	9.73	7.29	9.29	9.82	**	**	-	-
50	PLACE1005768	19.31	21.05	13.08	10.64	11.47	13.73	6.13	9.41	9.52	*		-	-
	PLACE1005771	24.23	23.82	24.14	14.86	21.27	9.53	16.05	19.49	20.2	*		-	-
	PLACE1005783	6.96	4.13	7.26	3.95	3.94	3.49	3.16	3.04	5.15			-	-
	PLACE1005799	43.95	40.56	57.56	28.57	25.86	15.96	30.85	26.7	32.18	*	*	-	-
	PLACE1005802	18.73	15.75	12.71	10.65	14.22	15.85	21.48	13.68	14.38			-	-
	PLACE1005803	14.16	12.88	18.69	6.94	7.06	7.31	4.95	5.48	3.9	**	**	-	-
55	PLACE1005804	16.14	16.06	21.67	10.66	8.62	11.86	4.49	6.03	5.63	*	**	-	-
	PLACE1005813	7.59	9.87	17.86	7.9	9.25	7.77	3.93	4.99	5.43			-	-
	PLACE1005815	17.11	19.5	18.51	7.94	18	6.6	9.57	8.13	8.77	**		-	-

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	PLACE1005828	21.32	17.86	17.66	18.38	28.15	11	8.41	12.77	17.42				
	PLACE1005833	19.04	15.23	17.55	13.68	13.86	12.16	11.62	13.97	12.02	*	*	-	-
5	PLACE1005834	31.23	40.41	42.31	19.53	15.14	12.45	22.97	22.37	27.18	**	*	-	-
	PLACE1005835	8.38	4.15	8.95	3.69	3.05	3.25	2.72	13.93	4.26				
	PLACE1005836	6.34	4.47	7.11	2.95	2.55	2.1	1.11	4.41	2.67	*		-	-
	PLACE1005845	7.96	5.73	10.94	3.26	4.7	1.75	3.2	4.47	3.62	*	*	-	-
	PLACE1005850	7.12	8.63	11.96	4.89	4.51	3.39	2.96	4.97	6.83	*		-	-
	PLACE1005851	49.92	45.46	36.8	28.76	36.45	21.25	9.27	9.06	15.36		**	-	-
10	PLACE1005856	9.13	9.45	9.68	4.42	6.52	4.26	5.66	4.96	7.88	**	*	-	-
	PLACE1005875	19.11	12.96	14.66	10.98	11.89	11.34	7.25	9.07	9.2		*	-	-
	PLACE1005876	6.84	5.72	8.26	3.52	3.77	3.26	2.47	4.32	3	*	*	-	-
	PLACE1005878	6.18	5.12	8.15	3.65	4.35	1.9	2.1	7.39	4.67				
	PLACE1005880	10.13	10.1	15.44	15.29	7.51	5.59	11.17	12.56	8.92				
	PLACE1005884	15.13	11.77	15.14	4.99	6.58	3.8	5.03	3.76	7.31	**	**	-	-
15	PLACE1005890	14.12	12.54	15.15	4.55	6.88	4.96	4.84	4.65	10.58	**	*	-	-
	PLACE1005898	22.47	43.11	28.59	9.23	15.21	13.1	10.14	6.45	7.84	*	*	-	-
	PLACE1005913	11.08	12.76	18.39	6.03	9.77	5.43	8.89	7.87	5.55				
	PLACE1005921	38.7	26.83	45.11	14.95	20.53	13.93	14.46	15.3	19.69	*	*	-	-
	PLACE1005923	35.55	28.6	35.14	8.99	9.9	10.33	7.55	9.92	9.16	**	**	-	-
	PLACE1005925	9.28	6.52	9.69	4.22	6.79	3.62	4.36	4.97	3.85		*	-	-
20	PLACE1005927	8.32	7.66	16.91	2.68	3.86	2.87	2.78	4.08	4.5				
	PLACE1005932	17.99	14.04	15.58	5.88	10.67	7.85	11.54	8.65	8.07	*	*	-	-
	PLACE1005934	7.56	7.52	8.85	2.45	3.18	2.78	2.65	3.47	4.68	**	**	-	-
	PLACE1005936	8.91	7.48	10.96	2.6	4	2.78	2.64	2.57	2.62	**	**	-	-
	PLACE1005939	14.59	14.49	13.88	5.4	8.87	6.89	7.24	6.14	6.85	**	**	-	-
	PLACE1005951	184.11	138.22	202.24	63.95	124.2	100.53	163.66	124.76	76.11	*		-	-
25	PLACE1005953	4.12	2.98	5.89	2.81	3.65	1.89	1.88	2.73	1.8				
	PLACE1005955	147.21	90.51	163.74	157.35	162.66	147.78	83.65	73.22	67.87				
	PLACE1005966	21.58	17.57	18.88	12.22	12.03	11.48	18.97	16.95	19.33	**		-	-
	PLACE1005968	7.85	6.96	6.59	3.18	3.12	3.27	2.21	3.25	2.08	**	**	-	-
	PLACE1005975	6.58	6.62	8.7	2.59	2.3	2.44	2.13	2.22	2.24	**	**	-	-
	PLACE1005990	13.31	13.53	10.46	5.9	8.19	4.45	5.05	6.3	5.08	*	**	-	-
30	PLACE1005997	11.27	8.34	8.61	3.34	7.86	4.32	3.83	4.17	2.65		**	-	-
	PLACE1006002	7.2	9.3	8.62	4.13	3.01	2.96	3.03	3.74	3.08	**	**	-	-
	PLACE1006003	19.13	15.27	13.68	6.84	9.41	7.04	14.37	14.53	15.21	*		-	-
	PLACE1006011	14.53	12.13	13.55	5.17	8.37	6.39	12.92	13.32	12.8	**		-	-
	PLACE1006017	17.66	15.33	13.64	7.8	6.85	7.26	3.44	3.4	5.68	**	**	-	-
	PLACE1006037	19.54	15.54	16.94	5.06	9.69	7.93	15.52	15.45	11.65	**		-	-
35	PLACE1006040	21.73	18.19	20.02	8.22	10.07	7.19	9.12	8.1	8.15	**	**	-	-
	PLACE1006063	18.04	22.51	29.29	15.12	25.84	15.72	12.74	9.35	9.64		*	-	-
	PLACE1006071	24.45	22.47	19.59	9.7	14.01	7.6	15.44	10.65	16.68	**	*	-	-
	PLACE1006073	38.01	25.19	30.05	16.58	19.75	14.04	20.88	12.98	14.52	*	*	-	-
	PLACE1006074	21.69	19.68	21.99	13.65	9.89	8.37	10.34	8.49	11.16	**	**	-	-
	PLACE1006076	6.98	23.32	28.44	3.28	24.98	6.58	8.27	11.5	12.4				
40	PLACE1006079	5.36	7.59	6.02	3.43	3.4	2.8	2.82	1.59	5.77	*		-	-
	PLACE1006093	17.29	20.55	15.5	11.28	11.48	8.91	6.51	3.34	7.24	*	**	-	-
	PLACE1006116	6.66	4.88	6.43	2.05	2.48	1.97	3.15	0.18	1.1	**	*	-	-
	PLACE1006119	9.01	6.23	8.79	2.16	3.34	2.75	3.83	1.45	4.03	**	*	-	-
	PLACE1006129	11.8	19.99	13.49	6.74	8.91	6.37	6.93	6.6	9.52	*	*	-	-
	PLACE1006139	11.03	9.2	11	5.5	4.05	3.54	5.37	5.2	8.18	**	*	-	-
45	PLACE1006143	34.11	32.02	23.21	13.95	17.22	16.38	5.72	10.56	8.1	*	**	-	-
	PLACE1006157	20.08	16.11	21.21	6.21	8	10.58	9.26	6.55	9.67	**	**	-	-
	PLACE1006159	22.74	19.17	16.53	5.42	7.39	5.18	11.09	3.24	9.93	**	*	-	-
	PLACE1006164	10.4	12.06	12.25	3.81	6.89	2.98	4.98	2.08	3.84	**	**	-	-
	PLACE1006167	150.43	130.54	128	105.79	82.45	55.54	118.18	93.17	93.5	*	*	-	-
50	PLACE1006170	12.04	9.61	11.88	3.48	3.73	3.68	2.75	2.82	3.04	**	**	-	-
	PLACE1006181	14.32	10.9	10.36	5.74	6.23	4.42	6.29	2.91	4.76	**	*	-	-
	PLACE1006187	23.98	21.9	19.46	7.26	12.29	5.92	18.37	17.04	21.06	**		-	-
	PLACE1006195	27.43	19.87	20.2	13.18	6.92	6.66	10.17	6.16	5.89	*	**	-	-
	PLACE1006196	14.88	10.51	8.01	6.22	7.31	2.89	4.66	4.93	4.37		*	-	-
	PLACE1006197	25.54	27.48	23.66	11.8	19.78	16.24	17.7	18.29	21.21	*	*	-	-
	PLACE1006198	12.15	16.37	13.46	4.05	5.5	3.12	5.11	3.17	4.8	**	**	-	-
55	PLACE1006205	8.36	7.44	9.1	4.62	5.35	3.49	12.53	5	7.53	**		-	-
	PLACE1006208	10.95	10.22	9.53	5.04	9.25	5.28	4.47	4.13	4.33	**		-	-

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	PLACE1006211	18.15	19.46	15.85	7.8	6.56	8.15	10.56	8.16	8.98	**	**	-	-
	PLACE1006219	29.22	24.03	22.82	13.99	7.2	9.8	23.91	20.19	22.03	**		-	-
5	PLACE1006223	33.12	26.98	22.85	14.69	11.86	8.81	23.65	22.74	28.77	**		-	-
	PLACE1006225	9.38	7.86	6.1	4.18	4.91	3.81	6.34	5.77	7.67	*		-	-
	PLACE1006236	23.05	26.18	25.58	13.5	14.02	10.31	12.5	8.37	11.47	**	**	-	-
	PLACE1006239	7.77	5.03	5	2.21	3.14	2.06	2.98	3.13	3.81	*		-	-
	PLACE1006245	11.97	10.97	10.73	4.72	5.26	4.25	5.6	4.62	4.52	**	**	-	-
10	PLACE1006246	14.07	10.52	9.12	4.17	12.12	4.44	10.44	8.15	11.84			-	-
	PLACE1006248	10.3	9.17	8.56	6.54	7.06	2.85	7.67	4.65	5.48	*		-	-
	PLACE1006262	19.08	26.43	25.66	10.77	26.8	17.9	14.07	10.91	15.08	*		-	-
	PLACE1006269	6.36	4.8	5.62	2.78	2.48	2.42	4.23	3.67	2.13	**	*	-	-
	PLACE1006275	7.84	6.83	8.11	7.79	9.46	8.46	5.82	11.38	4.94			-	-
	PLACE1006277	18.16	15.2	14.15	12.95	19.65	15.77	6.69	13.62	7.81			-	-
15	PLACE1006288	23.16	25	24.73	14.26	21	15.27	15.12	19.66	20.01	*	*	-	-
	PLACE1006290	3.79	4.35	4.22	1.07	3.07	1.54	0.76	2.83	1.89	*	*	-	-
	PLACE1006298	31.99	33.57	40.35	21.62	22.17	18.83	30.18	26.42	31.31	**		-	-
	PLACE1006311	24.06	25.54	26.15	17.19	20.35	18.67	6.49	6.41	12.35	**	**	-	-
	PLACE1006318	23.92	22.31	22.74	9.17	11.04	10.73	16.57	17.39	15.35	**	**	-	-
	PLACE1006325	10.97	6.18	13.93	5.64	6.43	6.48	6.34	4.38	3.68			-	-
20	PLACE1006331	322.49	249.29	312.14	284.34	344.95	317.78	261.41	376.24	167.86			-	-
	PLACE1006335	6.01	6.97	9.42	6.43	10.77	6.27	4.79	4.63	3.75	*		-	-
	PLACE1006357	23.6	23.65	28.41	15.45	19.92	11.71	10.11	13.97	13.07	*	**	-	-
	PLACE1006360	39.03	55.89	60.83	32.56	29.33	36.42	18.81	22.42	24.3	*		-	-
	PLACE1006364	4.49	3.79	4.52	5.2	5.32	3.04	3.31	4.72	3.85			-	-
	PLACE1006365	8.87	13.33	7.94	4.35	7.31	4.11	4.93	6.19	6.08			-	-
25	PLACE1006368	7.6	5	7.22	4.35	3.51	2.72	3.12	4.28	3.68	*	*	-	-
	PLACE1006371	12.84	8.89	13.13	6.85	5.51	3.89	5.93	6.19	7.36	*	*	-	-
	PLACE1006373	31.88	31.57	27.89	11.44	15.9	12.05	24.23	17.9	24.85	**	*	-	-
	PLACE1006382	15.81	18.11	17.64	20.83	24.97	21.9	28.68	49.67	48.66	*	*	+	+
	PLACE1006385	23.74	24.67	19.54	18.57	28.47	23.59	6.72	12.92	8.24	**		-	-
	PLACE1006391	7.09	8.24	10.32	5.76	7.9	5.35	7.26	7.31	6.16			-	-
30	PLACE1006412	14.35	15.98	15.55	14.85	16.87	8.6	8.42	8.73	11.54	**		-	-
	PLACE1006414	30.64	63.89	32.69	29.17	49.53	18.72	7.89	13.37	10.44	*		-	-
	PLACE1006419	23.86	16.38	19.21	8.34	10.82	5.22	6.84	8.36	7.76	*	**	-	-
	PLACE1006438	16.88	12.75	13.77	5.93	7.83	5.98	6.47	9.15	5.41	**	*	-	-
	PLACE1006443	7.62	8.28	7.5	4.32	3.07	4.42	2.72	3.77	2.68	**	**	-	-
	PLACE1006445	53.01	52.47	65.34	48.09	51.7	50.7	24.1	26.92	30.98	**		-	-
35	PLACE1006447	16.45	17.73	17.35	9.64	12.61	9.03	5.67	7.16	5.82	**	**	-	-
	PLACE1006466	5.01	5.76	10.4	3.6	5.26	3.03	3.62	2.47	3.82			-	-
	PLACE1006469	9.97	6.93	12.7	4.45	5.94	2.99	6.14	5.96	3.89	*		-	-
	PLACE1006470	14.91	13.1	13.03	5.44	14.24	9.05	12.65	15.12	16.52			-	-
	PLACE1006472	32.56	24.9	52.53	14.86	22.47	15.58	27.13	60.66	18.13			-	-
	PLACE1006476	75.24	88.04	95	49.93	69.66	43.58	73.04	95.42	77.62	*		-	-
40	PLACE1006482	19.52	14.87	22.77	7.46	8.75	5.8	9.29	24.88	15.09	**		-	-
	PLACE1006488	13.42	9.61	14.11	5.93	5.56	7.22	5.43	7.77	6	*	*	-	-
	PLACE1006492	53.41	60.91	65.09	29.78	38.14	28.4	41.31	52.42	43.57	**	*	-	-
	PLACE1006506	8.93	8.04	10.96	3.97	6.16	3.99	2.77	5.01	4.34	*	**	-	-
	PLACE1006515	6.57	6.17	10.41	2.69	4.8	3.13	3.49	3.57	2.51	*	*	-	-
	PLACE1006516	7.77	7.4	8.18	2.65	6.76	3.8	4.8	4.81	1.69	*		-	-
45	PLACE1006520	85.74	60.72	84.5	67.76	73.09	68.07	40.48	30.38	37.31	**		-	-
	PLACE1006521	5.4	3.13	7.19	3.67	3.58	2.13	2.56	2.69	1.53			-	-
	PLACE1006529	21.37	16.93	24.45	11.55	12.23	11.32	13.1	15.15	16.91	*		-	-
	PLACE1006531	8.98	4.63	8.46	3.15	2.87	3.1	2.57	4.69	2.69	*		-	-
	PLACE1006534	11.34	12.38	19.26	6.83	8.12	7.2	8.08	5.98	8.82			-	-
	PLACE1006540	17.3	13.48	19.89	6	9.01	6.33	5.04	4.77	5.56	**	**	-	-
50	PLACE1006549	57.43	76.29	59.13	33.67	55.25	39.07	49.85	36.47	56.34			-	-
	PLACE1006550	27.31	23.34	17.69	10.6	24.86	11.76	7.55	11.98	6.46	*		-	-
	PLACE1006552	41.43	35.42	38.21	18.37	17.9	12.42	28.67	34.48	34.92	**		-	-
	PLACE1006557	58.91	37.26	57.05	36.71	38.26	34.22	31.47	33.21	28.65	*		-	-
	PLACE1006563	12.53	9.16	14.73	7.21	10.95	7.06	5.43	4.33	7.28	*		-	-
	PLACE1006579	8.16	5.5	6.78	3.56	3.74	3.1	2.74	1.94	3.28	*	**	-	-
55	PLACE1006594	8.47	4.75	7.36	2.29	3.19	1.42	2.51	1.45	1.95	*	*	-	-
	PLACE1006598	14.33	13.22	15.98	9.86	13.18	9.6	7.97	4.5	6.78	**		-	-
	PLACE1006607	18.95	13.98	15.61	10.13	11.36	9.36	8.88	8.34	9.06	*	**	-	-

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	PLACE1006610	9.23	9.13	6.93	3.56	3.78	2.24	3.21	1.79	1.8	**	**	-	-
	PLACE1006615	5.13	4.58	7.74	3.64	4.24	3.19	3.42	3.13	4.2			-	-
5	PLACE1006617	10.84	9.51	10.64	5.44	6.44	4.54	8.05	7.55	8.94	**	*	-	-
	PLACE1006618	16.8	17.21	17.66	12.4	9.99	12.65	9.96	9.85	12.85	**	**	-	-
	PLACE1006626	9.9	9.38	11.8	4.89	3.64	3.15	3.8	3.9	3.22	**	**	-	-
	PLACE1006629	97.87	77.5	62.9	75.16	89.13	71.45	50.39	46.85	45		*	-	-
	PLACE1006637	20.62	30.53	27.31	15.03	24.3	12.77	12.77	11.41	9.09	**		-	-
	PLACE1006640	146.09	116.55	121.62	98.73	144.79	100.95	65.85	61.12	81.72	**		-	-
10	PLACE1006644	10.36	13.76	11.01	6.08	7.62	8.85	6.47	3.27	4.59	*	**	-	-
	PLACE1006657	9.47	8.7	8.11	3.37	3.88	4.59	4.46	4.41	6.15	**	**	-	-
	PLACE1006673	128.37	101.12	117.47	60.38	47.28	69.57	78.35	78.65	91.83	**	*	-	-
	PLACE1006678	13.14	7.54	6.57	3.78	6.24	6.14	3.95	3.22	3.7			-	-
	PLACE1006682	5.12	3.88	4.9	2.21	2.14	1.84	2.5	1.43	2.09	**	**	-	-
	PLACE1006684	8.48	6.37	7.5	1.9	2.47	2.03	3.67	2.97	2.03	**	**	-	-
15	PLACE1006698	24.65	21.3	17.88	6.94	8.35	11.27	7.31	3.9	5.72	**	**	-	-
	PLACE1006704	10.75	10.1	9.67	7.04	6.45	4.58	4.88	2.24	3.52	**	**	-	-
	PLACE1006708	6.82	6.62	4.54	1.43	4.58	2.49	4.44	1.95	2.6		*	-	-
	PLACE1006711	7.97	5.26	8.07	5.12	5.44	5.92	5.18	4.48	3.42			-	-
	PLACE1006714	19.78	16.32	14.11	6.39	7.42	10.52	4.46	5.02	4.69	*	**	-	-
	PLACE1006716	21.34	19.47	16.01	5.39	7.72	5.97	12.01	9.74	13.28	**	*	-	-
20	PLACE1006731	8.76	6.59	9.88	4.19	4.28	3.45	3.4	4.54	3.95	*	*	-	-
	PLACE1006754	12.83	10.26	11.39	6.83	5.2	6.24	8.13	4.13	6.6	**	*	-	-
	PLACE1006760	17.66	24.39	15.04	22.5	23.46	11.75	21.46	9.03	14.39			-	-
	PLACE1006779	14.53	14.99	8.23	6.82	4.21	3.38	5.07	3.29	2.36	*	*	-	-
	PLACE1006782	13.34	14.85	8.6	8.19	13.03	7.71	10.87	6.95	6.98			-	-
25	PLACE1006783	26.1	20.43	20.94	18.8	23.33	15.04	25.48	18.52	26.77			-	-
	PLACE1006786	16.5	11.01	11.97	10.81	6.14	7.77	7.76	8.87	8.16	*	*	-	-
	PLACE1006792	43	29.6	28.89	12.14	32.07	8.88	14.31	11.42	11.6		*	-	-
	PLACE1006795	6.46	5.54	6.42	3.27	4.53	2.37	5.98	1.9	3.55	*		-	-
	PLACE1006800	14.69	12.26	14.82	7.42	7.86	5.36	11.02	8.63	12.6	**		-	-
	PLACE1006805	297.4	379.55	330.72	251.58	242.8	138.41	164.1	78.29	121.42	*	**	-	-
30	PLACE1006809	17.57	15.02	14.01	6.89	5.54	5.55	12.59	5.67	9	**	*	-	-
	PLACE1006815	36.78	37.15	24.97	22.04	27.53	19.08	12.45	10.62	14.81	**	**	-	-
	PLACE1006819	8.55	8.96	7.82	3.54	3.27	1.58	3.56	2.07	3.34	**	**	-	-
	PLACE1006820	11.34	11.23	10.69	7.26	7.6	3.88	6.72	6.8	7.48	*	**	-	-
	PLACE1006826	11.68	10.21	8.37	4.26	6.11	3.55	4	5.42	6.14	*	*	-	-
	PLACE1006829	8.66	7.12	6.95	4.95	4.5	3.35	3.73	4.63	3.79	*	**	-	-
35	PLACE1006853	7.76	9.04	10.06	4.43	5.8	3.94	5.55	3.81	3.65	**	**	-	-
	PLACE1006860	13.3	14.13	11.82	7.29	7.57	5.64	7.39	5.43	7.17	**	**	-	-
	PLACE1006867	20.52	19.65	17.03	7.58	12.2	4.52	8.89	4.5	9.57	*	**	-	-
	PLACE1006875	6.86	5.29	3.98	1.69	3.65	1.95	4.64	3.37	3.97	*		-	-
	PLACE1006878	5.96	7.5	9.4	3.45	4.02	4.56	4.29	5.32	7.08	*		-	-
	PLACE1006883	17.58	24.05	25.14	11.43	14.88	9.68	8.41	13.21	13.16	*	*	-	-
40	PLACE1006898	34.11	35.72	38.43	15.89	26.64	17.27	29.81	38.71	32.24	*		-	-
	PLACE1006901	35.59	25.34	29.52	17.57	24.59	23.14	7.06	14.35	10.26	**		-	-
	PLACE1006904	283.91	237.86	265.1	210.53	264.05	203.01	176.62	324.88	215.9			-	-
	PLACE1006917	8.87	8.87	10.42	4.77	9.67	4.27	2.96	3.43	5.44	**		-	-
	PLACE1006932	13.9	19.05	15.16	17.43	14.76	12.47	12.23	11.92	6.34			-	-
	PLACE1006935	5.15	5.68	5.5	4.25	5.6	3.94	4.66	3.59	4.94			-	-
45	PLACE1006956	73	65.43	79.54	37.1	42.04	37.7	45.33	35.06	47.75	**	**	-	-
	PLACE1006958	14.71	17.1	17.16	7.75	10.57	5.67	10.62	14.42	12.92	**		-	-
	PLACE1006959	6.43	6.88	7.06	3.86	5.4	3.09	3.53	7.7	6.81	*		-	-
	PLACE1006961	11.78	13.88	26.99	6.58	7.47	6.43	7.89	10.93	8.94			-	-
	PLACE1006962	8.5	7.71	10.43	6.5	8.54	6.61	4.94	6	6.79	*		-	-
	PLACE1006966	30.69	63.35	44.81	30.7	31	25.61	17.51	20.36	25.7			-	-
50	PLACE1006979	9.85	10.88	9.97	5.88	6.1	5.13	5.32	5.52	6.47	**	**	-	-
	PLACE1006989	23.14	43.35	32.93	27.05	47.4	17.28	23.49	21.59	16.62			-	-
	PLACE1007001	14.41	12.66	17.15	10.97	5.54	6.74	6.74	7.87	8.22	*	**	-	-
	PLACE1007014	9.24	9.35	10.83	6.4	6.04	5.94	4.96	6.16	5.52	**	**	-	-
	PLACE1007021	56.53	38.34	63.46	20.03	40.71	38.97	20.72	29.77	27.88		*	-	-
	PLACE1007026	65.54	56.8	77.56	57.55	60.7	57.93	57.5	56.64	67.29			-	-
55	PLACE1007028	8.5	10.76	17.58	7.89	7.62	6.26	3.31	5.38	3.91	*		-	-
	PLACE1007038	7.96	7.89	13.66	4.19	6.33	3.79	2.05	3.52	4.03	*		-	-
	PLACE1007040	8.13	9.51	15.11	4.74	7.09	4.87	8.84	8.35	6.98			-	-

Table 483

	PLACE1007045	15.78	21.85	22.19	13.09	30.39	13.83	9.78	12.74	10.75	*	*	-
	PLACE1007048	19.3	14.44	24.23	9.41	10.57	11.83	9.91	12.06	15.93	*	*	-
5	PLACE1007053	9.31	5.29	12.35	5.07	3.06	4.56	5.35	25.19	5.41			
	PLACE1007068	8.67	4.77	10.34	5.02	4.28	3.54	2.63	5.02	2.74			
	PLACE1007070	18.55	13.15	15.29	11.03	10.78	10.43	6.96	7.21	5.68	*	**	-
	PLACE1007076	17.03	17.73	24.8	24.48	28.32	20.68	16.51	16.83	13.48			
	PLACE1007077	7.35	10.92	12.26	4.54	5.11	3.6	6.43	5.8	5.66	*	*	-
	PLACE1007081	41.36	35.79	51.18	37.04	46.87	29.31	28.18	20.46	26.31	*	*	-
10	PLACE1007082	14.74	14.27	12.93	7.51	10.12	5.83	13.51	10.86	10.42	*	*	-
	PLACE1007092	9.52	6.79	8.77	4.99	5.23	4.04	4.42	5.84	7.46	*	*	-
	PLACE1007096	8.7	7.04	11.33	3.9	6.35	2.61	4.31	10.62	7.33	*	*	-
	PLACE1007097	5.03	2.47	6.96	1.99	2.48	1.11	1.28	4.01	1.45			
	PLACE1007099	14.43	9.17	8.68	4.57	6.07	4.14	4.7	5.17	7.04	*	*	-
	PLACE1007105	9.93	9.89	19.72	4.22	5.46	3.96	5.83	6.27	9.12			
15	PLACE1007108	7.87	5.2	13.72	3	3.64	1.32	1.96	5.82	6.69			
	PLACE1007111	24.26	33.98	33.96	8.75	19.56	14.7	10.61	6.46	7.98	*	**	-
	PLACE1007112	13.01	15.69	10.39	7.41	17.53	7.08	9.51	4.37	5.03	*	*	-
	PLACE1007130	7.28	5.04	7.51	3.97	3.76	4.18	4.15	3.12	4.45	*	*	-
	PLACE1007132	11.01	5.03	12.54	6.14	8.23	7.16	4.79	4.84	3.32			
20	PLACE1007140	8.1	6.86	9.35	5.74	3.15	5.4	5.1	3.71	4.08	*	*	-
	PLACE1007143	7.85	4.78	7.3	2.76	4.42	3.52	3.05	2.29	1.7	*	*	-
	PLACE1007169	21.25	20.42	20.37	9.68	16.47	8.01	13.15	12.99	9.63	*	**	-
	PLACE1007178	5.69	6.23	10.18	2.7	4.22	2.51	2.33	2.04	2.65	*	*	-
	PLACE1007190	9.72	11.86	11.22	5.23	6.85	7.11	6.69	5.59	16.1	**	*	-
	PLACE1007201	11.31	9.93	8.97	4.82	6.82	3.46	5.63	4.72	7.11	*	*	-
	PLACE1007202	14.96	8.93	16.56	5.53	5.66	4.16	5.42	6.71	5.73	*	*	-
25	PLACE1007226	110.77	93.69	99.41	39.5	91.72	72.21	82.39	66.08	68.98	*	*	-
	PLACE1007238	53.4	44.43	54.82	32.05	30.06	27.04	24.59	23.68	27.03	**	**	-
	PLACE1007239	22.01	21.57	16.94	9.88	9.77	7.42	7.13	6.76	5.92	**	**	-
	PLACE1007242	8.39	6.41	6.58	2.97	3.53	2.45	2.76	1.3	1.2	**	**	-
	PLACE1007243	51.6	47.43	46.65	38.48	53.48	36.76	30.03	24.3	28.99	**	**	-
	PLACE1007247	13.13	15.22	14.84	6.24	10.32	8.42	5.62	3.59	3.12	*	**	-
30	PLACE1007257	10	9.05	8.75	2.44	7.1	2.96	4.72	2.48	2.64	*	**	-
	PLACE1007274	7.6	6.25	7.77	4.39	3.79	3.63	3.01	2.85	2.82	**	**	-
	PLACE1007276	4.51	6.36	6.4	3.01	2.72	2.17	2.35	3.34	6.03	**	*	-
	PLACE1007282	6.97	4.05	5.61	2.64	2.11	3.56	3.82	3.22	3.39	*	*	-
	PLACE1007286	11.57	9.64	10.32	4.04	6.1	5.17	5.17	3.51	3.72	**	**	-
	PLACE1007296	16.68	11.68	9.05	4.46	6.87	6.7	3.08	3.72	1.93	*	*	-
35	PLACE1007301	14.64	13.62	12.24	3.61	5.07	2.97	5.09	2.86	3.16	**	**	-
	PLACE1007314	8.78	10.14	10.9	5.59	4.99	2.5	3.88	2.16	3.2	**	**	-
	PLACE1007317	8.02	7.14	6.45	3.78	5.35	2.25	2.6	5.13	4.46	*	*	-
	PLACE1007329	6.93	6.45	9.13	3.46	3.47	2.66	3.68	2.3	2.77	**	**	-
	PLACE1007338	57.3	54.81	50.58	25.62	27.62	24.63	49.58	43.5	58.48	**	*	-
40	PLACE1007342	41.9	26.92	32.51	26.5	30.16	25.56	24.13	20.5	25.41			
	PLACE1007345	5.67	4.07	4.44	3.74	2.2	1.81	1.89	2.39	3.75	*	*	-
	PLACE1007346	20.5	15.07	16.53	8.68	6.27	3.82	4.58	3.48	4.29	**	**	-
	PLACE1007359	41.26	41.58	38.73	21.16	26.14	23.96	27.05	27.12	33.74	**	**	-
	PLACE1007367	8.65	8.31	7.96	1.51	3.49	1.31	3.83	1.42	3.11	**	**	-
	PLACE1007375	12.55	10.83	9.7	1.39	5.63	1.68	2.54	2.85	2.14	**	**	-
45	PLACE1007377	6.98	4.2	6.44	4.26	4.62	2.93	3.59	4.11	3.58			
	PLACE1007386	12.07	10.56	14.15	4.68	4.55	5.21	6.12	7.62	8.27	**	*	-
	PLACE1007392	24.21	18.68	19.13	13.92	12.02	7.51	28.83	13.55	12.42	*	*	-
	PLACE1007402	16.76	19.32	15.87	8.17	8.78	7.34	11.49	10.03	10.79	**	**	-
	PLACE1007409	9.51	9.82	11.04	5.11	5.51	7.23	4.08	2.01	3.77	**	**	-
	PLACE1007416	22.54	28.88	22.62	18.84	13.11	6.16	9.22	5.36	7.49	*	**	-
50	PLACE1007420	14.67	16.22	16.74	8.73	9.19	6.79	10.55	5.47	7.91	**	**	-
	PLACE1007431	28.03	25.88	21.18	15.73	16.55	11.3	26.89	15.55	26.27	*	*	-
	PLACE1007450	6.82	6.06	4.68	4.06	4.16	1.71	5.65	4.38	4.35			
	PLACE1007452	14.4	7.71	4.99	5.04	6.12	1.89	4.23	8.8	6.06			
	PLACE1007454	49.36	46.08	36.43	21.1	38.54	20.65	11.86	16.68	14.49	**	*	-
	PLACE1007460	11.52	10.93	12.45	8.16	8.35	4.82	9.8	9.12	12.38	*	*	-
55	PLACE1007478	12.6	13.38	10.86	4.17	8.16	7.05	7.4	4.59	6.97	*	**	-
	PLACE1007484	10.71	6.45	6.68	3.65	4	2.5	4.9	2.97	5.47	*	*	-
	PLACE1007488	14.59	14.99	17.16	7.24	4.48	5.55	6.08	3.67	8.77	**	**	-



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	PLACE1007507	16.63	14.22	12.4	6.49	10.52	5.63	19.33	11.77	17.21	*	-
	PLACE1007511	13.25	11.24	10.12	3.93	3.98	2.6	3.01	2.43	4.23	**	**
5	PLACE1007513	4.53	2.47	3.69	3.11	1.64	1.97	3.06	2.87	2.04		
	PLACE1007524	49.4	41.73	37.58	21.38	27.05	16.04	48.44	42.69	43.18	*	-
	PLACE1007525	7.48	5.19	4.73	2.29	4.06	1.12	3.74	3.09	4.25		
	PLACE1007537	8.42	7.3	9.61	4.91	5.72	3.83	6.57	5.7	5.93	*	*
	PLACE1007544	5.67	4.7	5.81	1.28	3.36	2.37	4.39	1.96	2.74	*	*
	PLACE1007547	16.52	13.81	13.32	8.64	13.2	6.38	11.36	9.38	8.52	*	*
10	PLACE1007557	22.7	26.33	16.93	8.14	13.6	7.63	24.98	15.24	20.74	*	-
	PLACE1007560	25.9	29.34	29.57	9.23	13.41	19.28	21.02	29.63	20.17	*	-
	PLACE1007565	3.88	2.26	3.15	1.89	4.77	2.57	1.98	2.22	2.43		
	PLACE1007580	4.59	3.09	5.83	2.2	6.97	1.42	1.87	5.45	1.54		
	PLACE1007583	3.85	2.11	3.18	1.64	4.14	4.12	2.02	2.49	2.5		
	PLACE1007591	5.53	6.61	10.65	2.9	4.26	2.95	4.34	4.96	5.37		
15	PLACE1007598	9.38	9.28	9	2.96	15.1	3.88	2.92	7.29	5.52	*	-
	PLACE1007610	3.93	7.09	11.32	4.32	11.34	3.52	4.35	8.81	6.31		
	PLACE1007618	4.85	4.13	5.18	3.66	4.39	5.01	3.62	3.16	4.04	*	-
	PLACE1007621	20.28	8.69	15.56	6.24	12.9	7.98	10.43	10.06	8.81		
	PLACE1007626	35.43	28.05	45.42	25.74	50.46	26.54	38.37	49.51	35.74		
	PLACE1007632	8.18	6.61	8.24	5.02	13.18	12.74	5.22	7.37	5.53		
20	PLACE1007635	17.84	21.72	22.91	16.26	21.82	12.51	7.83	15.31	12.34	*	-
	PLACE1007645	29.46	44.32	50.79	23.79	28.69	29.97	18.24	19.23	26.32	*	-
	PLACE1007649	5.43	7.86	6.71	4.51	9.04	3.18	4.73	2.18	2.74	*	-
	PLACE1007659	23.48	33.01	29.15	18.02	23.66	14.9	25	27.47	23.31		
	PLACE1007669	17.27	10.25	11.99	6.18	6.01	5.07	11.02	11.92	11.97	*	-
	PLACE1007677	15.06	16.35	15.01	8.53	7.7	12.44	11.15	10.52	8.69	*	**
25	PLACE1007688	30.37	21.3	31.84	9.3	9.6	6.97	5.43	7.59	4.3	**	**
	PLACE1007690	16.29	14.9	13.94	8.07	9.45	10.99	5.55	6.43	7.69	**	**
	PLACE1007697	7.22	8.07	8.65	7.42	10.69	12.34	4.08	7.67	5.36		
	PLACE1007702	9.68	16.27	14.18	8.71	12.06	12.61	6.79	7.15	7.48	*	-
	PLACE1007706	14.91	16.84	14.3	10.72	14.81	6.93	5.13	7.31	8.61	**	-
	PLACE1007725	15.22	10.08	11.32	8.01	8.72	6.5	4.92	7.04	8.09	*	-
30	PLACE1007729	9.62	8.04	8.37	6.72	6.7	9.05	5.49	8.22	6.25		
	PLACE1007730	14.54	9.51	13.82	11.08	11.03	10.92	7.95	12.03	8.17		
	PLACE1007737	26.23	17.29	21.46	12.32	15.98	9.58	13.89	16.95	16.37	*	-
	PLACE1007743	15.62	16.04	17.86	8.71	10.59	7.11	6.26	11.61	4.77	**	*
	PLACE1007746	42.92	48.93	37.39	28.78	37.1	35.26	16.78	10.7	15.4	**	-
	PLACE1007753	14.39	18.43	15.85	13.55	30.64	24.37	6.15	10.27	7.82	**	-
35	PLACE1007769	10.21	11.59	12.77	11.76	15.29	7.33	6.11	7.79	6.57	**	-
	PLACE1007780	5.74	2.24	6.02	2.59	3.98	3.4	2.92	4.75	4.26		
	PLACE1007791	7.33	7.57	11.32	6.64	9.26	5.56	5.87	21.8	5.42		
	PLACE1007807	10.4	6.68	8.59	5.19	10.28	4.84	5.47	15.67	6.17		
	PLACE1007810	21.71	5.64	13.76	5.45	11.67	20.68	5.72	5.81	5.21		
40	PLACE1007814	23.92	18.73	27.74	15.47	17.03	13.06	6.08	14.46	7.51	*	*
	PLACE1007828	9.64	11.73	14.79	8.65	13.95	8.98	3.79	6.99	9.71		
	PLACE1007829	21.85	26.65	22.58	10.61	17.88	12.23	16.05	20.8	14.7	*	-
	PLACE1007841	12.3	14.26	16.38	8.52	14.37	8.97	13.64	10.06	9.74		
	PLACE1007842	7.29	10.66	10.16	4.04	8.15	4.63	12.33	6.69	8.73		
	PLACE1007843	8.16	7.8	8.23	4.71	8.29	4.31	4.49	6.71	2.94	*	-
	PLACE1007845	14.45	11.07	14.52	8.03	11	7.42	8.69	6.18	6.07	*	*
45	PLACE1007846	9.52	9.87	9.08	6.82	5.35	6.86	5.9	8.42	7.28	**	*
	PLACE1007848	10.96	7.82	17.21	7.21	6.58	4.31	3.05	6.37	4.05		
	PLACE1007852	38.45	42.72	20.94	14.02	16.83	14.13	8.86	9.78	9.37	*	*
	PLACE1007858	19.55	23.44	22.4	13.38	19.15	12.06	12.86	10.77	11.27	*	**
	PLACE1007866	106.06	120.7	80.75	100.84	136.45	101.33	115.22	114.23	135.63		
50	PLACE1007871	46.64	38.13	36.79	13.91	18.93	11.35	19.19	30.79	21.75	**	*
	PLACE1007877	11.11	8.45	11.03	7.02	8.84	8.93	6.39	7.32	5.13	*	-
	PLACE1007878	37.18	35.47	41.1	20.44	30.52	24.13	17.29	22.96	22.69	*	**
	PLACE1007881	7.08	8.99	9.43	6.21	6.72	5.42	3.38	3.24	2.37	*	**
	PLACE1007885	13.54	9.97	15.34	8.52	12.53	23.99	7.37	7.86	5.04	*	-
	PLACE1007897	9.52	10.47	10.76	6.15	8.22	8.75	3.33	3.79	2.67	*	**
55	PLACE1007908	27.14	31.91	21.03	11.57	16.17	12.14	8.02	9.92	9.32	*	**
	PLACE1007922	13.27	17.29	11.92	8.56	15.72	12.01	8.76	6.61	6.69	*	-
	PLACE1007946	8.9	7.88	9.69	3.7	5.72	2.73	4.49	7.73	5.93	**	-

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	PLACE1007950	123	99.57	90.18	75	73.07	58.93	91.95	114.45	65.58	*	-
	PLACE1007954	8.61	7.27	7.95	5.58	7.49	5.54	3.77	4.03	2.97	**	-
5	PLACE1007955	17.64	15.71	13.66	11.51	9.3	9.77	6.99	7.04	4.12	*	-
	PLACE1007956	11.86	9.09	7.66	6.57	9.25	6.9	4.06	4.11	3.44	*	-
	PLACE1007958	9.03	7.99	9.04	2.65	4.9	3.85	2.65	3.75	2.07	**	-
	PLACE1007965	15.3	16.37	14.75	7.93	11.66	10.38	7.23	6.65	5.87	*	-
	PLACE1007969	24.54	27.08	14.83	16.49	16.9	27.64	8.5	10.51	6.83	*	-
	PLACE1007971	14.86	11.23	10.66	4.6	5.77	4.48	5.47	4.42	6.63	**	-
10	PLACE1007990	13.72	7.91	11.82	6.44	6.58	7.05	6.02	6.86	7.23		-
	PLACE1008000	8.41	4.96	5.71	4.66	6.7	5.87	3.52	3.67	3.05		-
	PLACE1008002	8.38	10.22	5.77	6.22	6.73	3.91	3.28	5.34	3.3	*	-
	PLACE1008037	7.47	6.35	4.25	2.21	4.95	4.35	2.35	1.88	2.58	*	-
	PLACE1008044	23.79	15.95	12.5	7.05	19.86	9.73	6.75	10	6.08		-
	PLACE1008045	19.99	21.06	9.24	5.88	14.67	9.04	6.52	7.55	2.12		-
15	PLACE1008080	15.75	26.6	10.27	8.38	25.41	7.91	16.05	14.95	13.99		-
	PLACE1008092	7.67	5.27	5.41	3.04	5.53	3.46	4.86	3.3	3.17		-
	PLACE1008095	16.14	13.84	10.97	4.61	15.55	7.49	3.99	9.83	5.13	*	-
	PLACE1008105	10.75	13.42	9.63	5.46	13.95	7.7	10.03	7.96	6.35		-
	PLACE1008107	6.1	7.51	5.49	4.1	6.68	4.81	2.94	3.48	3.2	**	-
	PLACE1008111	12.94	8.4	7.21	4.85	8.37	6.82	4.56	1.47	2.41	*	-
20	PLACE1008113	48.12	32.36	36.95	30.18	28.53	18.75	11.39	9.55	15.2	**	-
	PLACE1008122	12.52	11.61	10.25	6.59	8.27	7	4.17	3.46	4.27	**	-
	PLACE1008129	12.19	11.22	9.29	6.85	14.96	11.14	8.9	8.46	6.51		-
	PLACE1008132	21.17	14.41	14.91	9.14	12.76	11.94	8.42	8.33	8.23	*	-
	PLACE1008137	10.44	6.69	4.43	4.58	5.26	3.39	2.11	5.99	2.53		-
	PLACE1008174	12.98	8.11	5.85	5.98	7.01	8.19	6.41	5.88	5.58		-
25	PLACE1008177	5.92	6.91	4.83	3.39	4.55	3.28	3.39	1.53	3.61	*	-
	PLACE1008181	12.18	13.31	12.04	4.81	8.68	5.04	4.65	2.16	4.62	**	-
	PLACE1008195	13.39	9.3	9.62	7.44	7.76	6.35	5.1	3.44	5.91	*	-
	PLACE1008198	12.57	11.23	9.83	6.75	6.36	4.49	7.75	4.45	5.55	**	-
	PLACE1008201	10.88	12.64	8.33	6.13	9.66	7.65	6.3	5.05	9.18		-
	PLACE1008209	10.96	9.72	8.1	4.34	4.16	5.71	10.15	7.4	9.7	**	-
30	PLACE1008226	27.87	17.88	18.73	12.29	14.5	8.3	21.53	17.31	27.74		-
	PLACE1008227	19.93	14.99	13.17	9.05	11.55	7.15	13.25	11.51	13.73	*	-
	PLACE1008231	7.21	4.7	4.12	4.59	4.49	3.26	5.49	4.08	3.39		-
	PLACE1008238	12.79	18.51	15.04	5.47	8.57	11.49	6.6	7.97	4.88	*	-
	PLACE1008244	10.53	9.75	8.28	4.31	8.05	4.21	4.37	5.37	5.5	*	-
	PLACE1008249	15.98	17.02	8.54	6.34	10.36	6.43	17.75	4.65	8.03		-
35	PLACE1008266	102.69	124.96	102.56	88.83	113.4	78.29	73.83	64.62	80.68	*	-
	PLACE1008273	14.29	12.39	14.99	6.95	10.06	11.71	9.42	8.24	5.42	*	-
	PLACE1008275	5.26	4.99	6.79	3.64	10.8	3.9	3.08	3.54	1.54	*	-
	PLACE1008280	6.85	6.62	6.82	4.72	8.46	4.99	3.58	6.79	2.98		-
	PLACE1008282	12.89	9.41	16.7	11.11	18.66	13.55	5.47	11.9	7.88		-
	PLACE1008297	12.14	13.11	10.26	7.3	9.97	7.71	3.51	6.91	7.44	*	-
40	PLACE1008303	11.47	15.79	13.39	11.12	14.28	7.92	5.84	6.87	4.96	**	-
	PLACE1008309	4.41	7.26	5.38	6.98	9.29	6.05	3.56	4.2	4.65		-
	PLACE1008315	19.59	15.1	15.12	9.86	9.1	7.96	7.41	8.94	11.54	**	-
	PLACE1008329	9.22	7.92	9.32	5.09	12.42	9.18	10.32	5.48	5.2		-
	PLACE1008330	11.04	9.94	11.21	6.66	7.9	5.74	7.19	13.56	9.01	**	-
	PLACE1008331	9	15.63	14.68	4.1	11.97	13.67	4.88	7.64	5.55	*	-
45	PLACE1008351	12.84	22	18.28	7.61	13.2	12.68	4.26	8.16	3.26	*	-
	PLACE1008356	13.82	13.87	16.44	11.31	18.42	14.21	4.74	8.97	9.76	*	-
	PLACE1008359	10.61	8.67	5.76	4.5	6.41	4.58	3.38	3.42	3.83	*	-
	PLACE1008368	15.16	18.55	16.33	11.79	13.53	6.82	4.87	5.65	5.64	**	-
	PLACE1008369	3.81	2.08	4.52	1.83	1.71	1.5	2.12	2.77	3.86		-
	PLACE1008382	11.15	8.41	9.64	4.52	7.73	5.42	7.63	11.47	6.48	*	-
50	PLACE1008394	11.83	9.98	11.91	7.27	9.44	5.81	12.55	9.98	4.42	*	-
	PLACE1008398	23.83	19.35	38.34	11.94	10.53	17.6	18.05	34.01	14.62		-
	PLACE1008401	9.05	11.72	16.92	8.36	9.24	6.49	5.59	6.98	7.72		-
	PLACE1008402	8.61	13.91	16.2	7.29	15.86	9.77	4.08	3.77	5.17	*	-
	PLACE1008405	93.35	102.54	109	58.1	65.02	51.5	64.76	63.76	63.34	**	-
	PLACE1008409	9.15	10.93	10.45	7.65	10.56	6.32	5.13	6.5	6.16	**	-
55	PLACE1008420	4.6	3.84	4.48	2.08	3.3	3.48	3.03	3.37	1.89	*	-
	PLACE1008424	8.77	7.89	8.59	4.05	4.03	4.43	4.27	11.48	5.37	**	-

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	PLACE1008426	9.02	4.49	7.91	3	6.94	4.35	2.2	4.69	5.02				
	PLACE1008429	6.72	4.48	8.18	2.61	5.16	2.94	4.14	3.81	3.51				
	PLACE1008430	14.21	10.67	13.56	6.18	13.27	13.78	7.02	13.13	6.7				
5	PLACE1008437	10.05	12.15	13.23	7.3	7.15	7.37	5.37	12.87	6.94	**		-	
	PLACE1008453	9.93	7.46	12.22	2.24	6.5	5.48	4.46	4.26	3.11	*	*	-	
	PLACE1008454	21.6	22.78	23.98	10.1	17.4	10.34	15.68	15.08	11.82	*	**	-	
	PLACE1008455	34.62	30.32	25.55	12.02	19.33	14.29	16.61	22	23.57	*	*	-	
	PLACE1008457	11.67	8.98	10.52	6.51	8.83	5.84	9.41	9.29	9.88	*		-	
10	PLACE1008465	7.78	1.83	9.65	2.4	6.54	3.49	3.66	7.05	5.33			-	
	PLACE1008469	9.74	7.14	10.33	5.36	5.23	4.43	4.05	9.23	7.36	*		-	
	PLACE1008488	7.69	9.06	16.27	2.87	27.47	11.79	3.3	10.09	3.95			-	
	PLACE1008519	13.67	13.58	16.65	12.54	13.83	10.17	7.48	12.69	9.26			-	
	PLACE1008524	16.01	17.28	16.34	7.24	7.92	7.96	6.91	6.21	5.65	**	**	-	
	PLACE1008531	10.83	9.9	10.84	3.6	7.89	4.88	5.5	5.84	4.3	*	**	-	
15	PLACE1008532	31.22	27.65	29.16	13.43	17.17	10.64	20	23.65	23.08	**	**	-	
	PLACE1008533	16.83	14.02	15.02	5.15	9.56	6.45	8.04	10.1	5.87	**	**	-	
	PLACE1008542	11.05	6.89	12.38	7.62	8.01	5.5	3.52	4.43	4.89	*		-	
	PLACE1008549	8.08	8.32	6.56	2.76	4.31	2.64	3.19	4.98	1.09	**	*	-	
	PLACE1008560	9.22	6.82	8.11	4.41	4.7	3.86	2.93	3	1.98	**	**	-	
20	PLACE1008567	12.46	12.8	11.19	3	4.87	3.75	6.88	4.77	3.6	**	**	-	
	PLACE1008568	11.23	14.36	12.98	7.02	10.07	9.2	4.7	4.88	4.71	*	**	-	
	PLACE1008569	26.76	24.83	18.12	14.19	21.2	18.33	7.27	6.81	8.32	**		-	
	PLACE1008584	12.08	11.9	8.94	4.22	7.86	8.69	3.89	8.17	12.55			-	
	PLACE1008585	31.41	26.84	21.37	12.16	16.5	14.29	13.28	12.03	8.95	*	**	-	
	PLACE1008603	88.44	58.86	85.85	77.22	107.17	81.02	46.69	50.43	38.76	*		-	
	PLACE1008621	8.51	5.24	9.31	3.02	5.85	4.1	5.45	4.49	4.31			-	
25	PLACE1008625	5.93	4.92	6	3.54	3.65	3.16	1.59	3.39	1.97	**	**	-	
	PLACE1008626	7.17	7.14	8.41	4.47	6	4.22	1.34	2.51	2.04	*	**	-	
	PLACE1008627	16.63	17.04	15.47	5.85	10.41	6.49	6.26	6.1	3.78	**	**	-	
	PLACE1008629	17.85	11.92	13.81	7.55	20.73	20.07	19.18	21.96	10.11			-	
	PLACE1008630	10.34	9.61	9.25	3.39	5.31	3.93	4.34	4.76	3.98	**	**	-	
30	PLACE1008643	13.74	8.06	11.06	4.37	9.48	6.43	6.52	10.46	6.53			-	
	PLACE1008650	8.08	8.41	6.76	5.59	6.65	6.55	3.49	3.07	2.46	**		-	
	PLACE1008657	20.07	16.69	13.65	10.15	11.39	11.63	13.41	12.65	11.83	*		-	
	PLACE1008664	16.27	13.14	9.24	7.33	8.26	11.12	3.83	4.48	3.67	*		-	
	PLACE1008693	19.24	12.55	11.48	5.9	7.48	8.22	10.23	10.76	7.26	*		-	
	PLACE1008696	15.27	18.92	13.52	8.56	14.35	6	9.09	6.63	6.3	**	**	-	
35	PLACE1008715	12.07	13.35	10.97	4.79	8.42	4.36	3.79	3.86	5.13	*	**	-	
	PLACE1008716	9.95	8.16	6.63	2.27	4.4	4.51	4.19	6.11	4.54	*	*	-	
	PLACE1008722	23.06	17.9	16.82	6.63	6.45	7.4	2.92	4.69	5.05	**	**	-	
	PLACE1008738	22.32	18.29	21.17	13.47	19.87	5.51	15.63	19.57	23.28	*	*	-	
	PLACE1008742	84.96	67.74	75.79	53.3	53.65	55.26	60.09	57.16	55.95	*	*	-	
	PLACE1008744	16.51	21.18	12.37	7.32	20.16	7.33	4.32	8.49	4.3	*		-	
40	PLACE1008748	11.7	8.68	7.89	3.6	3.19	1.95	5.93	2.92	4.46	**	*	-	
	PLACE1008757	11.86	10.89	13.3	7.9	13.9	4.82	5.45	7.52	5.79	**		-	
	PLACE1008766	12.58	9.83	17.07	7.19	5.62	5.22	3.78	3.59	4.47	*	*	-	
	PLACE1008785	10.19	7.64	9.9	4.61	6.56	4.55	5.8	6.94	7.6	*		-	
	PLACE1008790	13.83	10.34	7.69	5.61	9.25	7.49	3.5	9.44	5.2			-	
	PLACE1008798	38.55	17.87	28.15	8.39	18.4	13.81	20.54	7.92	18.2			-	
45	PLACE1008807	7.39	8.08	6.82	3.5	7.56	4.57	3.41	3.26	4.62	**	**	-	
	PLACE1008808	14.69	14.79	11.52	7.99	7.57	5.08	6.28	4.51	3.87	**	**	-	
	PLACE1008813	11.75	10.29	9.69	7.89	7.9	5.45	5.57	3.03	5.81	*	**	-	
	PLACE1008836	10.67	11.89	10.55	6.13	6.4	5.79	6.93	5.51	7.49	**	**	-	
	PLACE1008851	17.38	11.13	11	56.43	9.1	6.6	16.91	8.29	14.77			-	
	PLACE1008854	6.2	6.11	5.28	5.3	4.42	2.5	6.46	5.33	5.1			-	
50	PLACE1008864	19.27	13.51	11	10.42	10.96	6.46	14.43	10.21	14.23			-	
	PLACE1008867	23.06	15	11.22	6.2	9.84	4.86	5.54	7.61	6.44	*		-	
	PLACE1008876	176.15	214.21	204.76	126.27	307.85	120.09	159.59	163.82	275.73			-	
	PLACE1008887	10.24	8.9	12.49	4.83	6.78	7.76	5.17	4.7	6.53	*	*	-	
	PLACE1008902	13.44	7.31	7.6	4.55	6.21	3.19	5.49	3.64	7.36			-	
	PLACE1008911	20.57	23.29	15.12	14.15	10.76	7.02	9.39	4.72	9.35	*	*	-	
55	PLACE1008917	7.8	5.68	7.21	2.11	3.42	3.23	3.5	4.03	3.26	**	**	-	
	PLACE1008920	3.68	3.98	2.25	1.85	2.38	2.78	2.45	2.52	1.03			-	
	PLACE1008925	6.03	2.49	3.19	2.51	4.89	2.3	3.22	3.16	2.76			-	

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	PLACE1008930	19.58	15.04	12.13	4.18	13.75	5.17	6.22	5.55	4.1	*	-
	PLACE1008934	16.24	5.52	7.38	4.49	6.52	4.37	6.49	7.37	5.19		
5	PLACE1008941	7.73	6.12	5.84	2.96	5.21	1.59	3.04	3.68	3.45	**	-
	PLACE1008947	14.65	13.48	10.43	5.14	6.75	4.89	11.51	10.32	9.84	**	-
	PLACE1008984	13.25	12.98	9.34	5.45	4.62	4.47	6.01	1.98	3.15	**	-
	PLACE1008985	7.07	4.44	3.91	3.08	5.06	1.59	3.53	4.2	7.06		
	PLACE1008994	3.13	3.32	2.46	1.43	1.88	1.44	1.4	0.58	1.95	**	-
10	PLACE1009020	10.8	10.64	11.79	9.97	10.93	10.07	6.16	7.97	6.48	**	-
	PLACE1009027	3.76	1.41	3.27	1.39	2.64	1.03	1.54	3.8	0.71		
	PLACE1009039	4.77	3.08	3.94	1.85	3.67	1.57	1.09	2.8	1.86	*	-
	PLACE1009045	8.82	6.04	9.52	3.29	4.82	2.76	2.8	7.24	2.61	*	-
	PLACE1009048	2.06	2.51	4.63	1.04	3.38	1.38	0.62	1.42	2.18		
	PLACE1009050	3.79	3.3	4.62	1.78	8.12	1.71	2.85	3.16	1.84		
15	PLACE1009060	19.41	22.53	16.93	15.31	14.46	12.87	9.32	9.93	14.15	*	-
	PLACE1009067	9.68	7.46	10.13	4.56	10.58	6.42	9.09	6.46	12.36		
	PLACE1009071	20.58	20.38	20.82	12.02	12.73	10.86	11.69	13.76	13.78	**	-
	PLACE1009090	9.2	7.98	10.33	4.26	8.7	11	5.63	8.05	9.63		
	PLACE1009091	83.22	75.58	81.93	64.69	72.29	69.99	50.11	57.74	52.35	*	-
	PLACE1009094	10.97	9.99	9.32	7.26	14.47	8.52	5.42	12.88	9.03		
20	PLACE1009099	8.3	10.72	9.62	5.36	7.81	7.04	3.55	4.21	4.97	*	-
	PLACE1009110	7.1	4.33	5.05	4.77	6.82	3.04	3.19	5.04	4.48	**	-
	PLACE1009111	4.96	7.16	3.67	5.5	7.31	3.03	4.35	3.44	4.4		
	PLACE1009113	16.47	13.6	10.85	8.16	11.25	17.03	7.41	8	12.76		
	PLACE1009130	13.26	8.46	18.05	9.61	8.47	7.77	7.71	8.47	5.51		
	PLACE1009150	9.24	9.08	10.56	5.69	8.31	5.53	5.87	7.76	4.55	*	-
25	PLACE1009155	15.03	18.94	19.94	9.19	13.17	10.27	14.29	28.01	20.9	*	-
	PLACE1009158	11.31	7.28	10.08	9.16	8.65	7.93	4.47	5.84	5.53	*	-
	PLACE1009166	6.72	5.63	9.02	5.97	6.75	3.86	4.53	5.03	5.29		
	PLACE1009172	12.12	10.58	13.44	7.25	11.43	5.16	4.32	7.13	6.22	**	-
	PLACE1009174	15.11	18.12	12.65	13.74	20.86	11.26	7.87	11.41	11.21		
	PLACE1009183	26.21	21.05	18.45	14.71	13.12	9.63	13.01	10.13	17.14	*	-
30	PLACE1009186	16.33	12.69	14.24	9.34	9.66	8.31	3.27	14.09	4.74	**	-
	PLACE1009190	10.56	9.79	11.19	7.65	14.06	8.19	4	6.56	7.14	*	-
	PLACE1009196	13.22	10.75	11.8	7.38	9.71	7.53	10.55	12.57	8.91	*	-
	PLACE1009200	19.33	23.87	22.95	10.45	11.73	10.18	10.96	16.99	17.03	**	-
	PLACE1009217	14.13	24.09	16.64	11.71	10.57	10.58	3.82	4.64	6.12	*	-
	PLACE1009230	27.31	26.63	32.64	10.81	26.12	18.34	16.83	20.7	24.31	*	-
35	PLACE1009236	9.03	10.62	12.67	7.18	9.87	8.71	6.77	9.24	7.63		
	PLACE1009246	21.48	34.44	20.99	9.29	20.22	19.2	9.84	35.09	13.46		
	PLACE1009265	18.86	26.11	25.51	7.08	18.04	9.4	9.34	41.89	9.73	*	-
	PLACE1009279	13.38	8.53	11.2	5.1	7.71	6.09	11.6	8.18	8.91	*	-
	PLACE1009298	49.41	26.44	34.52	26.24	34.87	27.55	30.84	25.04	29.21		
	PLACE1009308	9.89	13.34	12.22	3.57	6.53	4.13	6.2	4.88	5.8	**	-
40	PLACE1009319	11.98	14.82	14.36	7.73	14.05	5.85	5.29	9.69	4.23	*	-
	PLACE1009328	12.86	13.58	15.59	6.43	10.45	5.86	7.1	8.23	11.41	*	-
	PLACE1009335	8.34	6.5	7.11	3.99	9.88	4.55	4.35	7.62	2.32		
	PLACE1009338	14.56	12.99	17.79	6.9	13.74	10.92	6.69	5.83	8.27	**	-
	PLACE1009344	6.92	5.13	5.98	3.02	11.98	4.73	3.18	3.89	2.88	*	-
	PLACE1009355	23.17	22.99	26.45	20.27	18.4	17.42	10.13	10.79	9.83	*	-
45	PLACE1009368	8.63	5.09	6.32	3.35	3.66	2.95	3.35	6.92	2.66	*	-
	PLACE1009375	8.35	5.94	11.71	3.65	4.61	3.52	3.31	4.45	3.97	*	-
	PLACE1009388	18.28	22.47	42.99	8.1	17.38	17.02	11.33	10.99	17.5		
	PLACE1009398	16.02	15.66	15.45	5.65	12.56	7.13	6.81	5.4	4.18	*	-
	PLACE1009404	17.98	10.01	28.67	4.73	28.94	16.4	9.28	9.88	5.15		
	PLACE1009410	13.78	15.39	9.6	5.62	6.24	5.55	5.28	4.64	5.63	*	-
50	PLACE1009417	16.73	9.41	10.65	12.79	9.15	6.2	6.71	6.82	7.05	*	-
	PLACE1009424	9.71	6.5	9.08	4.75	4.94	4.28	3.44	4.18	4.16	*	-
	PLACE1009434	21.73	12.22	10.01	6.12	7.87	5.95	3.69	5.83	2.87	*	-
	PLACE1009443	7.33	14.79	8.94	2.98	3.24	2.54	4.85	2.06	4.82	*	-
	PLACE1009444	13.13	14.77	17.33	7.6	10.32	8.01	6.52	5.24	6.76	*	-
	PLACE1009459	8.33	7.91	9.2	3.33	5.72	4.79	3.49	3.56	3.33	**	-
55	PLACE1009460	9.94	14.6	11.32	7.7	8.3	7.62	5.02	3.61	2.95	*	-
	PLACE1009468	12.43	12.85	9.11	5.4	5.98	4.76	4.66	5.65	8.17	**	-
	PLACE1009476	7.02	4.9	5.38	3	3.07	3.32	3.74	3.76	3.61	*	-

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	PLACE1009477	13.59	11.11	12.8	10.3	9.83	6.89	8.75	11.15	10.89				
	PLACE1009493	5.63	4.68	4.85	3.04	3.33	2.25	3.06	2.29	1.49	**	**	-	-
	PLACE1009502	11.43	9.62	8.39	5.92	5.81	5.8	4.63	7.61	3.19	*	*	-	-
5	PLACE1009524	7.56	7.26	7.63	1.87	3.86	2.97	2.66	3.37	2.46	**	**	-	-
	PLACE1009527	18.34	12.36	9.71	6.88	11.49	9.95	6.88	5.14	3.52		*	-	-
	PLACE1009531	25.38	45.76	31.03	26.02	25.63	22.82	19.07	17.64	15.03				
	PLACE1009535	12.3	11.08	8.3	3.83	6.2	5.84	3.36	3.71	4.06	*	**	-	-
	PLACE1009539	8.83	10.23	7.02	4.34	7.56	5.81	5.39	6.61	6.43				
10	PLACE1009540	37.43	26.63	27.99	14.5	25.74	28.63	21	11.9	8.26	*		-	-
	PLACE1009542	12	5.45	5.7	3.62	4.51	6	3.18	3.69	2.67				
	PLACE1009546	12.67	10.42	6.26	3.72	5.36	5.98	4.35	10.8	3.66				
	PLACE1009556	7.91	6.37	6.72	5.1	4.62	3.16	3.16	2.46	2.95	*	**	-	-
	PLACE1009569	11.99	15.44	10.67	4.76	13.77	8.59	5.94	5.33	6.24		**	-	-
	PLACE1009571	7.82	9.37	5.59	3.8	7.13	3.69	5.84	2.83	4.48				
15	PLACE1009573	22.09	15.96	12.31	9.76	17.27	9.7	8.26	8.91	7.87	*	*	-	-
	PLACE1009576	13.53	9.49	9.65	4.21	6.31	4.13	5.49	5.78	4.15	*	*	-	-
	PLACE1009580	9.86	9.33	7.56	5.13	7.69	4.5	8.75	3.59	4.85				
	PLACE1009581	12.95	12.1	8.15	7.19	5.84	4.99	3.45	2.48	3.53	*	**	-	-
	PLACE1009587	13.3	7.18	8.26	7.06	6.26	5.41	3.85	4.9	4.28				
20	PLACE1009593	18.08	14.97	12.54	14.73	10.76	9.75	5.8	5.66	6.75		**	-	-
	PLACE1009595	24.28	22.3	15.19	12.22	14.76	12.77	19.19	14	13.81				
	PLACE1009596	8.31	5.39	3.71	3.49	5.52	2.24	4.95	2.48	3.3				
	PLACE1009600	19.52	17.07	12.01	6.59	8.79	3.99	8.49	7.24	8.2	*	*	-	-
	PLACE1009604	19.98	10.38	8.96	4.18	6.3	6.58	3.83	5.54	4.55				
	PLACE1009607	17.2	18	14.19	8.35	9.63	7.56	19.54	17.62	14.33	**		-	-
25	PLACE1009613	8.31	8.44	6.06	5.1	6.18	4.22	4.39	2.55	3.96	*	*	-	-
	PLACE1009621	18.02	17.88	15.95	7.12	14.76	8.85	8.46	6.45	12.83	*	*	-	-
	PLACE1009622	16.93	9.51	8.44	5	5.84	4.46	4.96	3.18	4.98				
	PLACE1009624	23.04	19.02	15.23	8.31	9.71	5.05	7.94	5.67	7.85	*	**	-	-
	PLACE1009637	8.56	7.93	7.76	3.81	7.55	4.55	3.93	3.27	4.29		**	-	-
	PLACE1009639	14.9	6.92	3.57	7.62	5.31	8.34	6.06	5.69	7.84				
30	PLACE1009654	23.03	16.88	13.87	7.6	11.88	8.66	7.4	8.09	10.22	*	*	-	-
	PLACE1009659	17.62	16.71	15.38	8.59	15.54	12.83	6.78	8.01	7.95		**	-	-
	PLACE1009665	13.55	12.11	8.08	5.71	10.66	10.87	8.53	10.59	6.01				
	PLACE1009669	10.91	11.58	11.44	5.71	8.38	5.23	8.32	8.02	8.98	**	**	-	-
	PLACE1009670	10	4.03	5.32	3.93	4.76	8.45	5.57	4.18	5.29				
	PLACE1009708	13.41	10.39	7.63	11.97	12.63	3.57	6.84	3.75	9.58				
35	PLACE1009721	15.79	10.82	9.31	5.16	6.52	4.42	9.11	3.24	6.91	*		-	-
	PLACE1009731	5.6	6.57	11.06	5.5	8.58	5.78	5.45	4.8	9.13				
	PLACE1009735	9.43	10.36	12.52	8.67	8.77	6.91	8.15	10.58	12.7				
	PLACE1009737	8.36	8.02	10.98	5.74	17.02	9.89	4.98	11.47	4.66				
	PLACE1009741	8.67	7.59	11.34	6.59	7.8	4.16	2.63	4.89	4.5	*		-	-
	PLACE1009752	9.51	12.78	18.39	7.46	12.57	11.15	4.36	9.17	6.85				
40	PLACE1009763	16.81	19.39	15.73	12.5	15.24	13.69	4.1	8.02	6.41		**	-	-
	PLACE1009766	7.54	8.76	7.16	6.98	11.81	6.16	9.17	7.21	6.61				
	PLACE1009772	12.62	18.28	13.46	16.58	26.84	15.97	7.94	11.57	13.51				
	PLACE1009782	7.96	6.95	7.99	4.24	6.2	9.33	6.26	4.41	4.35		*	-	-
	PLACE1009794	8.71	9.98	15.31	6.91	7.94	5.64	5.81	8.68	9.35				
	PLACE1009798	15.7	11.58	19.23	8.55	9.28	7.81	5.76	14.83	6.68	*		-	-
45	PLACE1009845	5.69	8.07	10.29	5.79	6.81	9.4	3.27	3.21	4.35		*	-	-
	PLACE1009849	4.29	6.11	7.54	5.25	6.21	5.82	3.81	4.56	5.57				
	PLACE1009857	5.97	7.92	9.09	4.47	4.42	3.88	4.36	2.37	3.86	*	*	-	-
	PLACE1009861	21.52	19.65	20.31	10.08	12.87	8.67	13.97	16.84	16.62	**	*	-	-
	PLACE1009872	225.97	496.72	352.07	405.22	548.08	335.22	583.26	839.73	801.36		*	+	+
	PLACE1009877	93.23	95.23	121.84	37.51	29.99	31.46	33.83	34.28	50.76	**	**	-	-
50	PLACE1009879	8.31	6.4	8.23	4.6	3.94	4.45	5.4	6.04	6.14	**		-	-
	PLACE1009886	6.21	5.71	6.04	3.1	4.43	3.64	3.76	3.74	3.91	**	**	-	-
	PLACE1009888	16.61	15.12	18.96	7.12	11.3	10.4	7.67	15.82	6.68	*		-	-
	PLACE1009908	10.69	13.22	16.94	7.9	15.1	13.2	5.89	21.59	11.16				
	PLACE1009919	18.85	20.8	15.18	25.14	44.25	16.53	6.38	10.08	17.42				
	PLACE1009921	12.5	11.43	13.89	6.9	11.45	10.84	6.74	7.53	6.61		**	-	-
55	PLACE1009923	37.38	53.14	35.03	28.71	69.72	45.4	23.4	36.13	28.69				
	PLACE1009924	26.03	16.67	21.48	6.94	14.99	12.69	29.73	40.32	10.81				
	PLACE1009925	10.23	25.64	14.3	6.85	14.35	14.82	6.32	35.83	7.94				

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	PLACE1009931	29.02	24.07	26.54	12.24	15.5	14.51	9.57	9.79	10.08	**	**	-	-
	PLACE1009935	8.86	7.44	9.7	2.78	11.02	5.42	14.95	3.43	6.35			-	-
5	PLACE1009947	6.29	6.77	9.33	4.25	4.43	3.14	2.04	2.93	4.01	*	*	-	-
	PLACE1009961	7.86	10.21	16.93	5.24	6.64	4.49	4.58	6.45	5			-	-
	PLACE1009971	7.79	7.18	10.26	3.38	7.18	3.34	3.67	4.69	3.08		*	-	-
	PLACE1009982	20.35	18.31	15.25	6.6	11.54	11.1	7.87	5.59	13.47	*	*	-	-
	PLACE1009992	12.32	8.01	11.62	6.39	8	6.72	5.24	5.76	6.38		*	-	-
	PLACE1009995	21.27	22.11	27.33	13.99	19.4	11.61	8.12	16.7	12.66	*	*	-	-
10	PLACE1009997	23.76	8.03	15.66	6.79	12.9	5.63	10.63	9.44	8.19			-	-
	PLACE1010002	14.56	6.35	12.19	4.66	8.08	5.35	5.32	14.28	7.75			-	-
	PLACE1010011	15.51	14.11	17.86	6.19	7.34	6.29	9.9	6.46	10.43	**	*	-	-
	PLACE1010013	6.16	5.13	12.68	2.37	2.99	1.56	3.53	4.24	2.98			-	-
	PLACE1010021	15.95	20.29	19.12	7.11	14.51	9.31	5.22	8.04	6.15	*	**	-	-
	PLACE1010023	27.49	31.11	21.32	17.41	29.7	20.44	16.49	7.28	6.33		*	-	-
15	PLACE1010031	20.87	15.58	32.54	10.16	16.34	7.15	9.85	8.36	10.28			-	-
	PLACE1010039	20.5	6.62	10.22	3.99	6.51	3.25	2.91	6.23	3.6			-	-
	PLACE1010045	11.17	9.8	13.16	5.75	8.43	6.1	5.11	5.8	5.51	*	**	-	-
	PLACE1010053	7.04	5.22	9.04	6.47	4.19	2.39	2.32	2.12	1.16		*	-	-
	PLACE1010060	18.9	18.89	15.21	7.4	8.59	8.37	12.03	13.21	10.77	**	*	-	-
	PLACE1010069	10.06	6.9	13.66	5.33	6.93	4.79	2.86	4.42	3.79		*	-	-
20	PLACE1010070	8.15	7.09	9.72	2.34	9.93	4.09	3.65	3.87	2.87		**	-	-
	PLACE1010074	63.56	56.74	39.11	24.21	42.72	26.72	25.32	15.29	17.22		*	-	-
	PLACE1010076	60.58	44.35	55.45	21.22	23.2	19.4	13.41	12.75	17.59	**	**	-	-
	PLACE1010078	13.76	11.23	14.35	6.69	10.2	8.63	4.38	4.87	4.45	*	**	-	-
	PLACE1010081	27.34	19.16	21.57	12.55	15.05	11.39	11.73	7.47	11.77	*	*	-	-
	PLACE1010083	7.1	7.48	5.64	1.97	2.64	2.62	1.69	2.61	1.96	**	**	-	-
25	PLACE1010089	11.95	9.65	9.57	5.5	5.81	4.38	4.84	2.48	4.43	**	**	-	-
	PLACE1010096	14.85	29.75	16.35	5.81	14.35	9.63	7.28	8.67	5.49			-	-
	PLACE1010102	22.29	34.08	23.15	9.26	16.03	13.51	7.63	9.06	7.61	*	**	-	-
	PLACE1010105	18.16	20.35	15.99	6.52	12.73	7.6	4.02	4.82	4.1	*	**	-	-
	PLACE1010106	19.44	22.57	15.73	8.29	8.94	12.84	10.96	10.43	10.44	*	*	-	-
	PLACE1010130	6.82	6.56	4.7	3.25	3.39	2.18	3.26	3.47	3.87	*	*	-	-
30	PLACE1010132	20.18	25.39	20.56	20.18	19.1	12.29	12.71	11.47	12.5		**	-	-
	PLACE1010134	10.35	11.42	9.66	6.05	6.05	5.55	6.72	4.12	2.88	**	**	-	-
	PLACE1010139	74.68	88.11	79.85	37.26	51.16	43.94	15.68	26.17	18.6	**	**	-	-
	PLACE1010148	10.48	7.43	9.71	13.14	7.54	4.86	3.27	4.13	7.63			-	-
	PLACE1010155	9.79	7.58	7.63	3.3	5.89	2.96	2.11	2.26	2.53	*	**	-	-
	PLACE1010156	32.59	25.06	24.61	14.7	18.09	11.09	7.29	10.58	14.48	*	**	-	-
35	PLACE1010161	8.48	13.16	10.69	5.15	8.21	6.03	4.47	3.31	5.46		*	-	-
	PLACE1010181	8.66	8.08	6.51	2.62	6.54	5.02	3.74	4.12	2.93		**	-	-
	PLACE1010194	8.57	7.46	6.67	3.93	4.98	3.84	2.86	2.08	2.37	**	**	-	-
	PLACE1010202	8.39	6.76	12.45	8.31	10.9	5.79	3.56	3.42	2.04		*	-	-
	PLACE1010231	12.97	10.31	14.49	7.96	15.61	7.14	8.93	9.42	8.37		*	-	-
	PLACE1010235	12.62	15	11.24	4.59	11.54	4.53	6.11	5.14	4.76		**	-	-
40	PLACE1010237	5.04	3.77	4.4	2.18	2.37	2.25	2.72	0.64	1.32	**	*	-	-
	PLACE1010251	9.46	4.47	6.29	5.09	4.79	10.14	3.78	5.92	3.88			-	-
	PLACE1010261	8.26	6.41	4.7	3.42	2.86	2.61	4.52	5.73	4.64	*		-	-
	PLACE1010270	7.53	8.07	6.36	3.29	6.44	3.19	3.88	4.95	3.8		**	-	-
	PLACE1010273	8.97	10.55	5.7	2.72	5.68	3.04	2.78	2.04	3.83		*	-	-
45	PLACE1010274	20.97	18.72	29.56	10.88	16.29	14.38	6.73	5.73	6.16		**	-	-
	PLACE1010277	15.29	14.99	14.3	8.87	13.93	8.53	11.24	4.25	6.68		*	-	-
	PLACE1010293	16.94	20.61	17.07	9.41	11.63	8.24	17.5	8.1	13.23	**		-	-
	PLACE1010297	38.08	33.94	34.95	17.91	31.69	15.63	31.8	20.1	25.32			-	-
	PLACE1010300	21.55	15.58	11.87	9.15	8.78	7.88	3.82	5.36	5.08		*	-	-
	PLACE1010310	323.02	293.14	231.29	170.36	221.96	136.69	214.56	235.35	207.22	*		-	-
50	PLACE1010321	10.7	10.58	7.81	4.96	7.93	6.91	5.6	6.6	6.56		*	-	-
	PLACE1010324	6.25	5.69	6.54	2.88	4.51	2.6	4.43	3.34	2.72	*	**	-	-
	PLACE1010329	14.25	11.37	11.93	5.93	10.64	4.89	9.64	9.84	9.32		*	-	-
	PLACE1010330	12.28	14.21	10.49	11.84	10.18	7.63	12	7.94	17.86			-	-
	PLACE1010335	27.7	52.66	38.23	18.39	9.7	13.5	16.61	15.38	28.61	*		-	-
	PLACE1010341	6.44	4.91	4.72	2	3.7	1.35	4.14	2.93	4.21	*		-	-
55	PLACE1010342	2.35	2.93	2.85	2.16	1.61	1.84	1.14	1.19	0.83	*	**	-	-
	PLACE1010346	10.42	6.88	7.23	4.08	5.74	2.77	5.84	6.92	5.88	*		-	-
	PLACE1010362	13.25	8.57	9.24	6.56	7.06	3.39	11.5	13.76	14.05			-	-

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	PLACE1010364	11.29	7.43	7.22	2.26	3.51	2.16	4.95	3.65	4.16	*	*	-	-
	PLACE1010368	10.78	8.61	7.03	3.98	6.56	5.19	7.58	7.15	5.73			-	-
5	PLACE1010373	30.2	28.61	24.17	14.82	22.58	10.46	24.63	20.09	20.87	*		-	-
	PLACE1010383	18.56	18.15	16.04	10	15.54	3.52	27.13	12.41	12.03			-	-
	PLACE1010385	2.48	1.73	1.18	0.83	2.33	0.49	2.65	1.19	2.06			-	-
	PLACE1010389	8.48	7.51	8.42	3.76	4.47	5.47	3.96	4.51	2.91	**	**	-	-
	PLACE1010401	3.24	0.96	4.6	2.29	2.49	1.63	2.81	2.31	1.6			-	-
	PLACE1010410	22.91	15.39	21.28	8.31	20.95	12.79	12.79	10.9	11.3	*		-	-
10	PLACE1010418	18.78	19.01	17.17	5.75	13.45	6.67	11.25	18.37	11.11	*		-	-
	PLACE1010425	10.58	10.75	18.36	4.2	4.88	3.19	8.87	11.17	8.75	*		-	-
	PLACE1010443	12.48	14.66	16.77	5.6	14.99	6.09	8.79	8.23	11.76	*		-	-
	PLACE1010445	36.17	45.7	37.43	17.56	20.28	18.29	39.23	32.46	41.56	**		-	-
	PLACE1010481	60.4	46.95	65.37	22.92	26.42	21.44	27.71	30.53	27.4	**	**	-	-
	PLACE1010482	127.4	82.31	84.53	104.64	120.51	109.85	62.48	50.87	49.97	*		-	-
15	PLACE1010491	71.28	72.3	73.41	43.51	47.95	35.09	68.63	86.51	74.84	**		-	-
	PLACE1010492	20.32	20.74	19.72	20.62	27.04	23.27	9.07	12.55	10.15	**		-	-
	PLACE1010509	11.2	13.07	17.83	8.18	12.58	8.24	5.79	8.34	7.68	*		-	-
	PLACE1010518	9.76	12.31	18.67	8.17	8.57	7.5	8.04	6.33	6.73			-	-
	PLACE1010522	8.32	9.35	9.63	6.71	11.42	6.63	6.37	5.88	7.65	*		-	-
	PLACE1010529	13.09	22.15	14.64	11.31	17.05	8.58	7.61	9.45	9.29			-	-
20	PLACE1010547	36.79	34.33	38.34	12.39	16.81	11.19	21.21	24.3	23.05	**	**	-	-
	PLACE1010560	10.15	9.34	9.56	6.09	4.54	5.89	6.02	5.35	6.13	**	**	-	-
	PLACE1010562	4.79	4.39	12.01	8.8	8.65	6.38	6.41	7.48	4.4			-	-
	PLACE1010579	74.54	67.98	59.08	46.33	48.92	48.24	56.27	84.49	60.31	*		-	-
	PLACE1010580	38.79	45.7	46.75	22.24	30	17.17	31.95	38.27	36.2	*		-	-
	PLACE1010589	29.35	25.54	32.71	12.61	15.12	14.18	19.83	24.34	23.16	**		-	-
25	PLACE1010606	31.76	30.37	40.62	15.46	19.15	14.23	22.77	25.83	28.81	**		-	-
	PLACE1010616	16.39	26.11	18.04	12.86	17.78	7.33	3.49	3.67	4.92	**		-	-
	PLACE1010622	9.08	4.75	12.08	2.52	4.26	2.63	11.54	11.12	6.28			-	-
	PLACE1010624	292.79	228.16	204.46	212.8	278.86	210.51	166.11	171.99	155.01	*		-	-
	PLACE1010628	48.66	44.83	51.05	27.25	26.82	37.41	15.79	19.04	21	*	**	-	-
30	PLACE1010629	19.03	17.43	20.71	12.12	16.38	15.36	14.93	10.66	11.67	*	*	-	-
	PLACE1010630	15.62	16.61	29.46	8.82	19.7	10.88	11.96	14.1	11.42			-	-
	PLACE1010631	22.99	34.46	25.54	20.07	21.82	17.69	19.23	10.89	16.98	*		-	-
	PLACE1010651	8	10.03	11.34	5.4	9.54	5.75	4.35	5.43	5.06	**		-	-
	PLACE1010661	13.76	16.34	32.78	7.67	13.64	27.31	6.28	10.55	7.26			-	-
	PLACE1010662	28.68	22.75	30.53	8.67	12.27	9.85	25.45	28.04	24.56	**		-	-
	PLACE1010668	37.33	37.7	40.55	22.62	25.66	20.72	36.78	44.21	37.46	**		-	-
35	PLACE1010702	12.3	6.26	13.51	6.5	7.73	5.88	8.16	17.08	6.46			-	-
	PLACE1010709	70.65	75.49	68.95	55.09	47.9	57.04	50.07	52.69	55.39	**	**	-	-
	PLACE1010713	80.41	68.48	77.71	36.46	48.82	48.26	28.63	32.14	23.64	**	**	-	-
	PLACE1010714	14.85	12.78	15.24	4.19	7.98	4.28	3.33	8.97	5.69	**	*	-	-
	PLACE1010716	10.07	15.73	17.8	4.88	22.94	9.1	5.99	13.73	3.7			-	-
40	PLACE1010717	16.27	25.02	15.64	13.63	18.64	10.49	10.76	15.16	3.55			-	-
	PLACE1010720	27.49	32.65	34.2	14.65	18.34	8.25	20.45	22.85	22.74	**	*	-	-
	PLACE1010739	32.05	33.62	24.71	15.33	21.42	15.16	17.5	28.68	18.95	*		-	-
	PLACE1010743	44.76	28.81	34.77	15.52	24.11	19.41	14.02	9.67	5.8	*	**	-	-
	PLACE1010752	26.13	19.45	22.02	11.29	9.49	11.37	16.27	24.35	13.97	**		-	-
	PLACE1010761	15.13	12.05	32.55	15.98	9.45	8.78	11.14	13.99	12.89			-	-
45	PLACE1010771	28.91	75.96	37.99	25.83	90.51	39.2	31.02	18.86	25.47			-	-
	PLACE1010784	98.45	116.91	93.11	48.56	63.14	52.26	30.32	31.37	33.38	**	**	-	-
	PLACE1010786	16.19	15.53	16.87	8.23	15.52	9.85	7	6.49	9.87	**		-	-
	PLACE1010789	46.25	33.26	40.6	14.8	19.17	10.09	44.64	47.22	35.88	**		-	-
	PLACE1010800	13.97	9.78	14.67	8.91	6.6	5.82	4.05	5.43	4.76	*	**	-	-
	PLACE1010802	13.35	16.74	27.18	16.21	23.96	4.91	12.32	5.78	37.85			-	-
50	PLACE1010811	26.9	21.58	31.28	13.09	18.01	12.69	11.33	11.86	10.25	*	**	-	-
	PLACE1010813	10.21	6.96	9.67	4.84	4.38	4.87	3.92	2.83	2.64	*	**	-	-
	PLACE1010827	10.79	10.81	12.05	5.43	7.46	5.87	6.65	5.02	3.76	**	**	-	-
	PLACE1010833	9.18	9.98	8.82	3.14	6.94	3.42	1.97	2.07	1.97	*	**	-	-
	PLACE1010839	24.14	30.08	20.18	11.7	20	12.82	16.21	11.13	15.42	*		-	-
	PLACE1010856	15.47	10.08	17.88	6.16	6.58	4.26	11.23	8.32	12.26	*		-	-
55	PLACE1010857	32.67	31.48	18.71	21.99	18.34	15.41	16.23	15.82	15.61			-	-
	PLACE1010870	5.83	4.92	4.28	3.87	3.55	2.92	2.91	2.04	1.94	*	**	-	-
	PLACE1010877	26.07	20.6	20.89	14.13	8.42	9.71	13.42	12.71	7.25	**	*	-	-

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	PLACE1010882	17.06	13.54	8.42	6.17	5.69	5.82	7.13	5.03	5.37	*	-	-
	PLACE1010891	27.43	30.32	21.15	13.46	14.41	7.46	15.38	15.07	24.71	*	-	-
5	PLACE1010896	13.62	18.23	16.16	6.92	8.03	5.78	3.54	4.62	4.06	**	**	-
	PLACE1010900	66.6	75.65	67.62	55.68	59.03	45.47	67.12	53.92	39.14	*	-	-
	PLACE1010916	104.52	71.53	76.5	35.13	35.16	33.1	29.84	23.73	27.17	**	**	-
	PLACE1010917	14.21	14.67	11.27	7.82	5.59	7.41	7.69	7.06	8.76	**	**	-
	PLACE1010924	5.86	2.7	4.5	2.89	4.47	3.08	2.47	3.1	1.31			-
	PLACE1010925	4.94	4.55	4.99	1.88	2.53	1.67	3.09	1.69	1.78	**	**	-
10	PLACE1010926	13.94	11.16	11.63	5.87	7.64	6.22	5.6	4.23	4.29	**	**	-
	PLACE1010942	207.77	196.21	175.46	147.15	130.24	102.36	197.42	120.16	123.73	*	-	-
	PLACE1010943	31.5	26.2	22.98	12.49	22.16	9	15.12	16.22	13.62	*	-	-
	PLACE1010944	83.2	92.75	68.43	51.82	78.63	47.87	87	58.47	73.16			-
	PLACE1010947	33.76	22.26	22.3	12.84	13.89	8.22	22.66	11.99	13.89	*	-	-
	PLACE1010954	10.33	11.3	11.05	5.3	5.81	5.51	5.34	5.12	4.22	**	**	-
15	PLACE1010960	15.62	30.44	20.31	7.94	8.28	7.04	11.37	9.05	8.5	*	*	-
	PLACE1010965	13.17	14.34	9.79	7.54	4.78	3.78	4.15	4.73	5.18	*	**	-
	PLACE1010968	18.41	14.95	14.27	6.84	9.6	5.59	12.62	6.34	9.37	**	*	-
	PLACE1010978	57.65	54.74	36.05	40.68	34.09	13.7	16.85	10.36	20.32	*	-	-
	PLACE1010982	21.44	26.06	15.9	7.42	6.54	11.09	10.66	7.85	9.32	*	*	-
	PLACE1010990	327.98	344.55	256.15	258.07	367.78	240.66	208.45	171.08	173.44	*	-	-
20	PLACE1011017	100.16	59.4	54.99	23.72	27.4	15.8	91.94	75.46	99.74	*	-	-
	PLACE1011019	13.37	8.64	6.46	8.37	6.37	4.79	6.61	7.41	7.81			-
	PLACE1011026	17.67	16.91	13.69	8.74	11.48	8.93	15.71	13.37	15.94	*	-	-
	PLACE1011032	5.5	8.88	7.51	2.84	5.75	2.99	4.5	3.38	3.21	*	-	-
	PLACE1011041	11.32	11.72	11.41	4.79	6.17	4.9	2.74	0	1.85	**	**	-
	PLACE1011045	30.68	27.07	24.09	20.73	22.77	14.24	25.88	22.96	30.06			-
25	PLACE1011046	10.75	10.03	9.15	3.68	6.42	4.38	4.21	3.5	2.56	**	**	-
	PLACE1011054	23.11	26.67	18.54	13.24	17.45	11.68	27.3	21.77	27.93	*	-	-
	PLACE1011056	5.67	3.31	3.16	3.73	4.11	8.46	6.33	3.05	6.91			-
	PLACE1011057	10.04	10.53	7.99	8.15	6.14	3.72	11.95	6.55	7.6			-
	PLACE1011059	19.4	17.96	11.33	7.08	9.45	9.52	6.53	6.86	9.19	*	*	-
	PLACE1011066	9.28	7.31	5.97	5.75	7.03	4.1	2.13	5.18	0.49	*	-	-
30	PLACE1011087	26.84	40.15	33.04	57.32	27.46	16.29	127.9	19.42	37.4			-
	PLACE1011090	10.52	7.52	6.48	3.01	5.18	3.1	6.04	4.61	6.16	*	-	-
	PLACE1011109	43.09	16.58	13.76	6.5	19.94	4.84	12.2	7.21	13.97			-
	PLACE1011114	17.98	24.04	19.89	13.12	19.15	8.13	12.09	13.25	14.96	*	-	-
	PLACE1011116	30.03	28.53	37.37	10.98	8.87	7	8.26	10.18	5.99	**	**	-
	PLACE1011122	5.9	6.6	5.93	4.16	4.82	3.11	3.97	4.69	2.89	*	*	-
35	PLACE1011133	6.47	4.35	6.51	3.81	3.93	3.81	2.72	5.84	2.91			-
	PLACE1011134	5.48	5.99	6.34	4.28	4.27	3.64	3.72	3.86	3.76	**	**	-
	PLACE1011143	4.76	9.67	5.59	2.21	5.45	3.27	2.93	3.83	4.13			-
	PLACE1011146	10.48	13.56	12.48	9.3	11.11	4.11	4.38	6.69	4.48	**	-	-
	PLACE1011160	7.71	9.99	6.71	4.98	7.77	3.25	6.45	4.47	3.78			-
	PLACE1011165	21.99	27.95	32.58	8.87	19.75	11.93	12.6	15.59	9.42	*	*	-
40	PLACE1011181	5.25	3.37	6	2.06	4.49	2.29	2.61	4.09	3.85			-
	PLACE1011185	60.3	36.78	36.17	37.68	34.15	24.31	17.32	33.87	29.05			-
	PLACE1011186	25.07	30.45	27.42	12.69	20.01	15.83	19.93	27.9	21.4	*	-	-
	PLACE1011203	10.27	18.2	13.8	9.36	12.5	6.63	8.02	13.49	10.02			-
	PLACE1011214	7.39	9.12	10.92	5.57	5.78	3.95	1.49	2.02	3.84	*	**	-
	PLACE1011219	7.03	5.86	7.27	8.39	4.52	4.58	9.07	4.64	3.23			-
45	PLACE1011221	10.63	11.42	9.42	5.44	10.51	4.92	4.92	5.52	6.28	**	-	-
	PLACE1011229	13.76	13.72	12.78	9.23	7.48	4.86	6.43	7.1	4.99	**	**	-
	PLACE1011231	34.58	28.7	50.02	23.03	24.8	13.83	19.12	24.97	26.97			-
	PLACE1011236	13.02	10.94	13.96	5.99	7.59	5.06	4.42	6.98	4.82	**	**	-
	PLACE1011247	571.8	409.73	639.71	528.63	738.01	566.23	553.23	542.58	267.58			-
50	PLACE1011263	4.49	7.26	9.65	4.09	5.29	4.39	2.77	4.83	3.37			-
	PLACE1011273	9.77	15.11	15.29	8	7.81	4.87	6.04	5.28	3.97	*	*	-
	PLACE1011278	21.08	26.71	20.88	9.67	19.17	11.18	9.31	5.1	7.74	**	-	-
	PLACE1011289	8.76	9.56	9.49	5.47	7.47	4.38	4.05	4.14	4.61	*	**	-
	PLACE1011291	3.27	1.73	2.37	1.38	1.37	0.09	2.52	4.22	1.75			-
	PLACE1011296	15.1	14.79	20.48	7.86	6.09	7.28	12.72	18.07	15.96	**	-	-
55	PLACE1011310	49.57	40.91	47.27	26.08	24.65	29.49	26.25	31.46	34.3	**	*	-
	PLACE1011311	12.85	11.18	13.64	5.84	6.4	7.88	4.02	7.29	3.99	**	**	-
	PLACE1011321	316.11	225.18	251.29	230.23	241.81	208.08	340.56	284.43	231.07			-



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	PLACE1011325	67.49	68.67	34.36	32.79	55.55	25.52	26.06	16.66	23.25	*	-
	PLACE1011332	37.6	32.99	20.69	24.89	22.84	17.06	26.8	25.99	39.36		
5	PLACE1011340	6.86	4.22	8.9	7.42	3.33	10.93	4.69	3.22	3.76		
	PLACE1011353	13.06	9.45	9.31	4.05	5.07	3.21	9.83	8.83	10.17	**	-
	PLACE1011360	7.09	6.29	7.09	5.01	4.64	2.08	4.25	9.92	6.13	*	-
	PLACE1011364	36.2	48	46.69	18.82	32.17	16.48	29.76	23.08	23.29	*	*
	PLACE1011365	56.47	40.06	43.45	30.4	25.78	22.53	35.29	36.44	44.51	*	-
	PLACE1011371	8.03	11.85	15.3	3.37	4.12	3.15	3.67	7.88	4.18	*	-
10	PLACE1011375	7.04	6.27	10.93	2.06	3.1	2.3	1.72	3.77	5.21	*	-
	PLACE1011386	164.83	196.07	182.53	143.65	164.65	123.82	185.62	179.87	160.52		
	PLACE1011399	13.53	14.93	12.77	5.31	8.23	5.03	14.49	12.53	13.08	**	-
	PLACE1011406	24.35	18.36	25.14	17.24	17.93	13.01	14.05	16.63	13.24	*	-
	PLACE1011407	11.96	8.15	11.8	4.39	4.52	4.88	4.7	7.06	4.99	**	*
	PLACE1011419	45.6	33.74	47.01	28.72	27.55	25.25	33.12	24.14	29.66	*	-
15	PLACE1011433	12.4	6.05	13.11	5.89	9.23	4.52	4.03	6.39	4.28		
	PLACE1011440	22.91	21.43	16.68	17.18	6.65	6.34	4.22	2.79	3.13	**	-
	PLACE1011452	21.99	27.18	21.9	7.47	5.58	8.33	1.98	2.55	3.76	**	**
	PLACE1011465	8.59	10.4	8.63	4.43	3.74	3.61	3.27	3.42	2.9	**	**
	PLACE1011472	12.35	11.03	8.39	5.76	5.63	4.74	4.12	4.06	4.53	*	**
	PLACE1011477	6.89	4.15	8.42	3.82	3.1	2.49	5.68	5.36	7.03		
20	PLACE1011478	147.8	127.45	151.17	98.43	129.14	92.91	97.94	88.28	67.65	**	-
	PLACE1011492	8.86	4.94	8.71	5.63	3.6	3.44	4.78	2.62	3.91		
	PLACE1011498	11.86	13.27	11.87	6.42	7.11	5.44	7.49	6.76	6.34	**	**
	PLACE1011501	5.51	5	4.76	1.97	2.88	1.92	1.53	1.09	0.63	**	**
	PLACE1011503	8.36	7.18	8.72	3.16	3.42	2.41	3.54	1.96	1.63	**	**
	PLACE1011509	6.79	8.76	6.6	2.67	3.22	3.57	3.54	1.66	2.46	**	**
25	PLACE1011514	39.36	42.6	35.59	29.05	24.04	21.59	28.05	21.32	28.44	**	*
	PLACE1011516	2.25	2.2	3.02	1.65	1.39	0.92	2.22	1.19	1.28	*	-
	PLACE1011520	56.28	54.22	44.97	60.14	59.13	46.66	37.37	33.63	31.08	*	-
	PLACE1011538	3.92	2.67	3.99	1.41	2.25	0.89	1.63	0.52	1.52	*	*
	PLACE1011555	5.04	5.36	4.18	1.71	1.41	2.12	2.42	1.56	2.13	**	**
30	PLACE1011561	40.83	32.97	31.05	28.42	20.97	80.97	15.06	18.06	18.45	**	-
	PLACE1011563	10.59	8.43	6.69	4.39	3.31	1.28	2.74	2.46	2.05	*	**
	PLACE1011567	8.99	5.72	8.85	4.85	2.48	0.94	3.39	1.71	1.08	*	*
	PLACE1011569	17.38	15.57	12.39	8.98	14.17	5.41	4.61	3.24	6.59	**	-
	PLACE1011576	9.4	4.88	4.15	2.79	3.81	3.52	4.89	6.65	7.51		
	PLACE1011586	11.29	10.02	9.62	6.88	3.58	5.49	4.18	5.75	5.57	**	**
35	PLACE1011635	30.93	17.84	23.55	13.98	14.55	6.78	13.1	10.06	12.62	*	-
	PLACE1011641	17.21	13.31	15.5	11.83	10.3	8.13	12.16	8.31	8.02	*	*
	PLACE1011642	14.04	9.07	8.81	4.73	3.8	2.98	2.08	3.09	1.68	*	**
	PLACE1011643	21.88	15.91	14.62	9.69	7.73	4.5	12.37	9.92	7.66	*	*
	PLACE1011646	50.88	55.98	42.92	29.54	24.58	20.05	12.83	13.88	9.31	**	**
	PLACE1011649	101.51	209.33	140.08	111.98	127.38	61.19	33.86	36.5	31.67	*	-
40	PLACE1011650	21.23	16.3	17.27	6.34	7.58	5.35	13.14	9.77	13.14	**	*
	PLACE1011661	36.54	29.6	21.98	17.54	11.85	16.02	29.9	27.07	30.09	*	-
	PLACE1011664	4693.7	3704.8	3103.3	1925.9	2495.7	2690.1	3091.7	3779.5	2474.5	*	-
	PLACE1011672	14.58	19.19	17.05	4.82	11.54	6.52	8.71	6.37	8.66	*	**
	PLACE1011675	27.27	28.5	23.64	11.76	7.61	13.02	10.47	6.83	11.83	**	**
	PLACE1011682	31.95	30.83	21.79	24.47	12.69	9.16	19.26	16.69	17.56	*	-
45	PLACE1011708	240.54	265.47	223.19	186.79	250.35	199.96	147.11	130.97	144.28	**	-
	PLACE1011719	2115.1	1324.5	1826.8	1953.8	1265.9	1000.2	1428.6	860.26	1269.9		
	PLACE1011725	14.63	11.44	8.67	4.74	6.3	2.04	9.22	9.94	8.53	*	-
	PLACE1011729	17.92	12.45	10.92	5.48	6.85	3.57	9.59	6.92	10.12	*	-
	PLACE1011741	19.11	16.45	8.97	6.48	6.39	4.13	6.03	4.62	6.01	*	*
	PLACE1011749	198.63	245.38	186.1	98.37	139.73	93.5	146.64	106.95	169.56	*	-
50	PLACE1011757	55.97	64.31	51.13	22.6	27.43	20.99	59.9	47.96	65.48	**	-
	PLACE1011762	112.55	118.61	84.99	66.65	83.7	57.21	113.37	92.71	109.2	*	-
	PLACE1011778	14.17	14.57	14.58	9.09	8.23	7.54	9.58	8.34	17.29	**	-
	PLACE1011783	34.3	38.67	23.05	14.78	12.16	17.09	15.47	21.92	20.45	*	-
	PLACE1011795	26.86	17.86	14.49	8.41	7.89	4.41	13.16	9.37	14.56	*	-
	PLACE1011810	6.46	2.52	3.35	2.53	2.07	0.8	3.19	3.06	3.38		
55	PLACE1011824	86.62	55.93	50.79	29.92	21.66	12.01	21.62	24.56	19.64	*	*
	PLACE1011825	47.11	53.31	45.03	28.52	34.47	24.16	61.42	44.87	47	**	-
	PLACE1011835	12.82	11.42	11.32	5.55	7.84	4.84	7.39	9.98	8.67	**	*

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	PLACE1011836	18.92	14.13	10.67	5.56	9.72	5.44	13.34	9.9	14.01			
	PLACE1011847	18.99	16.08	12.62	9.39	11.06	5.84	18.15	10.26	13.1	*		-
5	PLACE1011855	44.57	41.99	25.3	17.11	33.33	14.76	55.6	42.68	40.57			
	PLACE1011858	17.26	16.38	17.11	5.33	7.08	6.53	6.22	8.74	5.1	**	**	-
	PLACE1011874	23.12	12.72	25.71	16.84	19.22	7.85	10.17	8.71	12.51			
	PLACE1011875	10.58	9.98	11.17	5.18	10.63	6.87	7.18	6.04	4.93		**	-
	PLACE1011877	4.39	5.14	4.95	3.7	5.52	3.78	2.59	4.05	4.24			
	PLACE1011891	21.71	17.57	18.99	7.39	14.47	8.67	8.21	9.15	7.86	*	**	-
10	PLACE1011896	15.35	16.64	24.3	10.41	10.14	12.14	5.01	8.13	7.98	*		-
	PLACE1011920	16.12	14.42	15.9	7.68	8.85	7.76	6.46	2.46	3.24	**	**	-
	PLACE1011922	9.14	7.55	8.03	4.49	8.39	4.08	7.97	6.15	5.33			
	PLACE1011923	166.86	139.43	146.9	104.2	117.42	86.95	136.93	140	124.61	*		-
	PLACE1011937	11.45	9.18	10.8	8.58	6.75	5.1	5.71	6.29	5.46	*	**	-
	PLACE1011939	20.33	21.55	26.93	12.79	15.19	13.44	14.58	11.31	12.67	*	*	-
15	PLACE1011940	46.38	48.76	46.73	35.11	34.53	31.67	43.31	41.44	39.86	**	**	-
	PLACE1011962	58.59	70.73	80.18	30.15	38.09	28.84	47.96	47.68	42.57	**	*	-
	PLACE1011964	53.78	49.36	46.95	41.43	47.33	36.34	22.23	20.62	20.74	**		-
	PLACE1011978	50.21	52.86	64.71	38.6	31.39	22.36	22.46	20.19	18.12	*	**	-
	PLACE1011980	13.57	18.54	10.96	9.65	15.28	6.53	4.68	9.99	8.31			
	PLACE1011981	46.23	28.89	45.44	16.98	15.61	9.98	14.66	11.01	11.18	*	**	-
20	PLACE1011982	116.69	99.4	123.56	57.42	68.6	45.01	97.45	90.55	115.07	**		-
	PLACE1011995	8.31	11.27	12.33	5	7.29	7.22	6.27	8.29	4.87	*		-
	PLACE1012023	36.36	36.13	39.16	21.46	26.03	23.3	20.6	21.06	24.79	**	**	-
	PLACE1012026	72.96	80.46	66.75	52.71	40.29	50.42	21.72	33.87	25.71	**	**	-
	PLACE1012031	6.69	7.34	9.86	2.73	6.11	3.89	3.41	3.11	3.97	*		-
25	PLACE2000003	144.75	222.75	62.64	74.47	133.88	40.79	39.01	32.21	30.64			
	PLACE2000005	20.72	25.78	18.16	9.79	22.43	11.52	5.79	8.65	14.3	*		-
	PLACE2000006	74.92	51.78	61.3	27.4	24.75	21.12	50.02	43.94	72.77	**		-
	PLACE2000007	11.31	11.29	12.53	6.68	7.02	5.2	5.63	10.02	7	**	*	-
	PLACE2000011	20.07	19.36	23.84	14.92	4.58	15.77	9.39	11.52	19.43			
	PLACE2000014	10.47	6.72	12.3	4.76	6.02	3.48	3.63	6.9	4.73	*		-
	PLACE2000015	63.77	83.22	43.62	34.06	43.14	43.39	19.29	26.64	36.8	*	*	-
30	PLACE2000017	64.44	66.07	78.07	40.68	48.09	29.95	59.7	61.53	44.91	*		-
	PLACE2000021	131	136.36	142.32	116.28	142.66	101.82	89.75	68.71	86.35		**	-
	PLACE2000022	6.52	6.75	7.52	3.85	5.14	3.55	4.53	1.84	5.72	**		-
	PLACE2000030	277.16	275.48	252.39	182.81	167.16	156.31	125.23	96.07	135.65	**	**	-
	PLACE2000032	8.03	6.4	8.8	4.38	5.33	2.81	4.32	15.18	4.01	*		-
	PLACE2000033	19.24	16.61	20.22	9.43	14.03	10.83	8.93	12.91	10.87	*	**	-
35	PLACE2000034	212.75	182.06	146.24	219.9	195.88	170.13	146.86	112.34	125.26			
	PLACE2000039	8.9	10.84	13.51	4.94	3.89	4.8	3.72	4.38	6.52	**	*	-
	PLACE2000043	13.64	20.44	15.11	6.28	13.12	6.04	6.05	7.64	6.22	*		-
	PLACE2000044	7.28	9.48	9.44	3.48	5.71	4.79	4.48	4.25	4.59	*	**	-
	PLACE2000047	17.41	19.39	12.83	6.83	12.83	7.05	7.81	8.54	5.78	*		-
	PLACE2000050	18.34	17.87	22.05	7.34	8.98	7.31	7.51	8.31	7.94	**	**	-
40	PLACE2000061	53.75	61.97	78.23	34.92	41.03	37.86	22.68	14.04	20.77	*	**	-
	PLACE2000062	44.19	44.8	62.08	41.54	45.17	33.58	38.88	38.06	40.24			
	PLACE2000072	216.69	181.79	181.98	200.73	185.27	186.23	111.76	113.44	105.53		**	-
	PLACE2000073	8.16	10.75	9.27	3.77	4.89	3.62	4.56	4.79	3.59	**	**	-
	PLACE2000097	120.94	128.07	120.9	148.48	131.74	105.73	90.14	87.25	86.79	**	**	-
	PLACE2000100	13.48	14.19	15.99	6.02	8.77	5.56	4.8	3.51	6.24	**	**	-
45	PLACE2000103	355.83	328.95	197.42	251.22	436.52	235.01	231.23	336.03	237.95			
	PLACE2000106	32.23	23.41	23.14	14.46	6.17	13.03	9.13	10.5	5.27	*	**	-
	PLACE2000111	152.37	157.38	125.3	88.6	105.91	83.66	90.52	44.23	69.19	*	**	-
	PLACE2000115	27.01	16.97	16.32	19.6	21.67	16.26	13.74	11.32	11.63			
	PLACE2000118	229.23	214.41	143.27	124.01	152.19	92.15	153.7	62.85	67.07			
	PLACE2000124	7.33	5.71	5.57	2.12	1.78	1.55	2.01	1.56	1.09	**	**	-
50	PLACE2000132	18.07	19.01	19.11	15.64	11.16	12.49	9.7	6.52	8.48	*	**	-
	PLACE2000136	33.6	40.68	26.33	13.95	42.68	22.54	9.98	17.8	18.28	*		-
	PLACE2000137	6.87	5.34	6.91	1.61	2.95	2.09	1.24	1.8	2.36	**	**	-
	PLACE2000140	11.37	11.51	12.2	8.07	9.45	9.49	11.48	11.25	10.8	**		-
	PLACE2000147	10.22	7.24	9.46	6.01	5.85	4.51	7.52	7.6	9.27	*		-
	PLACE2000153	17.95	21.42	13.85	5.51	9.57	6.43	4.84	5.27	2.27	*	**	-
55	PLACE2000164	8.53	12.11	9.44	3.18	4.26	4.12	4.98	3.97	2.13	**	**	-
	PLACE2000170	38.84	46.93	33	28	28.56	22.27	30.03	23.36	30.82	*		-

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	PLACE2000172	9.55	12.02	10.86	4.88	5.87	3.32	4.01	4.8	6.2	**	**	-	-
	PLACE2000173	16.63	20.86	19.04	9.66	11.13	9.7	6.74	6.23	3.14	**	**	-	-
	PLACE2000174	6.73	7.76	6.4	3.37	4.73	2.4	3.08	3.26	1.62	*	**	-	-
5	PLACE2000176	47.07	39.92	36.01	26.8	32.78	24.97	24.68	26.79	25.41	*	**	-	-
	PLACE2000187	11.49	9.44	7.22	4.28	4.58	4.45	2.47	4.64	3.94	*	*	-	-
	PLACE2000216	15.24	13.28	16.1	7.83	10.53	7.67	11.12	11.23	10.67	**	*	-	-
	PLACE2000219	43.32	28.21	37.3	18.17	6.67	13.94	7.68	7.79	6.4	*	**	-	-
	PLACE2000221	9.58	7.64	7.46	2.22	3.99	1.24	4.08	2.43	3.07	**	**	-	-
10	PLACE2000223	16.67	12.34	12.95	4.95	6.75	4.32	4.43	2.01	2.87	**	**	-	-
	PLACE2000231	8.48	8.65	7.01	3.78	5.92	4.27	4.19	2.32	3.59	*	**	-	-
	PLACE2000235	7.02	5.03	3.66	1.54	5.33	1.9	4.43	3.57	3.78			-	-
	PLACE2000246	21.31	17.8	13.21	7.9	13.4	6.47	11.52	9.6	10.91	*		-	-
	PLACE2000264	41.11	43.3	30.68	20.28	22.27	18.14	15.54	15.85	15.69	*	**	-	-
	PLACE2000274	6.8	7.42	7.36	4.35	3.04	1.89	3.84	3.12	4.31	**	**	-	-
15	PLACE2000287	32.11	30.76	24.99	20.39	25.61	21.53	17.96	15.3	19.45	**		-	-
	PLACE2000296	42.94	34.88	35.63	23.36	22.17	20.37	32.02	14.36	29.35	**		-	-
	PLACE2000302	252.74	304.77	237.45	265.35	267.99	217.29	124.09	112.58	108.48		**	-	-
	PLACE2000305	21.47	23.58	17.69	16.14	17.23	16.65	22.14	18.21	22.01			-	-
	PLACE2000317	37.2	38.12	23.24	20.01	28.38	14.37	31.05	33.16	31.64			-	-
20	PLACE2000324	18.44	17.84	10.35	6.13	8.75	4.98	3.24	8.74	3.2	*	*	-	-
	PLACE2000334	21.38	17.6	11.43	10.36	9.7	9.37	7.54	6.15	9.1	*	*	-	-
	PLACE2000335	71.59	66.59	54.82	51.15	35.99	40.86	33.77	36.69	29.67	*	**	-	-
	PLACE2000340	20.62	28.95	19	17.88	23.88	12.85	16.23	14.73	16.82			-	-
	PLACE2000341	14.8	11.92	10.45	5.66	5.34	5.33	5.38	5.46	7.66	**	*	-	-
	PLACE2000342	23.53	21.95	21.97	16.28	11.86	11.51	22.81	14.69	23.12	**		-	-
25	PLACE2000347	9.57	9.26	10.05	4.16	2.94	3.3	5.78	3.54	5.48	**	**	-	-
	PLACE2000357	112.17	70.59	69.73	83.45	100.62	78.25	23	68.79	48.54			-	-
	PLACE2000358	57.37	32.59	34.74	25.22	20.69	15.46	44.93	47.18	42.01			-	-
	PLACE2000359	66.39	48.68	57.2	40.91	54.54	32.45	1.96	27.1	55			-	-
	PLACE2000366	24.09	23.36	19.56	12.65	12.71	9.05	11.75	9.72	10.83	**	**	-	-
	PLACE2000371	12.17	9.37	8.13	5.98	7.76	4.49	7.64	10.97	6.2			-	-
30	PLACE2000373	8.3	7.58	8.83	4.52	6.25	4.81	3.89	1.17	2.44	**	**	-	-
	PLACE2000374	20.82	21.57	18.21	16.3	16.71	14.02	11.71	11.44	14.19	*	**	-	-
	PLACE2000379	109.97	110.55	125.02	99.68	141.5	89.14	84.64	65.75	71.64	**		-	-
	PLACE2000386	27.43	27.19	20.99	10.83	12.4	11.22	15.3	17.99	10.26	**	*	-	-
	PLACE2000388	250.97	170.84	203.4	172.85	236.63	173.11	130.31	109.84	93.57	*		-	-
	PLACE2000392	241.74	206.31	271.34	159.33	199.67	145.83	119.57	115.9	95.8	*	**	-	-
35	PLACE2000394	10.9	10.42	13.61	8.59	15.25	7.68	5.68	9.12	6.51	*	*	-	-
	PLACE2000398	16.83	19.82	17.04	9.21	12.98	10.99	7.5	15.14	8.57	**	*	-	-
	PLACE2000399	30.6	27.17	17.03	25.83	27.41	28.06	9.08	19.74	20.17			-	-
	PLACE2000402	5.25	8.04	8.31	4.2	9.81	3.39	4.84	3.89	6.41			-	-
	PLACE2000404	24.79	49.52	29.14	49.74	21.66	25.22	16.23	19.06	8.51			-	-
	PLACE2000411	5.67	8.96	6.76	7.21	11.84	6.13	5.19	4.54	7.08			-	-
40	PLACE2000418	10.3	8.94	9.67	6.1	3.09	4.67	4.68	5.3	4.11	**	**	-	-
	PLACE2000419	96.71	94.48	148.23	58.48	57.97	27.06	44.37	46.85	45.47	*	*	-	-
	PLACE2000425	9.83	11.3	13.49	7.49	11.26	6.24	5.84	7.49	5.62	*		-	-
	PLACE2000427	15.21	22.92	21.67	15.7	21.56	15.92	5.61	6.9	4.76	**		-	-
	PLACE2000433	25.58	27.32	26.12	13.97	18.4	14.15	21.62	27.64	18.08	**		-	-
	PLACE2000435	16.36	18.11	21.19	9.69	13.76	7.6	8.43	10.79	12.73	*	*	-	-
45	PLACE2000438	35.17	36.25	36.72	24.14	34.38	15.98	38.19	37.23	25.32			-	-
	PLACE2000450	24.38	41.59	23.11	16.35	37.33	18.21	23.47	16.65	30.25			-	-
	PLACE2000455	51.05	47.04	53.6	30.31	36.57	21.71	39.12	34.02	35.42	*	**	-	-
	PLACE2000458	13.07	11.58	13.21	6.82	7.75	7.03	6.6	8.78	5.76	**	**	-	-
	PLACE2000464	9.95	10.55	11.94	7.59	6.37	5.51	7.66	8.47	7.16	**	*	-	-
	PLACE2000465	182.2	189.36	208.18	166.02	148.04	156.91	139.29	234.97	151.61	*		-	-
50	PLACE2000473	23.66	24.51	24.43	18.65	18.15	16.44	24.18	30.07	29.1	**		-	-
	PLACE2000477	14.25	12.47	18.55	9.69	12.47	6.23	10.6	9.09	9.9	*		-	-
	PLACE3000004	49.49	41.47	56.9	42.63	53.35	39.93	39.48	28.43	32.45	*		-	-
	PLACE3000009	30.13	36.74	28.18	19.79	35.05	20.31	13.54	15.44	20.29	**		-	-
	PLACE3000020	27.99	24.44	23.74	13.45	15.64	8.65	14.29	14.44	13.63	**	**	-	-
	PLACE3000029	13.95	12.7	16.35	6.3	9.27	7.3	4.68	16.59	5.52	**		-	-
55	PLACE3000038	6.52	4.32	7.69	5.63	3.97	4.12	2.68	6.95	6.18			-	-
	PLACE3000052	8.21	5.21	10.48	3.53	4.29	4.15	2.75	5.07	2.29			-	-
	PLACE3000059	7.39	8.1	10.8	4	5.08	2.55	2.83	4.28	4.31	*	*	-	-

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	PLACE3000067	49.68	45.52	57.37	38.78	41.13	26.16	39.8	46.08	41.69			
	PLACE3000069	22.6	20.15	23	9.32	14.75	10.81	1.9	9.3	14.16	**	*	-
	PLACE3000070	28.36	29.24	22.17	14.93	25.34	18.73	8.92	18.55	16.21	*	*	-
5	PLACE3000103	7.35	7.9	9.44	5.25	4.6	6.13	2.42	4.32	5.29	*	*	-
	PLACE3000119	35.89	28.1	30.76	15.16	14.79	15.09	26.05	30.71	30.91	**		-
	PLACE3000121	42.11	31.92	37.82	38.13	38.16	27.02	30.65	23.15	27.55			-
	PLACE3000124	419.8	380.05	314.65	379.74	412.05	282.09	411.56	374.59	344.25			-
	PLACE3000135	20.62	25.87	26.77	15.03	9.64	8.12	18.24	11.89	14.6	**	*	-
10	PLACE3000136	7.68	8.11	13.16	2.72	3.39	4.18	4.52	3.19	1.88	*	*	-
	PLACE3000142	24.15	28.81	26.5	11.04	24.59	15.08	9.37	6.94	11.56	**		-
	PLACE3000145	16.45	12.13	16.32	7.23	16.52	6.93	8.46	9.12	6.76	*		-
	PLACE3000147	109.42	62.46	138.9	40.47	87.42	32.89	57.71	63.5	68.14			-
	PLACE3000148	66.44	59.97	67.42	62.74	65.96	38.34	37.63	26.14	36.79	**		-
	PLACE3000154	10.3	11.14	12.88	7.95	8.64	6.56	7.31	6.3	7.57	*	**	-
15	PLACE3000155	54.28	50.77	22.77	23.49	28.34	24.7	10.12	11.93	8.34	*	*	-
	PLACE3000156	9.77	6.45	8.44	2.67	5.36	4.07	2.62	2.16	2.62	*	**	-
	PLACE3000157	38.44	50.52	36.49	23.64	29.36	25.04	21.36	24.91	20.01	*	*	-
	PLACE3000158	10.22	9.34	10.13	4.45	4.83	3.36	2.93	2.25	3.02	**	**	-
	PLACE3000160	19.92	29.65	15.93	8.71	11.7	10.32	5.77	7.29	4.57	*	*	-
	PLACE3000169	4.65	6.89	7.95	4.88	4.57	2.21	2.88	2.72	3.49	*	*	-
20	PLACE3000181	12.63	9.87	13.46	6.15	6.69	4.33	5.58	7.04	5.47	**	**	-
	PLACE3000194	1627	2636.2	1913.4	1710.4	2606.8	2399	3320.1	2826.5	2357.1			-
	PLACE3000197	7.18	4.55	8.38	2.14	1.71	1.66	2.79	2.24	2.57	*	*	-
	PLACE3000199	19.46	15.17	17.17	4.98	8.73	7.24	6.33	5.56	6.07	**	**	-
	PLACE3000205	12.53	16.93	16.84	6.91	6.83	4.67	7.28	5.87	4.15	**	**	-
	PLACE3000207	7.97	6.69	7.83	2.48	4.45	2.85	2.71	2.19	2.08	**	**	-
25	PLACE3000208	5.49	5.5	6.02	1.68	6.49	-2.8	2.64	3.52	2.46	**	**	-
	PLACE3000213	40.02	27.48	31.62	27.29	30.91	23.89	26.59	30.58	23.2			-
	PLACE3000215	20.76	15.1	17.45	10.19	8.64	8.25	15.48	14.18	17.02	**		-
	PLACE3000218	13.39	10.52	10.44	6.03	3.81	4.29	4.65	4.57	4.68	**	**	-
	PLACE3000220	61.41	56.02	42.84	39.7	37	28.53	36.15	41.5	44.54	*	*	-
	PLACE3000221	12.37	9.42	8.54	5.7	3.63	2.33	5.09	3.54	2.87	*	**	-
30	PLACE3000225	180.89	144.07	131.66	176.14	175.29	127.3	77.77	64.65	86.2	**	**	-
	PLACE3000226	20.28	21.59	18.74	7.11	11.09	6.3	3.48	2.23	3.79	**	**	-
	PLACE3000230	17.46	18.98	14.94	6.27	14.11	10.52	4.65	3.25	5.88	**		-
	PLACE3000231	17.8	13.66	8.65	9.08	2.29	4.95	6.33	9.35	7.91			-
	PLACE3000235	9.61	7.55	8.28	4.48	5.65	4.02	5.72	2.93	4.77	**	*	-
	PLACE3000242	58.11	27.4	48.85	17.82	13.76	17.4	11.61	10.29	11.25	*	*	-
35	PLACE3000244	18.63	13.16	20	8.5	7.54	7.64	10.16	10.96	16.61	*	*	-
	PLACE3000253	56.99	47.97	42.85	32.37	25.93	24.8	32.98	24.76	32.96	*	*	-
	PLACE3000254	27.82	25.4	19.01	15.47	10.42	14.64	15.57	11.42	13.74	*	*	-
	PLACE3000271	14.58	20.8	13.28	5.71	8.52	5.71	8.32	6.43	8.38	*	*	-
	PLACE3000276	13.09	13.68	8.83	2.78	7.9	3.42	3.8	5.28	3.1	*	**	-
	PLACE3000304	37.31	49.14	39.5	28.72	17.9	18.26	33.17	28.5	40.23	*	*	-
40	PLACE3000309	12.29	9.64	9.42	6.2	5.6	4.27	5.42	4.79	5.47	**	**	-
	PLACE3000310	51.34	49.06	45.31	11.5	35.47	14.78	19.66	9.79	16.36	*	**	-
	PLACE3000320	24.3	28.51	23.33	14.31	20.51	12.27	15.7	15.03	15.45	*	**	-
	PLACE3000322	43.24	35.12	33.62	31.55	31.68	23.75	27.52	20.55	23.56	*	*	-
	PLACE3000330	28.37	27.71	24.49	12.33	15.5	11.35	20.66	17.37	21.33	**	*	-
	PLACE3000331	6.68	8.07	7.67	6.55	5.13	3.84	2.57	2.99	0.04	**		-
45	PLACE3000336	393.24	473.08	270.29	359.87	515.03	306.41	470.46	662.39	717.67			-
	PLACE3000339	11.78	5.98	6.82	3.79	5.41	2.48	9.74	10.29	11.53			-
	PLACE3000341	12.2	6.88	6.99	4.2	5.65	4.02	4.35	5.75	4.94			-
	PLACE3000350	13.71	12.66	10.21	4.86	8.13	4.84	5.77	4.37	7.49	*	*	-
	PLACE3000352	17.23	29.11	20.8	9.42	15.27	8.16	11.43	7.14	13.58	*	*	-
	PLACE3000353	14.74	14.96	16.82	8.78	8.26	6.98	10.37	5.48	6.79	**	**	-
50	PLACE3000362	57.42	93.8	72.53	67.02	59.59	35.38	59.68	38.27	60.6			-
	PLACE3000363	9.44	8.61	10.55	4.39	5.19	4.3	7.06	4.68	6.56	**	*	-
	PLACE3000365	5.59	7.45	4.94	1.48	2.65	3.2	4.78	2.37	2.95	*	*	-
	PLACE3000373	38.45	30.27	25.57	4.05	7.88	3.63	14.16	11.37	15.74	**	*	-
	PLACE3000374	48.65	44.25	34.93	16.2	26.01	11.78	24.23	27.25	23.51	*	*	-
	PLACE3000387	5.55	3.77	3.38	1.58	3.57	0.43	3.58	2.95	3.21			-
55	PLACE3000388	26.03	22.21	15.9	9.86	12.79	6.37	21.94	26.7	24.22	*	*	-
	PLACE3000399	15.37	13.07	9.83	5.64	4.9	3.93	10.68	11.05	9.52	**		-

Table 496

	PLACE3000400	42.78	33.52	30.29	11.43	26.51	8.47	52.76	33.47	38.46	*	-
	PLACE3000401	137.51	137.03	95.06	91.28	111.28	51.38	81.66	72.2	62.65	*	-
5	PLACE3000402	8.43	7.72	4.24	2.44	6.58	2.29	8.31	7.96	5.44		
	PLACE3000405	7.33	4.67	7.44	2.73	3.5	5.1	3.7	5.44	3.66		
	PLACE3000406	4.67	3.39	6.42	4.46	6.89	4.16	3.34	4.69	2.59		
	PLACE3000413	12.33	14.38	16.34	10.31	15.31	7.77	6.83	11.34	9.07	*	-
	PLACE3000416	84.6	58.17	41.71	94.16	126.08	86.52	51.61	89.65	63.01		
	PLACE3000425	2.87	4.19	4.03	2.67	4.11	2.12	2.08	0.77	1.54	*	-
10	PLACE3000437	6.08	4.62	9.74	3.57	11.5	3	3.57	3.67	4.77		
	PLACE3000455	6.66	7.45	7.23	5.48	5.38	4.19	5.5	5.74	3.82	*	-
	PLACE3000475	4.99	6.71	5.08	4.69	5.48	5.91	3.2	5.35	2.87		
	PLACE3000477	12.61	9.21	10.6	8.81	9.19	10.36	8.13	7.94	5.96	*	-
	PLACE4000003	30	20.47	39.94	8.43	18.43	9.82	12.11	10.52	8.23	*	-
	PLACE4000008	8.19	8.19	9.59	5.97	7.85	6.93	4.18	5.57	3.47	**	-
15	PLACE4000009	46.86	36	37.99	37.22	51.39	35.97	11.09	18.85	7.53	**	-
	PLACE4000014	18.34	18.57	19.39	16.62	19.49	16.59	6.08	13.2	15.87		
	PLACE4000029	5.3	5.07	5.95	2.91	4.87	2.62	3.69	3.02	2.87	**	-
	PLACE4000034	10.02	8.01	6.28	5.12	7.93	4.55	5.88	5.27	5.14		
	PLACE4000049	21.86	18.28	18.64	14.38	19.7	19.05	12.54	13.96	11.06	**	-
	PLACE4000052	47.63	33.03	40.39	17.99	15.08	20.28	24.01	22.07	24.29	**	-
20	PLACE4000062	53.46	46.6	50.02	32.69	40.48	28.08	39.71	36.99	45	*	-
	PLACE4000063	56.25	68.62	67.5	55.27	69.37	73.66	45.78	60.53	44.9		
	PLACE4000089	10.35	13.86	13.41	10.66	10.48	9.25	5.68	5.4	5.66	**	-
	PLACE4000093	15.33	18.02	19.57	10.49	13.84	10.33	17.17	14.6	14.04	*	-
	PLACE4000100	8.21	7.32	11.21	7.61	6.2	7.32	5.19	5.2	4.71	*	-
	PLACE4000103	13.85	15.73	12.84	8.67	14.38	6.43	4.02	8.73	6.65	**	-
25	PLACE4000106	32	18.81	23.23	18.35	21.38	15.86	17.78	20.58	18.06		
	PLACE4000128	22.05	18.53	23.14	8.88	10.24	9.57	11.18	17.49	11.76	**	-
	PLACE4000129	266.34	156.01	188.25	120.37	95.41	112.42	146.64	98.31	136.33	*	-
	PLACE4000131	59.1	45.51	65.57	41.68	34.82	39.78	18.29	19.7	30.83	*	-
	PLACE4000147	7.89	7.51	11.76	3.51	5.07	3.96	2.77	6.32	2.52	*	-
	PLACE4000156	15.48	18.75	19.37	9.1	12.85	10.65	15.8	15.48	10.02	*	-
30	PLACE4000175	12.45	10.41	18.08	11.94	9.67	2.46	6.38	6.69	6.89	*	-
	PLACE4000190	40.84	40.93	32.85	23.06	35.22	26.66	12.42	10.73	11	**	-
	PLACE4000192	35.69	24.13	23.88	16.77	21.59	17.55	17.75	19.51	19.4		
	PLACE4000206	33.82	29.03	26.48	11.73	17.97	14.5	17.45	20.16	20.02	**	-
	PLACE4000211	12.98	13.88	13.86	7.96	9.94	9.19	6.64	31.04	6.54	**	-
	PLACE4000214	13.12	6.23	9.29	3.45	7.5	4.16	4.96	7.25	13.71		
35	PLACE4000222	35.35	30.73	34.54	24.03	24.44	20.1	20.58	28.37	25.45	**	-
	PLACE4000223	14.88	14.83	15.03	7.36	10.28	5.52	4.16	7.67	5.85	**	-
	PLACE4000229	12.38	12.15	12.52	4.51	6.31	4.98	4.32	4.28	3.98	**	-
	PLACE4000230	9.56	8.77	9.56	4.68	7.06	5.7	4.97	9.82	3.71	**	-
	PLACE4000233	22.71	24.01	29.85	11.57	13.98	13.77	8.53	11.22	9.26	**	-
	PLACE4000239	10.07	7.4	9.42	6.8	7.34	6.09	4.49	4.54	3.54	**	-
40	PLACE4000247	15	11.82	15.56	9.41	13.91	8.87	8.67	6.24	7.39	**	-
	PLACE4000250	16.14	18.27	20.25	16.54	17.86	12.73	10.47	8.04	11.21	**	-
	PLACE4000252	10.01	5.15	12.75	1.39	3.96	3.1	2.21	3.92	2.7	*	-
	PLACE4000259	25.72	27.31	16.16	12.78	19.39	8.44	8.29	19.39	9.08		
	PLACE4000261	23.52	25.16	22.9	11.05	14.2	9.22	13.61	14.62	13.29	**	-
45	PLACE4000264	176.03	156.54	119.76	135.7	191.67	147.27	105.16	95.1	89.72	*	-
	PLACE4000269	71.18	49.07	62.08	23.03	41.63	24.74	71.71	82.6	52.18	*	-
	PLACE4000270	7.6	6.37	8.9	4.69	5.92	4.81	3.06	3.68	3.44	*	-
	PLACE4000281	15.26	16.07	18.29	6.09	10.92	7.61	6.44	6.66	5.1	**	-
	PLACE4000300	8.43	9.82	8.78	6.3	8.5	7.03	3.68	2.93	2.96	**	-
	PLACE4000320	12.37	11.22	11.92	6.27	10.09	6.43	4.47	4.26	2.85	*	-
	PLACE4000323	15.16	16.25	19.16	9.12	14.06	10.9	6.05	4.54	4.03	*	-
50	PLACE4000326	11.15	8.97	10.53	4.35	4.69	4.13	4.28	3.68	4.65	**	-
	PLACE4000344	27.71	32.93	24.51	14.27	30.44	19.64	5.14	9.78	8.98	**	-
	PLACE4000347	156.82	129.54	154.28	89.79	129.04	79.82	138.06	137.09	135.75		
	PLACE4000354	15.47	9.46	11.43	7.01	8.32	6.55	3.28	5.96	4.83	*	-
	PLACE4000367	8.63	5.47	7.82	5.38	5.39	6.72	3.84	3.95	3.64	*	-
	PLACE4000369	11.27	6.37	9.31	5.27	4.5	4.05	4.11	4.32	3	*	-
55	PLACE4000379	6.35	6	4.77	3.22	2.93	2.33	3.1	3.32	2.21	**	-
	PLACE4000387	25.99	34.88	32.06	17.28	20.68	16.67	6.75	8.86	3.97	*	-

Table 497

	PLACE4000392	8.31	9.76	11.03	3.63	5.95	3.64	5.73	2.01	2.93	**	*	-	-
	PLACE4000399	53.9	51.54	53.26	20.64	28.55	18.63	37.94	35.1	44.54	**	**	-	-
5	PLACE4000401	4.22	3.76	3.44	3.96	3.49	2.6	3.5	3.9	1.61				
	PLACE4000403	8.42	5.82	6.5	4.19	7.67	4.85	3.96	3.29	3.53		*	-	-
	PLACE4000411	20.23	15.5	15.73	8.23	11.19	9.81	14.98	10.1	11.34	*		-	-
	PLACE4000415	8.15	4.8	4.61	4.06	6.07	4.23	2.98	3.98	4.5				
	PLACE4000416	35.43	25.11	24.69	17.72	17.34	16.23	24.55	17.6	25.73	*		-	-
	PLACE4000424	43.93	33.38	31.83	13.69	19.37	13.98	27.93	23.64	33	**		-	-
10	PLACE4000431	10.44	8.78	8.78	5.88	4.85	3.5	4.69	2.33	4.08	**	**	-	-
	PLACE4000443	50.64	44.47	41.43	26.49	37.08	21.33	51.22	33.11	43.74	*		-	-
	PLACE4000445	5.42	4.17	3.6	3.57	7.43	5.38	2.23	3.95	2.66				
	PLACE4000450	9.85	6.68	6.23	4.72	6.64	4.07	3.56	7.58	3.73				
	PLACE4000455	167.91	132.51	128.81	98.87	124.22	95.79	172.16	139.08	172.24				
	PLACE4000465	31.84	25.74	18.83	10.79	23.42	11.27	11.29	10.8	17.69		*	-	-
15	PLACE4000466	13.01	11.54	9.57	6.56	6.92	4.59	5.76	4.65	5.6	*	**	-	-
	PLACE4000472	165.28	158.69	152.44	150.34	164.09	112.33	151.06	116.56	147.01				
	PLACE4000487	10.38	6.99	9.12	4.68	4.63	2.93	3.52	2.06	3.49	*	**	-	-
	PLACE4000489	6.8	7.97	5.85	3.99	5.8	4.43	4.22	4.11	4.53		*	-	-
	PLACE4000494	70.51	55.91	43.58	29.17	31.84	24.64	72.67	73.79	78.08	*		-	-
20	PLACE4000502	204.58	180.8	176.1	156.92	166.08	118.92	216.32	165.78	200.53				
	PLACE4000521	28.26	22.58	17.07	7.12	15.76	9	21.36	20.06	19.61	*		-	-
	PLACE4000522	18.46	20.38	16.27	10.46	14.51	9.51	16.91	13.88	17.23	*		-	-
	PLACE4000537	9.79	11.19	9.86	4.99	8.2	4.43	2.5	3.6	0.68	*	**	-	-
	PLACE4000548	12.35	10.52	9.27	3.9	4.07	4.41	4.08	3.04	3.64	**	**	-	-
	PLACE4000558	56.63	61.59	46.82	23.74	32.06	21.71	66.44	39.24	52.93	**		-	-
25	PLACE4000581	9.34	8.43	8.7	5.21	3.71	3.17	5.23	4.69	4.75	**	**	-	-
	PLACE4000590	4.28	4.39	2.54	2.29	1.9	1.58	2.69	1.47	1.72	*		-	-
	PLACE4000593	9.43	8.29	6.55	6.59	7.86	5.28	9.13	5.16	4.1				
	PLACE4000612	50.54	44.64	46.86	32.73	32.12	18.75	8.58	0	9.68	*	**	-	-
	PLACE4000638	8.47	6.12	6.11	6.07	5.18	3.4	1.44	4.91	1.37		*	-	-
	PLACE4000650	11.71	6	6.58	1.78	5.39	2.69	5.01	3.89	2.3				
30	PLACE4000651	10.02	10.01	7.86	4.63	8.67	3.43	7.21	6.04	5.23		*	-	-
	PLACE4000654	40.79	37.09	28.74	21.7	29.39	18.93	39.41	24.87	38.02				
	PLACE4000670	7.33	7.03	6.77	5.23	9.34	3.97	6.41	3.63	6.87				
	PLACE4000685	27.36	21.25	28.71	7.25	13.45	14.89	8.25	13.79	8.57	*	**	-	-
	PLACE4000687	5.87	2.72	5.94	3.75	3.52	3.04	2.8	3.66	2.1				
	PLACE5000003	13.69	15.66	16.08	8.92	15.85	13.17	6.36	9.93	8.84	**		-	-
35	PLACE5000005	17.05	13.36	13.46	14.47	17.35	13.76	5.61	8.29	7.64	**		-	-
	PLACE5000019	9.12	11.38	11.73	6.9	5.65	5.55	3.51	3.39	6.14	**	**	-	-
	PLACE5000021	28.4	29.38	31.96	18.99	19.21	16.52	23.2	21.13	21.28	**	**	-	-
	PLACE5000022	44.41	69.47	62.06	68.78	41.05	40.85	49.9	41.64	44.86				
	PLACE5000024	5.49	3.54	5.62	3.22	3.37	3.62	2.52	4.61	6.39				
	PLACE5000036	104.88	78.2	100.83	80.5	90.12	87.43	80.46	55.18	59.66				
40	PLACE5000059	13.88	12.58	10.61	5.28	9.26	6.17	6.41	11.67	8.16	*		-	-
	PLACE5000076	102.38	115.06	146.87	71.48	155.46	121.21	73.46	149.18	129.94				
	PLACE5000117	10.83	17.74	16.15	14.79	20.06	15.63	5.73	9.53	5.57		*	-	-
	PLACE5000143	12.99	9.49	15.16	8.13	9.83	8.06	5.81	8.66	8.8				
	PLACE5000152	183.88	202.8	96.28	147.85	104.4	116.95	74.92	70.73	75.92				
	PLACE5000154	90.81	108.58	44.13	75.4	77.68	45.59	40.84	23.33	50.85				
45	PLACE5000155	33.2	24.58	26.07	16.94	31.52	23.72	16.67	17.93	27.02				
	PLACE5000165	113.75	76.52	82.55	90.32	103.03	88.36	32.72	55.94	39.36		*	-	-
	SKNMC1000004	1323.5	940.91	1083.3	665.71	1250.5	673.39	1094.9	1184.2	1060.5				
	SKNMC1000011	8.28	9.06	11.81	4.48	12.47	5.45	4.79	5.44	8.03				
	SKNMC1000013	14.72	15.01	20.62	10.84	11.72	12.41	4.74	6.54	6.23	**		-	-
	SKNMC1000014	20.79	23.92	26.42	20.23	26.13	18.1	14.76	15.14	11.78	**		-	-
50	SKNMC1000018	9.56	8.87	12.44	5.32	9.73	4.54	3.81	4.41	5.25	**		-	-
	SKNMC1000020	25.49	27.02	25.39	13.63	25.33	12.68	18.7	20.72	21.65	**		-	-
	SKNMC1000046	24.6	15.36	17.74	13.48	22.27	16.07	12.53	14.97	15.86				
	SKNMC1000050	8.51	7.09	7.49	5.47	4.73	4.3	4.47	21.02	3.74	**		-	-
	SKNMC1000062	26.94	17.98	24.61	14.13	15.7	9.74	23.61	36.47	28.61	*		-	-
	SKNMC1000075	11.6	7.44	13.24	7.34	10.78	7.51	4.21	5.3	7.09				
55	SKNMC1000082	22.01	16.02	26.11	8.38	13.04	9.62	12.8	21.17	16.8	*		-	-
	SKNMC1000091	36.26	39.39	43.7	12.98	23.22	18.68	24.3	27.26	22.42	**	**	-	-
	SKNMC1000099	11.34	8.86	15.64	6.38	7.5	4.4	5.83	7.15	6.38				

Table 498

	SKNMC1000104	16.76	17.55	17.05	8.52	14.24	10.52	9.72	10.59	13.24	*	**	-	-
	SKNMC1000113	45.53	34.91	35.51	20.7	25.14	23.85	18.86	24.14	23.6	*	*	-	-
5	SKNMC1000119	17.58	14.67	21.54	10.33	12.31	8.53	8.83	13.02	8.17	*	*	-	-
	SKNMC1000142	16.52	20.57	23.49	7.26	16.72	11.75	8.01	11.68	14.09	*		-	-
	SKNMC1000170	242.49	183.41	211.38	201.28	226.18	182.82	247.45	216.7	250.73			-	-
	SKNMC1000178	15.01	12.68	14.32	6.9	9.12	6.49	4.97	7.82	9.01	**	**	-	-
	SKNMC1000194	7.33	8.61	11.61	2.23	3.73	3.19	2.64	4.74	3.45	*	*	-	-
	SKNMC1000198	18.76	29.87	24.52	7.87	13.1	9.06	5.41	5.23	5.02	*	**	-	-
10	SKNMC1000225	100.44	119.68	87.32	52.94	84.28	50.45	35.91	33.78	44.06	**		-	-
	SKNMC1000249	23.35	22.68	30.9	13.07	19.76	17.19	12.83	14.11	14.19	*		-	-
	SPLEN1000007	10.7	10.7	16.74	6.92	9.27	7.23	6.86	7.37	5.89	*		-	-
	SPLEN1000012	15.31	13.75	18.53	8.26	13.65	10.56	13.22	11.71	11.02			-	-
	SPLEN1000014	74.22	59.99	63.53	32.33	49.13	32.58	29.87	29.67	37.64	*	**	-	-
	SPLEN1000036	14.69	11.54	10.05	7.95	8.19	6.93	3.18	3.76	2.42	*	**	-	-
15	SPLEN1000059	39.71	33.5	32.87	12.1	19.81	12.24	19.97	18.35	17.18	**	**	-	-
	SPLEN1000068	20.63	22.57	21.07	11.6	16.29	10.46	9.19	11.89	8.79	*	**	-	-
	SPLEN1000072	19.88	16.93	14.96	6.06	9.86	7.47	5.18	4.49	6.78	**	**	-	-
	SPLEN1000101	71.97	43.16	57.46	18.69	27.56	26.8	32.73	40.27	19.97	*		-	-
	SPLEN1000108	7.69	6.28	7.07	3.65	4.35	2.67	3.12	2.84	2.04	**	**	-	-
	SPLEN1000113	11.47	6.64	12.13	7.54	8.23	7.26	5.5	6.27	7.59			-	-
20	SPLEN1000114	16.01	14.75	14.36	7.29	9.65	6.3	8.14	8.22	8.73	**	**	-	-
	SPLEN1000132	5.96	4.51	7.38	2.74	4.42	2.34	1.47	2.25	2.21	*		-	-
	SPLEN1000135	10.57	8.18	9.39	3.86	4.71	4.73	4.9	2.38	2.97	**	**	-	-
	SPLEN1000136	23.91	23.93	20.23	10.77	11.86	10.15	16.69	14.04	13.77	**	**	-	-
	SPLEN1000141	42.88	39.73	42.83	27.16	32.91	23.4	23.31	18.41	20.57	**	**	-	-
	SPLEN1000164	15.72	13.33	13.69	7.76	12.46	6.69	9.59	8.11	9.12	**	**	-	-
25	SPLEN1000166	12.98	9.08	11.45	4.56	6.01	5.04	6.49	5.17	6.32	**	*	-	-
	SPLEN1000175	19.26	16.94	15.5	7.48	9.23	6.92	11.34	13.49	13.41	**	*	-	-
	SPLEN1000182	67.34	58.35	68.22	30.69	30.43	27.88	28.16	29.1	23.7	**	**	-	-
	SPLEN1000185	6.38	8.35	5.56	4.69	4.56	3.06	2.86	2.31	1.51	**		-	-
	THYMU1000004	48.79	34.96	41.97	30.97	32.65	27.64	26.98	17.5	13.12	*		-	-
	THYMU1000009	14.59	13.55	14.88	8.47	10.1	5	7.34	4.91	5.62	*	**	-	-
30	THYMU1000015	19.34	18.55	12.08	8.34	11.37	5.93	10.39	10.96	13.03	*		-	-
	THYMU1000016	6.78	4.3	5.54	2.79	2.51	1.91	5.14	3.5	4.34	*		-	-
	THYMU1000023	6.35	6.23	6.53	4.39	3.65	4.2	3.1	5.69	3.98	**		-	-
	THYMU1000034	390.65	392.5	375.97	306.71	379.09	270.69	454.49	361.08	369.56			-	-
	THYMU1000035	8.93	7.8	9.14	5.88	4.95	4.81	5.06	3.93	4.36	**	**	-	-
	THYMU1000037	9.69	6.41	7.36	4.28	3.96	3.33	4.24	3.59	3.83	*	*	-	-
35	THYMU1000042	6.85	3.93	5.82	2.75	3.24	2.02	2.08	1.63	1.09	*	*	-	-
	THYMU1000047	25.64	25.03	24.74	13.43	16.94	11.38	26.77	21.68	23.81	**		-	-
	THYMU1000080	20.17	51.54	27.22	17.42	19.98	26.99	13.06	15.8	14.07			-	-
	THYMU1000094	11.12	6.99	9.51	6.45	6.49	4.35	11.14	9.41	9.31			-	-
	THYMU1000109	228.62	201.78	195.22	195.65	173.29	154.39	235.81	205.84	221.79			-	-
	THYMU1000127	44.2	30.97	37.5	12.05	18.11	17.75	24.49	15.04	18.2	**	*	-	-
40	THYMU1000130	21.64	17.3	15.84	7.65	12.45	8	10.24	3.41	8.22	*	*	-	-
	THYMU1000137	6.81	10.03	8.23	3.35	5.2	3.34	4.41	2.7	3.47	*	*	-	-
	THYMU1000146	11.97	7.39	7.48	8.11	7.24	6.17	5.13	3.03	6.19			-	-
	THYMU1000159	10.45	10.21	8.17	6.28	6.42	3.77	4.54	3.62	4.78	*	**	-	-
	THYMU1000163	8.08	8.93	9.7	5.33	5.95	3.66	7.57	4.17	4.21	**	*	-	-
	THYMU1000167	67.79	51.53	54.02	27.07	31.06	17.27	75.27	48.55	70.31	**		-	-
45	THYMU1000186	8.38	8.15	3.89	3.94	4.49	2.65	3.36	2.91	3.02			-	-
	THYRO1000017	24	17.58	11.71	8.21	11.63	5.25	6.04	5.8	4.42	*		-	-
	THYRO1000026	10.24	8.59	6.72	5.28	7.77	4.55	4.15	3.45	6.46	*		-	-
	THYRO1000034	39.83	32.92	35.9	29.82	39.02	28.83	26.88	25.91	22.08	*		-	-
	THYRO1000035	34.67	27.15	24.29	22.39	30.44	22.35	22.09	19.28	23.65			-	-
	THYRO1000036	16.2	14.28	11.79	9.92	10.8	4.36	7.94	4.75	8.23	*		-	-
50	THYRO1000040	9.47	7.71	9.48	4.32	5.83	3	5.07	3.54	5.01	*	**	-	-
	THYRO1000061	18.28	19.76	15.63	8.28	5.85	4.81	6.42	5.28	9.19	**	**	-	-
	THYRO1000067	16.85	13.02	12.06	8.02	8.96	4.34	7.22	6.1	5.44	*	**	-	-
	THYRO1000070	9.96	13.03	10.58	5.63	9.48	4.69	20.02	18.33	15.63	*		-	-
	THYRO1000072	21.57	19.92	18.73	19.89	17.94	12.39	9.77	9.74	9.5	**		-	-
	THYRO1000084	9.91	5.58	5.31	3.9	6.43	2.97	10.41	8.45	10.27			-	-
55	THYRO1000085	29.04	36.56	22.76	13.84	17.05	13.37	10.59	14.52	10.12	*	*	-	-
	THYRO1000086	13.56	10.42	8.08	7.5	9.36	4.87	6.64	6.5	4.47			-	-

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	THYRO1000087	51.14	69.3	41.47	29.99	58.4	26.89	61.05	53.08	61.77				
	THYRO1000092	26.07	28.19	30.84	13.75	13.51	9.94	17.56	21.51	22.34	**	*	-	-
5	THYRO1000093	4.26	2.01	4.16	1.77	3.46	3.25	2.69	3.3	2.41				
	THYRO1000099	9.62	5.87	9.26	3.68	8.63	4.69	5.9	7.16	4.32				
	THYRO1000107	70.48	59.74	59.68	39.34	64.57	40.78	35.76	61.82	50.34				
	THYRO1000111	13.96	11.92	12.38	7.04	9.78	5.89	9.55	11.53	9.66	*	*	-	-
	THYRO1000121	31.45	32.43	38.13	15.06	18.17	17.71	26.05	28.32	34.79	**		-	-
	THYRO1000124	54.83	35.35	48.22	37.6	35.37	31.52	34.87	27.99	31.75				
10	THYRO1000129	8.59	9.01	8.49	5.14	9.82	6.06	8.93	8.73	10.55				
	THYRO1000130	12.23	8.25	10.08	6.62	6.95	6.32	6.99	9.76	9.68	*		-	-
	THYRO1000132	7.93	8.79	12	5.35	7.15	7.04	4.12	4.66	3.86		*		-
	THYRO1000134	17.2	6.06	9.3	6.24	6.27	12.5	5.33	7.31	5.41				
	THYRO1000144	23.66	30.56	32.27	27.55	32.97	28.83	18.04	19.4	19.02		*		-
	THYRO1000155	35.26	37.35	35.3	18.99	24.31	20.42	31.31	40.6	29.86	**		-	-
15	THYRO1000156	37.13	43.79	38.99	24.77	34.58	23.66	18.78	36.39	21.81	*		-	-
	THYRO1000163	56.18	53.4	58.15	23.96	28.08	23.46	11.7	14.01	16.02	**	**	-	-
	THYRO1000173	8.52	8.35	6.58	5.25	10.18	4.15	3.25	4.22	4.73		**	-	-
	THYRO1000186	35.39	31.09	36.48	14.41	13.8	14.41	7.62	12.05	15.91	**	**	-	-
	THYRO1000187	17.39	15.95	24.02	6.63	8.73	8.87	5.49	7.02	6.9	*	**	-	-
	THYRO1000190	7.06	7.97	10.31	6.43	5.1	6.9	4.78	5.24	5.17		*	-	-
20	THYRO1000196	8.72	14.15	13.33	14.25	10.93	7.74	3.75	6.65	9.84				
	THYRO1000197	13.75	17.13	15.02	14.96	17.34	16.5	8.34	11.47	6.36		*	-	-
	THYRO1000199	6.8	9.71	11.38	6.6	11.32	10.32	5.5	6.51	7.17				
	THYRO1000206	20.09	21.74	25.04	13.14	17.5	12.03	7.45	6.8	7.63	*	**	-	-
	THYRO1000221	6.96	7.15	5.44	4.48	8.31	3.94	3.81	4.45	3.66		*	-	-
	THYRO1000222	56.33	56.17	63.27	37.58	40.7	31.29	35.13	33.5	43.65	**	**	-	-
25	THYRO1000228	148.64	127.09	184.25	73.36	64.55	57.59	55.06	55.21	55.09	**	**	-	-
	THYRO1000241	7.79	5.72	9.15	4.42	5	4.49	2.68	4.65	4.26	*	*	-	-
	THYRO1000242	18.16	23.99	29.76	25.09	51.85	27.45	12.5	20.02	16.61				
	THYRO1000246	21.57	18.12	24.56	19.46	20.13	15.33	9.29	10.17	9.72		**	-	-
	THYRO1000253	10.77	13.3	16.4	9.6	16.01	8.45	6.71	8.04	5.73		*	-	-
	THYRO1000270	12.58	12.99	17.24	8.11	13.02	8.87	9.06	8.16	7.99		*	-	-
30	THYRO1000279	15.04	13.53	16	8.28	14.2	7.73	7.71	7.11	4.92	**		-	-
	THYRO1000285	1215.2	1221.3	1148.5	961.64	1121.8	816.57	1261.8	1135.7	1518.7				
	THYRO1000288	24.11	22.65	22.01	13.89	25.53	14.41	22.83	21.93	20.34				
	THYRO1000296	40.86	36.2	38.51	33.51	37.84	29.24	32.78	49.02	40.29				
	THYRO1000320	12.29	9.4	14.15	6.59	7.17	6.08	5.28	11.64	9.29	*		-	-
35	THYRO1000322	37.49	34.76	35.08	17.69	26.05	19.02	19.43	23.34	20.74	**	**	-	-
	THYRO1000327	29.25	26.35	19.48	16.99	27.29	15.75	10.07	12.24	13.52		*	-	-
	THYRO1000343	16.65	12.58	17.82	8.18	11.42	7.21	10.1	9.05	8.44	*	*	-	-
	THYRO1000345	6.25	7.77	6.06	4.74	8.59	3.02	4.68	4.72	4.12		*	-	-
	THYRO1000358	13.06	10.33	11.35	6.24	8.76	7.32	8.15	6.51	9.21	*	*	-	-
	THYRO1000368	5.38	5.26	6.26	3.15	3.94	2.68	6.19	3.06	2.43	**		-	-
40	THYRO1000375	14.1	11.6	18.84	8.56	5.99	5.1	3.89	3.2	3.55	*	**	-	-
	THYRO1000381	10.31	8.3	9.78	4.37	5.3	5.96	4.17	5.35	3.59	**	**	-	-
	THYRO1000387	11.39	10.61	13.54	4.54	5.97	3.46	10.59	5.84	3.07	**		-	-
	THYRO1000394	61.78	50.97	22.02	14.67	26.91	8.08	6.98	9.73	11.33		*	-	-
	THYRO1000395	29.06	37.87	27.54	18.13	24.45	14.15	25.79	23.19	25.7	*		-	-
	THYRO1000400	10.51	10.51	9.69	3.23	12.01	5.83	3.72	3.73	3.08		**	-	-
45	THYRO1000401	10.42	9.53	10.77	6.74	5.06	4.73	3.24	5.18	5.6	**	**	-	-
	THYRO1000407	111.95	92.99	98.17	63.29	75.05	58.17	51.33	55.33	55.02	**	**	-	-
	THYRO1000420	15.01	13.25	17.92	11.1	11.62	8.56	12.79	12.37	14.41	*		-	-
	THYRO1000438	8.38	5.22	8.85	5.12	4.11	4.31	4.22	4.7	3.13		*	-	-
	THYRO1000452	15.04	12.59	12.97	5.92	10.6	6.13	2.16	3.93	4.57	*	**	-	-
	THYRO1000455	7.17	8.57	9.52	2.62	3.31	3.44	2.83	2.18	2.11	**	**	-	-
50	THYRO1000471	78.16	81.99	62.01	65.6	82.48	70.86	81.77	51.28	74.06				
	THYRO1000481	8.9	7.89	8.46	4.91	7.54	4.12	2.78	3.16	5.02		**	-	-
	THYRO1000484	19.83	12.76	16.87	10.37	11.59	9.38	11.21	9.7	11.91	*		-	-
	THYRO1000488	28.64	20.75	23.35	20.89	21.13	19.59	15.6	20.62	19.42				
	THYRO1000501	11.59	12.72	13.28	7.74	9.03	6.79	8.05	7.95	10.26	**	*	-	-
	THYRO1000502	55.86	52.65	49.31	44.07	46.78	38.57	44.58	40.93	38.11	*	*	-	-
55	THYRO1000505	9.64	7.65	7.27	5.56	5.82	3.06	3.98	5.47	2.02	*	*	-	-
	THYRO1000535	37.32	41.34	38.41	38.72	38.24	31.02	23.49	20.01	18.32	**		-	-
	THYRO1000556	102.92	92.57	85.3	76.31	104.96	62.73	51.56	50.77	49.93	**		-	-



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	THYRO1000558	8.54	7.17	6.38	4.15	8.61	3.01	4.26	2.04	3.45	*	-
	THYRO1000569	6.63	4.92	4.79	4.77	4	3.41	3.56	3.02	3.94	*	-
5	THYRO1000570	9.09	6.95	8.33	5.27	6.38	6.54	5.25	4.89	7.09		
	THYRO1000572	52.16	31.52	39.78	12.92	33.15	30.73	30.68	23.84	11.23		
	THYRO1000573	8.96	8.49	6.82	4.33	8.49	6.35	13.45	11.85	8.38		
	THYRO1000577	9.73	7.83	7.69	3.93	6.26	2.6	2.58	3.82	2.74	* **	- -
	THYRO1000580	40.56	32.54	29.95	22.22	19.86	19.81	24.19	17.34	25.52	* *	- -
	THYRO1000584	39.96	36.8	31.93	19.25	25.5	16.24	26.15	21.02	19.13	* *	- -
10	THYRO1000585	8.99	7.37	6.65	4.19	6.67	4.86	5.4	3.58	2.99	*	-
	THYRO1000596	43.85	33.14	32.61	22.94	31.65	11.59	15.52	10.88	14.47	**	-
	THYRO1000602	19.04	15.25	10.78	7.23	11.51	11.78	8.87	7.72	10.81		
	THYRO1000605	10.06	9.44	5.91	6.29	6.99	4.61	4.9	5.21	5.08		
	THYRO1000615	134.15	117.37	85.97	86.81	98.31	67.18	77.31	67	84.37		
	THYRO1000625	33.27	24.69	16.68	12.6	10.75	20.13	8.38	6.86	11.76	*	-
15	THYRO1000636	17.91	16.49	14.48	12.48	11.49	6.7	8.72	6.17	8.59	* **	- -
	THYRO1000637	18.22	22.2	13.43	10.39	14.05	9.78	9.07	5.2	7.26	*	-
	THYRO1000641	7.23	5.87	6.32	4.82	10.06	3.87	8.42	4.55	2.07		
	THYRO1000657	10.91	9.86	8.65	6.93	7.74	7.68	9.53	8.35	10.94	*	-
	THYRO1000658	14.37	9.48	5.1	6.28	6.83	5.43	4.59	4.62	4.77		
	THYRO1000662	10.63	9.43	8.46	6.7	6.85	6.96	7.92	7.09	10.89	*	-
20	THYRO1000666	30.51	33.5	45.43	12.9	20.33	13.81	14.6	13.53	16.48	* **	- -
	THYRO1000676	11.56	11.35	8.48	6.32	9.3	8.37	4.16	5.02	6.44	*	-
	THYRO1000678	23.44	18.73	20.73	10.13	15.99	8.49	9	7.38	9.87	* **	- -
	THYRO1000684	27.78	27.85	20.27	12.26	16.45	11.06	26.97	17.92	24.98	*	-
	THYRO1000694	16.87	11.78	10.72	5.47	10.25	5.99	12.29	9.36	8.6		
	THYRO1000699	9.11	6.36	4.55	5.62	6.31	3.48	7.37	3.08	5.06		
25	THYRO1000712	17.55	14.87	12.31	9.08	11.99	7.67	12.79	9.26	13		
	THYRO1000715	29.82	23.25	21.02	20.98	27.37	20.44	15.76	18.98	18.68		
	THYRO1000716	13.12	15.14	11.94	8.87	12	7.65	7.48	6.69	6.98	**	-
	THYRO1000717	11.89	15.21	12.45	6.9	9.22	5.08	30.93	6.96	7.18	*	-
	THYRO1000723	30.36	26.4	21.78	10.82	20.63	14.48	30.94	22.3	30.26	*	-
30	THYRO1000734	16.61	19.91	16.12	11.94	17.61	9.39	9.31	6.61	13.3	*	-
	THYRO1000748	17.46	14.06	15.87	5	7.52	5.42	7.82	5.84	7.09	** **	- -
	THYRO1000755	20.17	21.24	19.88	13.28	17.61	14.04	14.7	23.04	21.01	*	-
	THYRO1000756	369.81	334.57	369.63	298.51	345.41	273.28	259.37	366.07	273.4		
	THYRO1000776	4.97	4.99	7.55	4.25	6.18	4.82	2.58	5.02	3.55		
	THYRO1000777	5.42	5.63	6.34	5.34	6.01	4.03	3.82	3.75	3.21	**	-
35	THYRO1000779	483.37	458.9	483.51	453.87	549.42	449.1	368.6	510.93	458.47		
	THYRO1000782	17.27	20.25	23.35	14.58	17.12	13.37	15.61	16.4	16.35		
	THYRO1000783	5.74	5.45	6.68	5.43	9.62	4.88	3.62	5.19	3.8	*	-
	THYRO1000786	25.62	30.48	26.26	16.78	13.18	14.48	32.89	30.78	26.94	**	-
	THYRO1000787	50.52	37.21	54.05	28.71	18.06	26.25	20.11	24.5	22.66	* **	- -
	THYRO1000792	14.11	12.1	15.65	4.55	6.72	7.1	8.13	7.14	8.33	** **	- -
40	THYRO1000793	36.92	35.83	42.61	19.08	27.16	19.55	34.91	38.74	32.64	**	-
	THYRO1000795	37.33	45.29	88.32	42.19	57.36	40.15	12.57	21.17	13.38		
	THYRO1000796	10.25	11.83	14.01	6.19	10.21	5.98	7	11.89	11.1		
	THYRO1000798	9.87	14.22	12.83	9.06	8.1	7.49	5.04	7.33	5.2	* *	- -
	THYRO1000800	37.69	54.75	19.73	33.2	22.36	23.21	13.79	16.89	13.75		
	THYRO1000805	8.27	6.21	6.02	5.33	8.39	4.44	3.81	4.14	3.82	*	-
45	THYRO1000815	109.41	92.13	90.62	43.51	38.14	25.61	31.76	21.16	31.98	** **	- -
	THYRO1000829	33.86	25.13	34.71	19.68	21.68	18.45	16.87	14.34	12.65	* **	- -
	THYRO1000835	9.51	9.82	10.3	6.71	6.28	4.65	5.41	5.24	6.07	** **	- -
	THYRO1000843	27.06	16.5	24.96	16.28	19.34	15.73	6.22	7.81	8.06	**	-
	THYRO1000846	7.86	5.91	13.48	4.53	6.28	7.74	3.89	7.02	5.26		
	THYRO1000852	24.69	25.37	23.66	12.87	20.2	12.5	9.33	10.39	11.62	* **	- -
50	THYRO1000855	7.12	7.47	10.43	2.52	5.79	2.98	4.3	6.1	5.2	*	-
	THYRO1000865	9.21	5.67	8.64	3.4	6.56	3.18	5.99	8.76	7.67		
	THYRO1000866	57.27	46.1	51.69	32.85	43.74	27.97	46.24	39.05	41.55	*	-
	THYRO1000881	13.67	12.21	13.18	9.6	10.62	12.24	10.21	16.82	10.91		
	THYRO1000894	9.33	7.11	11.4	5.66	6.12	4.31	4.14	4.68	4.75	* *	- -
	THYRO1000895	8.9	5.89	10.11	3.35	4.07	4.72	4.32	4.09	3.45	* *	- -
55	THYRO1000916	9.19	7.72	16.87	5.02	6.67	5.27	4.16	6.12	3.42		
	THYRO1000917	6.89	10.63	12.32	4.97	9.51	5.39	6.77	7.94	6.2		
	THYRO1000926	14.99	10.81	12.37	6.79	9.95	6.06	7.42	7.03	11.27	*	-

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	THYRO1000934	9.21	6.94	9.67	4.17	7.52	4.26	6.41	5.73	4.96	*	*	-	-
	THYRO1000951	21.19	13.82	17.24	10.15	10.71	6.54	7.11	11.34	11.56	*	*	-	-
5	THYRO1000952	38.82	45.17	51.97	24.89	24.37	18.77	17.55	26.97	13.34	**	**	-	-
	THYRO1000956	11.42	8.41	13.85	5.27	6.34	6.15	5.07	6.61	6.85	*	*	-	-
	THYRO1000960	9.97	3.83	8.63	2.78	4.13	2.34	2.46	2.03	6.43			-	-
	THYRO1000961	33.04	35.26	36.48	15.01	15.48	15.21	21.6	24.41	21.14	**	**	-	-
	THYRO1000964	14.43	12.46	17.93	3.92	6.7	5.62	5.43	7.53	4.58	**	**	-	-
	THYRO1000971	15.18	16.5	16.14	8.34	13.54	9	9.38	8.59	10.52	*	**	-	-
10	THYRO1000974	7.51	5.29	9.43	2.24	6.94	1.8	3.55	5.59	3.45			-	-
	THYRO1000975	7.71	4.75	6.93	3.36	5.71	4.79	3.77	4.87	3			-	-
	THYRO1000983	8.4	4.14	7.44	3.86	5.03	3.36	3.1	3.21	4.03			-	-
	THYRO1000984	9.35	8.4	11.52	6.49	7.32	5.22	5.08	2.55	2.65	*	**	-	-
	THYRO1000988	10.2	6.57	7.62	4.27	4.23	4.6	2.94	2.66	2.92	*	**	-	-
	THYRO1000991	12.33	10.95	12.47	5.27	7.49	7.34	5.57	6.15	6.01	**	**	-	-
15	THYRO1000999	9.77	12.84	10.64	5.68	8.33	5.92	5.68	3.11	2.9	*	**	-	-
	THYRO1001003	324.55	443.5	324.63	353.93	491.59	377.12	509.02	394.65	380.17			-	-
	THYRO1001015	16.58	13.37	11.66	7.36	13.81	8.4	12.04	9.04	10.47			-	-
	THYRO1001016	34.7	29.76	32.31	14.48	17.7	10.51	27.97	31.88	30.58	**		-	-
	THYRO1001022	27.6	17.2	20.61	6.98	9.39	10.85	5.35	6.58	6.8	*	**	-	-
20	THYRO1001031	15.75	9.57	11.29	5.12	7.05	5.99	8.13	6.39	9.34	*		-	-
	THYRO1001033	11.34	7.57	8.58	7.55	5.52	6.01	4.3	4.01	4.9		*	-	-
	THYRO1001062	12.86	12.45	12.49	4.68	5.59	4.88	3.54	3.68	2.79	**	**	-	-
	THYRO1001063	10.18	8.38	10.08	5.14	7.17	4.58	3.55	4.32	2.35	*	**	-	-
	THYRO1001071	18.49	15.5	18.23	9.12	10.91	7.86	5.73	5.41	5.84	**	**	-	-
	THYRO1001080	11.77	12.06	11.47	3.65	12.27	3.17	3.08	4.59	4.41	**	**	-	-
	THYRO1001093	12.17	9.63	9.75	5.98	4.91	5	8.58	8.31	7.24	**		-	-
25	THYRO1001100	33.06	27.59	26.02	30.29	27.98	30.28	66.02	40.22	70.38	*		-	-
	THYRO1001102	10.18	6.7	5.95	5.04	6.9	4.52	4.36	4.71	4.45			-	-
	THYRO1001104	5.1	2.75	2.78	0.69	0.92	1.62	1.32	0.94	0.7	*	*	-	-
	THYRO1001109	19.62	18.07	14.26	10.98	10.98	9.76	8.55	11.06	8.68	*	*	-	-
	THYRO1001113	10.89	6.97	7.59	2.84	3.69	2.77	2.56	1.4	2.3	*	**	-	-
	THYRO1001120	9.27	9	8.82	3.46	4.66	2.98	4.02	3.07	2	**	**	-	-
30	THYRO1001121	20.41	16.36	16.91	9.1	13.05	6.93	13.22	15.3	13.97	*		-	-
	THYRO1001128	25.09	18.24	17.74	8.53	9.61	6.74	3.45	4.7	7.82	**	**	-	-
	THYRO1001133	7.42	6.4	5.88	4	5.05	4.23	3.88	4.14	3.81	*	**	-	-
	THYRO1001134	29.23	23.66	23.28	16.51	20.53	18.49	22.14	16.92	20.47	*		-	-
	THYRO1001142	5.04	4.99	5.1	2.78	3.05	3.47	2.44	2.26	1.6	**	**	-	-
35	THYRO1001173	31.85	26.04	28.94	20.36	18.72	13.59	18.5	15.33	18.17	*	**	-	-
	THYRO1001175	95.55	98.04	80.56	104.29	114.18	77.1	51.33	46.56	49.17	**	**	-	-
	THYRO1001177	10.9	11.18	11.71	5.13	7.17	5.9	4.63	5.82	5.02	**	**	-	-
	THYRO1001189	16.52	14.55	11.53	5.76	11.24	3.42	11.07	10.9	8.86			-	-
	THYRO1001194	11.83	6.2	11.19	5.29	7.22	4.28	5.84	7.01	6.86			-	-
	THYRO1001204	52.04	33.32	32.8	18.53	22.19	18.27	39.75	37.94	46.59	*		-	-
40	THYRO1001205	8.98	12.23	9.39	5.39	8.08	5.04	6.55	6.04	4.85	*	*	-	-
	THYRO1001213	41.54	37.73	35.86	23.36	25.7	20.79	37.67	32.41	38.62	**		-	-
	THYRO1001224	10.86	11.43	10.75	5.38	8.69	6.7	7.21	4.53	6.36	*	**	-	-
	THYRO1001237	16.76	20.25	15.97	16.59	13.69	5.38	9.78	5.69	6.27		**	-	-
	THYRO1001242	13.1	19.03	16.06	12.27	8.61	6.73	9.21	5.95	9.02	*	*	-	-
	THYRO1001258	27.32	21.68	20.65	9.74	18.76	12.77	10.51	6.86	13.04	*	**	-	-
45	THYRO1001262	8.57	4.74	4.06	3.76	5.55	4.02	4.79	3.93	5.05			-	-
	THYRO1001266	25.45	17.38	17.48	9.96	11.28	8.76	13.97	15.24	19.55	*		-	-
	THYRO1001271	27.85	25.6	17.14	13.77	18.43	9.74	22.54	18.92	23.05			-	-
	THYRO1001287	126.74	172.63	126.71	56.76	169.06	71.99	103.16	93.81	120.13			-	-
	THYRO1001290	11.3	8.82	9.68	4.97	7.48	6.55	3.86	5.84	8.41	*		-	-
	THYRO1001291	13.9	16.44	13.22	8.85	8.33	3.9	6.83	3.64	6.66	*	**	-	-
50	THYRO1001297	13.17	12.27	11.41	6.73	6.88	4.23	7.87	5.3	8.04	**	**	-	-
	THYRO1001302	28.98	24.47	17.01	9.99	19.11	8.25	41.39	28.42	36.98			-	-
	THYRO1001313	3.4	2.28	2.86	1.62	1.97	1.71	3.09	2.85	2.3	*		-	-
	THYRO1001320	4.85	2.3	4.45	3.81	2.95	2.21	2.67	2.22	1.94			-	-
	THYRO1001321	84.54	108.43	89.51	45.59	48.9	36.67	60.61	56.13	42.33	**	*	-	-
	THYRO1001322	15.07	13.59	11.8	5.6	6.9	4.45	5.91	6.73	6.71	**	**	-	-
55	THYRO1001327	61.14	62.79	47.56	27.21	36.08	29.25	40.32	44.89	30.36	**	*	-	-
	THYRO1001336	21.04	18.95	13.64	17.33	15.44	11.88	17.21	14.24	12.35			-	-
	THYRO1001347	42.47	35.49	29.56	20.44	37.43	12.7	20.26	16.34	15.93	**		-	-

Table 502

	THYRO1001358	6.96	7.77	6.52	4.41	8.39	3.78	5.37	5.5	4.22		*	-
	THYRO1001363	36.77	35.26	36.97	12.86	20.63	14.65	24.19	31.52	25.12	**	*	-
5	THYRO1001365	2.39	1.31	4.42	2.3	2.69	1.43	1.82	2.18	1.5			-
	THYRO1001374	10.11	11.14	11.66	5.19	7.75	3.64	2.84	5.3	4.44	*	**	-
	THYRO1001401	11.45	8.59	8.77	5.02	5.3	5.96	5.5	8.56	6.31	*		-
	THYRO1001403	3.12	3.62	7.98	1.61	2.43	2.61	3.73	1.98	3.91			-
	THYRO1001405	84.82	60.76	92.35	68.75	78.6	50.19	53.53	29.6	47.94		*	-
	THYRO1001406	13.59	7.57	12.02	4.76	6.87	3.76	11.69	13.59	9.54	*		-
10	THYRO1001411	4.72	4.15	5.65	3.88	2.4	3.38	2.52	2.5	3.6		*	-
	THYRO1001420	9.34	4.82	8.71	4.7	4.71	5.55	3.24	4.39	8.81			-
	THYRO1001426	9.26	4.52	12.27	5.65	6.22	4.37	4.27	8.59	6.13			-
	THYRO1001430	10.74	13.91	18.18	13.99	18.28	13.49	6.82	9.48	10.77			-
	THYRO1001434	7.66	6.66	12.91	8.64	10.68	8.13	5.38	8.91	2.99			-
	THYRO1001456	26.49	36.99	36.96	17.02	23.99	16.92	30.71	34.81	38.85	*		-
15	THYRO1001457	14.33	10.91	13.26	5.72	4.54	3.33	4.05	3.22	4.83	**	**	-
	THYRO1001458	15.32	13.83	12.78	10.99	10.13	5.72	4.4	7.29	6.97	*	**	-
	THYRO1001459	5.78	4.92	7.36	2.81	3.46	4.24	3.11	4.43	5.51	*		-
	THYRO1001471	13.48	10.81	13.3	5.13	9.62	6.19	6.36	8.85	9.45	*	*	-
	THYRO1001478	8.04	3.79	8.01	2.94	3.62	2.21	4.12	4.22	3.59			-
20	THYRO1001480	16.07	16.86	14.48	6.78	13.68	13.34	3.54	6.61	19.35			-
	THYRO1001481	16.23	13.97	17.19	13.3	15.2	13.73	4.94	6.01	3.76	**		-
	THYRO1001487	39.34	43.94	45.87	41.49	42.62	34.09	36.78	39.23	41.44			-
	THYRO1001495	6.21	3.33	12.71	2.18	5.51	4.67	3.43	3.46	4.85			-
	THYRO1001498	13.82	15.45	16.61	11.32	20.15	8.37	4.81	6.08	4.31	**		-
	THYRO1001510	9.97	6.87	19.31	8.41	6.21	3.55	4.99	6.45	19.57			-
25	THYRO1001512	11.51	8.21	10.34	5.87	6.36	6.84	4.43	19.67	5.22	*		-
	THYRO1001519	12.05	16.47	10.9	4.73	8.69	4.14	4.42	4.28	5.04	*	**	-
	THYRO1001522	10.39	6.84	12.83	6.15	7.71	8	5.13	5.33	7.56			-
	THYRO1001523	15.14	10.51	16.01	7.01	9.2	6.38	3.77	3.19	4.5	*	**	-
	THYRO1001526	5.67	5.48	12.84	2.85	5.19	3.09	4.51	3.63	4.01			-
	THYRO1001529	70.52	99.68	61.07	73.62	81.82	35.88	29.07	23.9	34.69		*	-
30	THYRO1001534	10.48	7.92	11.72	6.09	7.42	11.24	6.53	6.35	3.17	*		-
	THYRO1001537	5.9	3.05	5.93	3.4	3.75	2.75	3.26	2.87	4.91			-
	THYRO1001541	27.84	38.72	38.42	23.51	30.22	18.99	22.01	26.98	14.85			-
	THYRO1001545	12.87	9.76	11.61	3.56	6.9	5.41	4.16	22.14	4.44	**		-
	THYRO1001559	143.67	217.09	127.43	126.92	211.99	217.97	165.83	143.91	101.7	**	**	-
35	THYRO1001563	29.66	25.88	28.83	14.46	17.77	19.17	10.82	18.32	17.35	**	**	-
	THYRO1001570	5.85	5.24	10.72	3.21	3.79	2.31	2.47	4.03	3.05			-
	THYRO1001573	10.58	14.52	15.67	7.66	10.98	10.26	4.93	9.17	5.76	*		-
	THYRO1001584	11.71	9.79	13.05	7.75	12.43	7.3	8.19	4.92	4.88	*		-
	THYRO1001593	119.63	87.93	122.57	37.27	54.3	33.56	100.89	84.41	119.61	**		-
	THYRO1001595	9.11	9.13	10.8	7.84	8.88	6.77	4.62	12.97	7.82			-
	THYRO1001596	6.25	3.54	8.97	3.03	4.5	2.76	3.54	3.67	4.02			-
40	THYRO1001602	7.1	6.21	7.8	6.63	4.96	5.02	4.21	4.12	2.97	**		-
	THYRO1001605	28.22	39.54	25.87	13.48	23.89	22.57	11.83	10.02	13.09	*		-
	THYRO1001608	19.26	17.94	17.77	8.3	22	8.49	8.07	8.36	11.18	**		-
	THYRO1001617	7.36	9.07	12.26	4.4	5.61	3.53	3.83	3.37	4.51	*	*	-
	THYRO1001634	9.8	9.15	14.08	5.65	9.76	4.62	5.62	3.69	4.86	*		-
	THYRO1001637	6.56	2.42	6.39	2.18	3.8	2.31	2.41	3.7	6.48			-
45	THYRO1001641	12.87	8.05	12.44	6.03	4.87	6.49	3.32	2.86	2.92	*	**	-
	THYRO1001656	20.03	12.66	30.89	7	10.07	5.22	6.32	7.53	5.64			-
	THYRO1001658	7.58	6.85	10.14	4.65	4.77	3.94	3.38	2.8	2.5	*	**	-
	THYRO1001661	150.1	98.3	106.51	135.25	166.2	125.8	74	80.32	53.76			-
	THYRO1001671	10.97	8.43	12.21	5	5.04	3.97	5.12	5.12	3.84	**	**	-
	THYRO1001672	12.9	11.31	11.75	5.85	6.91	5.08	3.69	2.74	2.72	**	**	-
50	THYRO1001673	31.04	28.57	26.79	16.85	19.7	19.9	22.8	23.43	23.51	**	*	-
	THYRO1001677	8.63	6.86	9.97	3.55	4.9	4.2	5.4	6.55	6.85	*		-
	THYRO1001683	39.34	16.85	25.87	16.11	18.7	19.17	8.36	10.76	9.09			-
	THYRO1001700	12.31	7.03	9.15	3.61	4.23	3.04	2.79	3.63	4.8	*	*	-
	THYRO1001702	23.7	21.62	17.4	10.57	5.8	11.44	6.01	4.83	2.94	*	**	-
	THYRO1001703	7.22	4.23	5.14	2.63	3.23	1.81	2.37	2.42	2.04	*	*	-
55	THYRO1001706	8.39	5.62	8.09	3.72	3.11	3.37	3.24	2.65	1.26	*	**	-
	THYRO1001721	11.69	10.42	16.73	6.09	4.96	4.46	3.92	2.33	3.87	*	**	-
	THYRO1001725	147.69	144.4	144.74	111.99	128.3	86.63	130.43	106.61	93.76	*	*	-

Table 503

	THYR01001730	7.74	3.57	7.41	4.48	4.19	3.07	3.64	4.09	4.72			
	THYR01001738	1.57	3.03	2.24	0.97	0.17	0.58	0.7	0.99	1.64	*	-	
5	THYR01001743	5.12	3.48	3.39	1.67	2.12	2.94	1.98	2.6	2.48			
	THYR01001745	30.25	14.84	20.6	6.81	4.65	9.25	12.7	8.09	11.05	*	-	
	THYR01001746	10.78	5.89	7.69	2.83	3.1	3.64	3.64	1.32	2.13	*	*	-
	THYR01001770	20.01	12.02	16.57	10.05	13	10.49	5.37	6.07	5.43	*	-	
	THYR01001772	29.2	56.08	29.11	28.47	34.34	15.95	9.21	8.24	9.37	*	-	
	THYR01001778	39.03	35.61	22.42	13.39	32.45	16.04	9.42	8.03	11.2	*	-	
10	THYR01001793	9.35	3.26	5.98	4.02	4.49	3.37	4.45	4.26	5.77			
	THYR01001796	66.96	62.34	52.36	31.61	31.58	30.06	74.83	63.67	78.59	**	-	
	THYR01001800	25.21	17.42	21.74	19.92	16.43	13.71	8.41	10.02	11.59	**	-	
	THYR01001803	12.96	11.11	10.61	7.04	8.3	3.44	5.71	5.48	6.64	*	**	-
	THYR01001809	10.44	7.96	6.8	4.59	3.72	3.71	3.62	1.76	1.34	*	**	-
	THYR01001817	18.78	13.28	15.51	15.03	13.53	6.93	8.79	4.88	8.37	*	-	
15	THYR01001819	14.15	14.31	9.69	5.8	6.63	6.06	6.27	4.29	5.81	*	*	-
	THYR01001828	8.14	8.22	6.65	5.42	7.94	4.29	7.29	4.26	2.47			
	THYR01001854	50.53	32.88	37.71	33.17	34.18	22.81	22.16	27.13	21.15	*	-	
	THYR01001895	9.86	7.83	3.92	4.41	4.53	2.55	3.7	10.54	3.46			
	THYR01001907	27.03	13.41	12.49	9.48	10.54	7.02	4.92	4.41	6.47			
20	TRACH1000006	9.54	7.16	8.08	5.68	4.66	5.53	6.46	4.52	6.76	*	-	
	TRACH1000013	9.02	5.8	8.2	2.58	4.45	3.1	3.07	2.02	4.14	*	*	-
	TRACH1000074	13.69	9.32	8.63	4.66	5.76	4.06	6.37	3.07	3.63	*	*	-
	TRACH1000095	11.28	8.48	10.55	5.54	3.9	3.41	3.79	4.56	3.68	**	**	-
	TRACH1000102	26.86	26.3	20.1	15.81	18.57	15.2	32.52	24.6	27.09	*	-	
	TRACH1000108	88.66	59.61	40.48	28.57	26.39	20.8	69.3	56.08	66.91			
25	TRACH1000126	17.36	13.19	13.78	8.07	9.6	6.46	5.91	5.75	6.51	*	**	-
	TRACH1000146	7.25	6.83	5.07	5.29	3.75	3.17	3.49	3.25	4.97	*	-	
	TRACH1000160	11.76	11.24	7.7	4.05	5.59	4.95	5.32	4.22	5.87	*	*	-
	TRACH1000184	33.51	45.86	50.29	14.82	25.81	22.15	25.29	16.88	23.76	*	*	-
	VESEN1000004	11.35	8.9	8.13	5.46	9.59	6.32	5.53	5.44	6.01	*	-	
	VESEN1000007	32.64	30.13	26.81	16.7	21.99	18.54	37.52	29.73	33.89	**	-	
30	VESEN1000013	13.16	11.68	12.05	7.19	9.9	4.25	7.18	4.46	8.92	*	*	-
	VESEN1000028	23.17	20.53	28.94	10.16	15.29	14.76	9.13	12.72	8.48	*	**	-
	VESEN1000059	4.76	3.32	5.57	3.56	3.32	3.56	1.16	3.33	1.96			
	VESEN1000100	8.85	5.84	8.92	5.55	6.82	5.48	3.69	5.59	3.98	*	-	
	VESEN1000107	158.28	125.83	134.47	126.46	135.37	133.6	74.61	79.36	82.66	**	-	
	VESEN1000117	3.74	4.02	10.93	3.48	5.02	4.1	2.18	2.11	2.69			
35	VESEN1000122	5.84	5.31	7.17	3.91	7.47	3.29	2.52	3.75	2.41	*	-	
	VESEN1000137	7.93	10.91	7.7	8.31	5.46	4.02	3.34	3.36	5.77	*	-	
	VESEN1000195	12.47	4.75	10.07	4.43	4.22	7.07	3.11	4.32	13.25			
	VESEN1000215	89.55	69.15	78.83	74.46	93.71	81.06	50.08	36.95	43.24	**	-	
	VESEN1000279	16.42	11.12	19.97	7.86	19.23	9.52	8.84	13.86	21.33			
	VESEN1000363	40.43	29.46	56.48	41.4	53.72	50.13	17.51	33.82	20.25			
40	VESEN1000388	4.51	6.13	9.09	5.56	8.45	6.21	3.44	6.29	2.57			
	VESEN1000394	137.33	123.92	135.03	107.32	177.33	115.58	81.85	76.56	86.04	**	-	
	VESEN1000410	7.84	11.73	12.31	7.37	8.85	7.32	5.82	6.16	5.5	*	-	
	VESEN1000411	14.34	16.7	11.87	14.26	14.7	9.52	6.54	4.28	7.07	**	-	
	VESEN1000415	6.65	6.22	8.5	3.16	5.01	4.35	2.06	3.93	7.37	*	-	
	VESEN1000440	7.1	4.56	7.48	10.06	4.69	9.04	3.62	6.97	6.76			
45	VESEN1000452	127.08	114.54	102.58	100.33	106.23	122.79	77.87	58.16	82.71	*	-	
	VESEN1000539	57.4	47.68	67.32	36.3	45.7	42.57	51.56	51.15	50.18			
	VESEN1000554	7.29	12.24	14.13	6.05	4.57	6.75	3.69	3.4	3.85	*	-	
	VESEN1000557	4.5	6.91	10.86	5.64	5.73	4.35	3.05	2.96	4.75			
	VESEN1000575	16	18.27	24.28	11.3	16.07	11.77	13.59	13.83	16.27			
	VESEN1000585	14.4	14.28	13.38	9.87	13.37	6.72	4.91	4.08	5.01	**	-	
50	VESEN1000592	28.09	20.04	22.75	8.98	11.53	7	7.53	8.48	8.84	**	**	-
	VESEN1000658	9.27	5.98	6.99	4.92	3.93	3.11	3.31	12.18	6.06	*	-	
	VESEN1000669	7.65	11.62	18.09	8.2	9.11	7.91	4.21	6.96	3.61			
	VESEN1000743	27.12	25.27	28.49	19.46	23.17	19.77	12.01	15.14	12.53	*	**	-
	VESEN1000752	23.77	18.91	24.8	11.19	11.63	9.8	14.24	19.48	18.19	**	-	
	VESEN1000761	7.03	8.3	9.9	5.64	5.41	3.65	3.1	8.25	5.47	*	-	
55	VESEN2000039	16.58	20.4	16.46	7.12	12.23	7.45	5.23	4.66	6.91	*	**	-
	VESEN2000102	15.76	17.97	17.55	7.45	12.52	8.13	11.35	8.16	13.31	*	*	-
	VESEN2000164	69.66	54.85	54.07	18.32	20.39	15.6	15.69	21.51	20.97	**	**	-

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	VESEN2000175	7.45	6.95	7.39	3.43	6.1	3.72	4.64	8.1	4.35	*	-
	VESEN2000186	18.04	20.73	21.8	11.19	14.77	10.58	8.74	12.84	12.61	**	**
	VESEN2000199	11.71	6.48	9.96	8.59	9.24	5.52	6.89	6.26	14.79		
5	VESEN2000200	150.21	142.83	144.63	172.94	215.31	128.05	93.38	87.48	97.05	**	**
	VESEN2000204	7.05	7.07	9.65	4.56	4.24	3	2.19	4.63	3.19	*	*
	VESEN2000218	16.65	12.07	17.29	7.31	8.24	6.16	8.32	5	5.15	**	**
	VESEN2000230	12.09	13.48	13.57	4.57	10.45	4.08	3.93	4.19	2.98	*	**
	VESEN2000272	8.95	9.01	11.14	4.32	3.66	3.22	4.36	3.53	4.22	**	**
10	VESEN2000299	8.61	7.23	11.81	5.04	5.83	4.25	3.6	5.71	4.76	*	*
	VESEN2000323	17.3	12.74	15.22	15.36	17.47	14.24	5.84	6.35	4.65	**	
	VESEN2000327	18.5	9.19	14.45	6.81	8.17	7.45	3.2	5.07	5.85	*	
	VESEN2000328	7.53	7.78	8.38	3.45	4.17	4.12	2.35	2.19	1.81	**	**
	VESEN2000330	25.07	20.15	22.73	13.34	18.45	13.16	15.63	15.15	15	*	**
	VESEN2000336	7.29	9.37	11.82	5.86	9.09	5.78	3.64	3.5	5	*	*
15	VESEN2000354	10.99	9.78	10.4	5.27	8.22	4.93	3.58	3.58	2.59	*	**
	VESEN2000378	168.58	110.88	139.59	81.44	99.69	74.23	74.17	76.59	54.75	*	*
	VESEN2000379	32.08	21.47	28.34	16.72	15.12	13	22.77	26.45	21.84	*	
	VESEN2000397	21.17	10.11	25.4	12.77	12.2	10.8	15.72	16.01	17.99		
	VESEN2000416	5.92	5.21	7.48	3.5	6.28	4.01	2.87	3.94	3.48	*	
	VESEN2000420	8.47	4.35	7.18	4.04	3.81	2.46	2.31	4.27	1.92		
20	VESEN2000430	8.74	5.76	7.33	2.94	5.32	2.11	1.8	2.27	0.71	*	**
	VESEN2000448	14.67	14.58	16.08	4.71	4.34	2.88	3.91	2.23	2.27	**	**
	VESEN2000449	46.1	50.29	39.97	32.75	32.82	21.56	37.62	28.99	23.73	*	*
	VESEN2000456	45.88	33.52	32.47	18.88	21.08	19.47	15.48	22.28	22.31	*	*
	VESEN2000562	6.11	3.13	4.69	5.4	3.95	3.19	3.24	2.45	2.42		
	VESEN2000573	26.67	20.52	18.39	14.29	11.45	8.79	8.94	7.46	12.2	*	*
25	VESEN2000604	9.02	7.76	4.59	4.65	4.32	4.42	1.84	4.41	1.34	*	*
	VESEN2000614	9.59	7.78	6.05	4.77	5.05	4.35	3	3.94	2.87	*	*
	VESEN2000638	16.75	10.83	10.74	6.38	9.46	6.26	4.67	4.46	3.5	*	*
	VESEN2000641	15.71	14.29	14.25	7.95	7.6	6.71	8.94	7.41	6.6	**	**
	VESEN2000645	9.28	11.51	10.66	5.27	8.01	4.95	5.42	4.96	6.81	*	**
30	Y79AA1000013	24.66	15.88	15.09	6.08	5.43	5.53	13.59	13.07	18.88	*	*
	Y79AA1000030	19.52	16.62	14.47	8.07	7.77	10.99	7.86	7.77	10.02	*	**
	Y79AA1000033	29.91	18.65	28.38	16.37	15.72	11.59	28.15	19.64	28.85	*	*
	Y79AA1000037	4.94	2.8	4.89	5.26	3.24	0.91	1.44	1.94	2.43	*	*
	Y79AA1000041	79.98	53.74	54.67	39.77	36.14	29.21	42.77	30.09	45.97	*	*
	Y79AA1000059	9.8	7.3	8.44	4.37	5.08	2.06	5.32	3.01	5.11	*	*
35	Y79AA1000065	116.14	101.03	106.53	93.49	124.96	111.44	68.74	63.93	65.56	**	**
	Y79AA1000081	7.88	11.03	9.72	7.03	9.28	7.22	5.68	4.38	3.88	**	**
	Y79AA1000127	8	5.82	6.2	3.17	4.25	2.35	5.28	6.34	4.47	*	*
	Y79AA1000130	20.16	11.01	14.68	13.04	8.43	8.05	14.41	16.35	14.16		
	Y79AA1000131	17.14	8.99	11.18	6.93	10.63	6.92	6.82	8.55	6.52		
	Y79AA1000134	6.34	7.52	5.68	7.86	5.61	3.09	4.16	2.2	3.07	*	*
40	Y79AA1000143	8.89	7.38	8.14	3.93	5.83	3.75	3.23	2.53	3.96	*	**
	Y79AA1000144	11.79	8.62	9.18	5.64	6.37	5.56	3.97	3.84	3.36	*	**
	Y79AA1000150	28.57	28.05	20.04	12.4	17.77	10.86	24.46	16.09	20.29	*	*
	Y79AA1000153	11.32	11.62	7.41	5.89	9.36	6.53	6.84	5.59	6.52		
	Y79AA1000166	13.75	6.3	9.45	4.16	5.68	2.88	7.42	8.85	8.76		
	Y79AA1000179	13.15	8.67	7.74	7.91	7.5	4.67	13.52	5.81	9.18		
45	Y79AA1000181	14.37	9.22	8.77	6.64	8.41	3.93	3.41	3.97	4.65	*	*
	Y79AA1000202	22.9	17.78	19.17	14.55	12.31	8.36	18.27	13.59	20.94	*	*
	Y79AA1000207	52.28	63.3	44.9	24.04	38.89	23.79	15.85	13.31	14.27	*	**
	Y79AA1000214	9.44	4.9	5.66	4.71	4.79	4.18	5.54	2.28	3.2		
	Y79AA1000222	11.34	8.61	7.95	5.13	7.04	2.26	4.7	3.53	4.67	*	*
	Y79AA1000226	27.21	25.59	19.24	12.19	15.74	11.35	24.75	16.69	21.48	*	*
50	Y79AA1000227	9.07	6.57	6.62	3.66	4.45	3.9	7.4	6.45	7.51	*	*
	Y79AA1000230	32.97	25.47	29.26	12.55	10.05	6.68	4.18	3.82	4.93	**	**
	Y79AA1000231	65.27	41.2	48.87	47.4	47.89	24.64	28.97	32.14	28.29	*	*
	Y79AA1000239	74.35	85.68	67.35	68.07	52.75	45.41	64.49	54.97	44.91		
	Y79AA1000258	8.42	5.48	5.2	4.36	4.01	3.09	3.34	2.93	4.62		
	Y79AA1000268	80.53	75.19	49.36	22.18	30.03	27.42	30.39	28.87	31.5	*	*
55	Y79AA1000269	73.43	71.24	52.77	41.13	70.01	36.67	77.91	62.7	65.45		
	Y79AA1000270	10.85	7.03	4.1	4.98	7.95	3.4	5.03	5.7	4.72		
	Y79AA1000280	25.49	25.11	28.96	8.6	12.9	9.27	5.74	8.76	6.26	**	**

Table 505

	Y79AA1000285	22.27	16.31	18.63	6.85	10.3	7.36	15.47	22.31	18.9	**	-
	Y79AA1000295	4.35	2.68	5.01	1.59	3.76	2.11	2.3	2.59	2.22		
5	Y79AA1000307	6.82	4.93	8.12	6.39	9.3	7.36	3	5.88	4.49		
	Y79AA1000313	4.28	2.34	3.94	1.66	3.1	3.25	1.93	2.47	1.62		
	Y79AA1000314	1.57	1.83	4.11	1.4	1.41	0.98	0.87	0.14	1.73		
	Y79AA1000328	3.78	3.39	5.43	2.09	10.7	2.68	3.27	3.33	3.32		
	Y79AA1000334	9.59	9.06	7.49	5.79	6.64	3.5	5.12	3.62	4.02	* **	- -
	Y79AA1000342	17.48	13.29	18.31	13.02	15.9	13.67	34.2	31.79	30.43	**	+
10	Y79AA1000346	17.08	11.48	18.69	8.72	9.82	6.74	5.35	5.97	4.15	* **	- -
	Y79AA1000347	28.82	26.71	31.26	22.14	31.96	28.74	20.9	20.82	19.69	**	-
	Y79AA1000349	15.95	20.35	20.7	17.44	19.4	18.58	5.37	7.08	5.15	**	-
	Y79AA1000355	11.9	11.6	17.89	14.98	13.32	9.11	5.25	6.54	7.95	*	-
	Y79AA1000368	5.31	4.56	7.88	4.89	6.47	3.77	2.77	3.21	1.95	*	-
	Y79AA1000388	9.85	11.63	11.71	9.62	9.75	4.51	5.03	4.57	5.04	**	-
15	Y79AA1000392	13.05	13.68	11.25	7.92	12.06	6.34	12.1	13.67	13.52		
	Y79AA1000405	100.68	62.31	79.28	103.67	109.59	81.35	71.19	52.24	66.44		
	Y79AA1000410	8.13	6.1	10.22	6.13	5.36	5.28	4.83	4.8	5.17		
	Y79AA1000420	11.1	11.77	13.46	5.41	8.52	5.43	6.77	7.21	5.64	* **	- -
	Y79AA1000423	7.61	9.21	8.96	4.46	6.29	5.4	4.36	2.75	3.4	* **	- -
20	Y79AA1000426	5.75	6.96	10.06	4.68	5.08	3.97	3.38	2.69	2.24	*	-
	Y79AA1000432	5.62	5.18	10.2	4.71	5.75	4.03	2.85	3.99	8.12		
	Y79AA1000453	32.42	33.52	37.01	20.21	25.21	18.7	36.98	32.84	33.05	**	-
	Y79AA1000465	4.43	1.91	3.14	1.7	4.29	1.76	2.57	2.29	2.11		
	Y79AA1000469	35.31	28.37	27.42	30.17	34.28	32.32	21.89	31.66	24.15		
	Y79AA1000480	11.78	8.51	13.38	5.22	5.02	5.9	5.84	10.93	8.28	*	-
25	Y79AA1000502	19.24	16.15	21.16	8.66	14	12.35	16.39	18.08	18.17	*	-
	Y79AA1000521	75.16	71.09	84.73	74.85	78.28	67.85	48.04	51.73	45.89	**	-
	Y79AA1000534	13.31	15.15	20.4	13.25	14.05	10.71	13.15	11.71	11.75		
	Y79AA1000538	12.36	14.67	20.45	9.58	11.27	5.96	3.97	0	4.64	**	-
	Y79AA1000539	15.51	16.32	14.99	9.48	12.74	10.1	5.39	5.2	6.13	* **	- -
	Y79AA1000540	10.2	7.44	12.08	3.41	6.65	4.35	12.15	10.44	10.32	*	-
30	Y79AA1000560	180.34	128.09	149.28	162.08	194.06	150.66	118.75	125.1	108.26		
	Y79AA1000574	12.15	9.72	10.83	5.66	8.8	4.53	10.59	16.21	10.56	*	-
	Y79AA1000584	40.26	35.5	37.1	23.89	28.68	25.51	26.96	34.59	37.41	**	-
	Y79AA1000589	9.65	4.15	9.45	2.79	3.53	2.1	3.54	8.38	4.6		
	Y79AA1000598	34.26	29.42	37.32	17.43	15.95	16.46	24.99	27.55	21.09	** *	- -
	Y79AA1000600	44.58	45.66	51.58	51.4	52.23	39.65	32.06	30.08	26.05	**	-
35	Y79AA1000609	7.91	6.61	8.76	1.95	5.66	3.3	3.74	4.36	7.05	*	-
	Y79AA1000618	20.27	20.13	21.51	6.61	13.31	6.56	19.86	14.92	16.1	**	-
	Y79AA1000627	18.35	16.53	18.66	9.09	10.58	9.21	14.78	8.21	19.69	**	-
	Y79AA1000636	5.21	2.52	7.03	3.36	4.46	4.2	2.54	3.13	1.94		
	Y79AA1000649	19.51	21.35	25.26	12.58	12.75	9.69	16.99	19.63	19.13	**	-
	Y79AA1000656	7.37	5.14	7.46	2.86	2.97	2.28	2.83	3.72	2.99	** *	- -
40	Y79AA1000673	8.38	7.17	11.58	4.74	3.99	5.74	1.87	4.27	2.18	* *	- -
	Y79AA1000674	131.64	157.11	127.73	143.89	140.32	116.2	111.11	118.96	120.08		
	Y79AA1000678	22.12	27.62	25.96	12.61	21.55	13.08	21.7	19.94	19.36	*	-
	Y79AA1000682	14.62	11.86	13.44	6.55	8.13	6.38	12.74	13.35	11.29	**	-
	Y79AA1000683	37.64	24.6	33.28	19.88	16.2	12.73	33.87	33.73	36.17	*	-
	Y79AA1000697	46.01	35.33	48.41	23.15	27.46	23.15	15.24	20.88	15.95	* **	- -
45	Y79AA1000700	3.64	3.69	5.68	3.34	3.06	2.62	3.53	2.27	2.51		
	Y79AA1000702	50.6	33.01	36	23.71	24.96	18.05	18.21	11.97	15.36	* *	- -
	Y79AA1000704	93.86	71.31	88.5	110.92	93.16	106.68	74.22	61.46	46.95		
	Y79AA1000705	6.23	6.74	7.37	1.82	2.22	2.09	2.28	0.26	2.39	** **	- -
	Y79AA1000717	8.36	6.77	8.13	4.96	8.96	4.55	2.44	3.74	2.84	**	-
	Y79AA1000722	10.83	11.52	10.81	4.97	5.79	3.98	6.28	5.41	5.45	** **	- -
50	Y79AA1000724	42.59	35.15	44.52	31.42	30.43	23.04	24.2	29.89	31.56	* *	- -
	Y79AA1000726	8.78	4.43	7.31	5.15	4.77	4.25	2.41	3.94	2.09	*	-
	Y79AA1000734	5.72	4.05	6.45	2.81	2.76	3.46	2.68	2.98	0.98	* *	- -
	Y79AA1000748	7.45	7.72	6.69	2.89	2.82	2.75	2.52	2.6	2.35	** **	- -
	Y79AA1000750	41.52	33.1	33.65	18.03	22.65	18.6	26.15	29.63	22.6	** *	- -
	Y79AA1000752	9.11	9.26	10.14	4.75	3.47	2.23	2.34	2.01	1.29	** **	- -
55	Y79AA1000774	19.25	19.31	26.89	10.74	13.71	10.53	12.54	14.59	12.73	* *	- -
	Y79AA1000776	12.05	9.97	9.69	5.12	6.81	2.36	10.58	10.24	7.92	*	-
	Y79AA1000777	17.61	11.59	13.15	7.32	8.15	7.21	6.02	5.12	6.68	* *	- -

Table 506

	Y79AA1000778	20.06	13.62	11.66	10.8	9.69	8.29	13.52	13.51	12.96			
	Y79AA1000782	11.43	7.55	9.19	7.76	8.46	7.38	6.62	5.21	4.82	*		
5	Y79AA1000784	13.14	10.21	12.84	4.67	6.08	6.71	10.7	9.6	9.71	**		
	Y79AA1000794	46.19	39.88	38.82	22.35	24.71	16.75	37.28	33.24	34.17	**		
	Y79AA1000800	7.18	3.91	5.09	0.48	0.36	0.17	2.34	0	0	**	*	
	Y79AA1000802	11.45	13.12	10.85	5.78	8.8	4.96	3.89	4.75	3.77	*	**	
	Y79AA1000805	21.22	18.33	12.77	6.7	11.14	4.1	15.87	12.52	16.72	*		
	Y79AA1000814	27.49	21.74	19.65	16.59	17.35	12.96	22	17.22	22.17	*		
10	Y79AA1000823	14.24	7.73	9.85	4.94	4.36	5.06	6.73	6.96	8.36	*		
	Y79AA1000824	16.24	10	9.76	8.11	9.28	6.16	6.82	5.83	8.72	*		
	Y79AA1000827	9.71	3.82	4.6	3.63	3.22	2.56	3.51	2.06	2.83	*		
	Y79AA1000831	7.38	5.79	7.27	4.13	3.32	2.68	4.43	0.57	1.26	**	*	
	Y79AA1000833	22.35	19.25	16.88	12.38	7.9	8.89	19.38	11.86	18.04	**		
	Y79AA1000850	33.44	40.57	26.99	19.52	21.81	14.62	28.93	23.5	32.01	*		
15	Y79AA1000856	6.26	7.4	4.9	2.81	6.29	2.12	4.31	2.48	3.63	*		
	Y79AA1000862	8.84	4.04	5.05	7.04	4.31	3.07	5.61	5.34	5.05	*		
	Y79AA1000876	21.17	10.25	11.73	7.67	6.82	6.01	5.79	7.01	6	*		
	Y79AA1000888	32.02	25.94	21.68	17.64	17.29	12.59	18.41	20.33	23.17	*		
	Y79AA1000902	6.26	5.68	6.17	4.27	4.4	2.72	2.73	2.97	2.19	*	**	
	Y79AA1000935	76.11	52.08	52.32	70.65	71.58	69.22	39.77	35.2	32.3	*	*	
20	Y79AA1000959	48.22	40.7	37.08	25.45	33.48	19.11	26.33	21.44	21.93	*	**	
	Y79AA1000962	46.82	45.31	38.99	22.79	24.29	17.48	60.82	38.12	53.14	**		
	Y79AA1000963	25.33	35.17	19.37	13.71	17.32	12.79	14.75	14.39	13.92	*		
	Y79AA1000966	41.31	37.86	31.25	27.6	23.69	23.7	32	18.68	25.22	*		
	Y79AA1000967	19.13	9.69	10.03	8.88	7.99	4.65	1.27	8.2	0.25	*		
	Y79AA1000968	25.81	16.48	14.41	11.57	12.79	6.94	25.2	19.6	28.68	*		
25	Y79AA1000969	40.02	39.97	33.37	23.55	39.74	36.04	32.93	30.52	18.66	*		
	Y79AA1000976	22.75	15.17	16.99	14.98	19.84	15.88	14.85	10.98	11.26	*		
	Y79AA1000978	8.83	7.09	6.8	4.57	5.39	2.66	4.35	3.43	4.33	*	**	
	Y79AA1000985	8.02	3.9	5.83	4.32	4.39	1.76	4.37	2.17	1.99	*		
	Y79AA1000989	295.68	243.92	218.77	78.52	138.6	77.87	70.03	46.49	61.43	**	**	
	Y79AA1000991	12.26	8.35	10.64	5.63	5.93	8.76	7.23	8.65	6.01	*	*	
30	Y79AA1001013	42.37	37.07	51.31	24.72	27.17	18.23	24.27	34.59	22.31	*	*	
	Y79AA1001014	16.53	17.99	19.41	12.93	20.24	14.74	13.35	18.92	15.51	*	*	
	Y79AA1001019	8.07	6.21	8.29	4.14	6.05	5.04	2.84	5.3	3.51	*	*	
	Y79AA1001020	13.89	16.72	13.86	21.03	12.53	10.76	9.5	10.16	11.46	*	*	
	Y79AA1001023	7.28	6.24	9.28	4.31	8.03	5.29	3.01	3.87	2.51	*	*	
	Y79AA1001030	28.41	43.95	33.86	36.62	21.08	22.74	16.86	22.85	18.21	*	*	
35	Y79AA1001035	10.6	13.73	10.93	9.68	10.73	7.69	7.26	7.72	8.91	*	*	
	Y79AA1001041	14.5	11.14	15.3	8.73	9.98	7.28	9.17	13.51	15.31	*	*	
	Y79AA1001043	22.79	19.12	22.36	8.78	13.48	10.29	9.42	13.86	17.78	**	*	
	Y79AA1001048	12.86	13.5	12.88	6.65	11.19	7.59	6.44	7.55	6.3	*	**	
	Y79AA1001056	6.67	9.77	12.37	5.42	9.5	6.82	2.1	3.99	2.72	*	*	
	Y79AA1001061	11.12	17.1	15.18	5.75	10.72	7.78	8.04	10.36	12.77	*	*	
40	Y79AA1001062	4.7	4.96	6.24	2.95	3.71	2.56	2.92	2.19	2.28	*	**	
	Y79AA1001068	6.22	3.59	5.75	4.34	5.98	4.49	3.29	3.38	3.07	*	*	
	Y79AA1001073	17.6	17.56	20.08	5.98	13.24	7.19	16.17	13.71	20.42	*	*	
	Y79AA1001077	7.3	2.86	6.26	7.08	4.43	3.45	1.86	5.22	1.86	*	*	
	Y79AA1001078	7.29	5.05	6.25	3.73	4.63	2.99	3.3	5.06	3.66	*	*	
45	Y79AA1001081	7.84	5.5	8.85	3.05	3.81	3.52	2.8	3.1	3.74	*	*	
	Y79AA1001088	36.17	40.23	42.34	24.5	22.27	19	24.36	30.94	32.13	**	*	
	Y79AA1001089	332.88	366.62	308.34	284.36	390.54	406.65	237.36	376.46	392	*	*	
	Y79AA1001090	7.05	4.26	8.66	4.12	3.36	2.71	3.39	1.8	2.5	*	*	
	Y79AA1001105	22.53	22.64	23.57	8.51	14.07	9.94	17.11	15.32	15.62	**	**	
	Y79AA1001142	114.5	98.72	131.88	102.55	114.58	143.24	69.56	60.81	74.51	*	*	
50	Y79AA1001145	98.33	98.57	100.63	125.36	121.38	91.71	78	59.2	74.76	**	*	
	Y79AA1001162	126.48	83.55	107.65	92.38	93.62	73.32	97.56	124.59	105.84	*	*	
	Y79AA1001167	12.61	7.85	13.06	7.92	8.62	6.56	7.15	16.96	9.58	*	*	
	Y79AA1001176	75.12	80.1	84.48	76.52	65.54	64.34	46.71	59.03	47.45	**	*	
	Y79AA1001177	8.46	7.48	10.23	4.06	5.51	3.51	3.45	4.68	2.96	*	**	
	Y79AA1001179	54.1	53.61	67.63	28.64	33.09	26.42	13.82	47.33	10.91	**	*	
55	Y79AA1001185	32.79	30.94	36.04	15.68	21.34	16.32	19.9	17.65	25.06	**	**	
	Y79AA1001201	45.08	50.33	41.06	13.71	31.35	17.81	48.16	43.78	38.95	*	*	
	Y79AA1001205	18.73	12.88	21.83	8.38	8.46	6.14	7.31	11.86	11.81	*	*	

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	Y79AA1001211	21.15	21.66	22.83	13.08	12.91	10.43	0.44	20.18	19.17	**	-	-
	Y79AA1001212	128.68	116.33	107.84	151.9	151.84	105.91	80.87	83.57	67.14	**	*	-
5	Y79AA1001215	31.68	27.07	33.84	18.3	19.09	14.63	17.05	18.24	23.12	**	*	-
	Y79AA1001228	7.97	5.25	12.95	3.35	3.4	3.64	3.41	10.17	4.89			
	Y79AA1001233	8.26	6.53	16.79	3.45	3.77	2.51	2.28	3.79	3.13			
	Y79AA1001236	8.84	5.25	11.14	5.02	5.53	3.13	4.08	4.7	2.24			
	Y79AA1001239	74.22	59.48	53.54	45.62	83.11	43.05	50.35	42.44	46.18			
	Y79AA1001240	70.83	49.07	64.4	30.83	35.04	20.32	48.49	59.48	54.67	*	-	-
10	Y79AA1001255	8.89	10.29	10.55	7.47	6.78	6.42	0.72	6.35	0.76	**	*	-
	Y79AA1001264	14.2	10.19	13.36	9.71	10.05	8.67	4.58	4.84	6.39	**	**	-
	Y79AA1001272	15.16	12.6	13.5	3.77	6.76	5.59	8.86	7.59	6.53	**	**	-
	Y79AA1001281	8.87	7.72	6.68	4.17	4.8	3.47	2.65	2.22	2.28	**	**	-
	Y79AA1001299	9.39	10.08	9.6	4.21	5.3	4.49	3.28	3.68	3.29	**	**	-
	Y79AA1001312	40.47	42.72	35.81	17.92	27.92	14.77	29.7	20.85	25.67	*	*	-
15	Y79AA1001319	31.92	23	20.23	23.19	28.4	16.96	30.43	20.02	18			
	Y79AA1001323	32.99	27.82	34.32	14.07	19.03	14.31	25.9	23.32	27.9	**	*	-
	Y79AA1001328	28.33	16.1	28.16	14.56	12.93	12.69	4.94	7.51	4.42	*	*	-
	Y79AA1001343	12.56	8.01	10.99	6.43	7.59	7.49	6.83	9.08	8.27			
	Y79AA1001351	6.64	4.21	8.23	2.99	1.8	1.8	2.08	2.52	1.68	*	*	-
20	Y79AA1001364	8.06	5.02	6.85	3.26	2.98	2.12	4.06	2.93	1.74	*	*	-
	Y79AA1001367	145.27	118.42	143.46	117.7	132.8	94.77	76.65	57.61	66.99	**	**	-
	Y79AA1001384	45.86	52.17	41.89	27.43	34.83	21.42	31.33	29.86	26.76	*	**	-
	Y79AA1001391	10.96	12.22	10.34	2.99	9.55	4.77	7.43	7.31	6.01	**	*	-
	Y79AA1001394	24.73	14.05	14.28	9.7	6.32	9.07	6.42	10.16	9.01			
	Y79AA1001402	12.42	7.77	9.12	5.62	4.8	4.67	4.74	3.87	4.52	*	*	-
25	Y79AA1001410	5.24	2.77	3.09	3.28	1.53	1.95	2.62	0.78	1.99			
	Y79AA1001414	27.49	18.53	20.44	10.78	9.47	10.2	16.16	13.43	11.92	*	*	-
	Y79AA1001426	271.77	221.23	225.78	200.19	221.07	217.77	202.63	211.55	197.64			
	Y79AA1001427	15.18	10.97	10.9	6.77	10.81	5.39	6.71	6.07	6.74	*	*	-
	Y79AA1001430	22.25	17.58	19.52	10.25	13.63	7.85	11.32	11.76	10.84	*	**	-
	Y79AA1001439	6.75	4.58	4.31	2.6	4.23	1.25	2.94	2.35	2.98	*	*	-
30	Y79AA1001485	17.57	9.99	14.92	13.26	10.56	8.25	5.32	10.37	14.36			
	Y79AA1001493	20.47	12.23	13.25	9.02	11.27	6.64	13.37	13.83	16.06			
	Y79AA1001511	14.52	8.05	9.32	8.33	6.58	5.82	5.2	6	5.96			
	Y79AA1001523	10.03	6.72	7.33	6.48	4.81	3.84	4.54	3.21	2.59	*	*	-
	Y79AA1001530	11.44	7.57	8.59	6.64	8.84	5.29	6.2	7.76	5.77			
	Y79AA1001532	13.55	14.73	11.04	5.35	5.16	4.93	5.08	4.52	6.49	**	**	-
35	Y79AA1001533	56.5	68.51	50.9	29.97	36.82	26.92	69.28	61.19	56.58	*	*	-
	Y79AA1001541	8.12	8.52	5.25	4.02	4.89	2.24	4.69	2.24	2.18	*	*	-
	Y79AA1001548	67.38	47.55	44.48	30.61	26.42	21.92	46.07	51.22	51.86	*	*	-
	Y79AA1001555	14.35	9.75	8.13	8.86	4.86	4.97	8.19	7.68	10.98			
	Y79AA1001562	18.44	13.73	12.82	8.99	10.6	7.19	10.2	9.39	15.75	*	*	-
	Y79AA1001581	24.34	18.91	17.62	9.8	12.04	10.4	15.9	9.96	16.33	*	*	-
40	Y79AA1001585	30.32	20.83	22.83	20.22	25.12	15.45	0.69	15.13	0.14	*	*	-
	Y79AA1001592	28.53	25.65	26.36	29.33	16.66	7.28	20.69	8.44	14.72	*	*	-
	Y79AA1001594	23.28	21.85	24.28	14.25	15.59	10.11	22.55	14.53	20.27	**	*	-
	Y79AA1001603	12.47	11.04	10.84	6.8	11.48	6.78	22.63	14.33	27.5			
	Y79AA1001613	25.09	18.27	18.81	23.47	16.84	13.34	20.3	16.35	18.99			
	Y79AA1001630	22.94	13.91	12.22	13.14	13.53	8.02	11.73	12.98	17.67			
45	Y79AA1001647	33.54	24.86	22.66	23.22	25.84	16.49	26.93	21.3	26.55			
	Y79AA1001664	12.2	10.56	13.13	7.78	6.05	5.54	10.34	8.1	11.69	**	*	-
	Y79AA1001665	11.52	9	9.75	6.87	7.31	6.13	5.92	6.12	7.69	*	*	-
	Y79AA1001679	24.51	18.98	17.88	11.13	12.84	9.27	24.02	13.28	18.8	*	*	-
	Y79AA1001692	7.23	6.72	8.1	2.24	2.83	2.63	3.64	2.31	3.06	**	**	-
	Y79AA1001696	14.23	12.31	9.21	5.29	8.48	4.61	14.27	13.28	13.01	*	*	-
50	Y79AA1001705	12.04	11.4	8.55	9.76	11.8	6.21	4.61	5.98	4.57	**	*	-
	Y79AA1001711	13.72	7.72	10.63	6.49	4.11	3.08	6.08	4.06	7.4	*	*	-
	Y79AA1001717	4.71	1.55	3.26	3.34	1.71	0.7	1.49	1.63	1.39			
	Y79AA1001719	22.12	12.72	16.33	9.89	12.72	6.53	12.21	11.1	11.76			
	Y79AA1001727	38.96	27.16	22.35	13.65	17.35	9.31	38.01	28.39	34.23	*	*	-
	Y79AA1001750	21.5	17.52	18.42	10.15	15.4	8.01	11.94	9.9	11.41	*	**	-
55	Y79AA1001760	127.24	115.03	77.78	58.26	73.6	43.62	140.25	100.84	138.73	*	*	-
	Y79AA1001777	6.77	6.32	6.37	2.57	5.24	2.46	5.26	4.15	4.71	*	**	-
	Y79AA1001781	2.86	2.24	2.15	1.61	1.86	2.55	0.74	1.53	1.3	*	*	-



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	Y79AA1001787	5.04	3.62	6.16	2.83	4.49	3.23	3.33	2.97	2.01			
	Y79AA1001793	120.15	97.84	90.95	70.69	108.02	70.38	56.01	50.79	40.18	**	-	-
	Y79AA1001795	5.66	5.4	6.21	4.2	5.9	3.1	3.91	2.49	2.28	**	-	-
5	Y79AA1001799	15.09	14.95	16.22	8.14	9.02	8.13	5.96	8.67	5.96	**	**	-
	Y79AA1001800	25.64	16.41	26.8	14.68	31.06	13.67	17.04	13.04	14.7			-
	Y79AA1001801	18.54	13.81	14.73	8.69	14.72	7.61	10.02	6.35	8.81	*	-	-
	Y79AA1001803	4.48	5.85	6.44	4.5	2.73	1.98	4.84	2.96	2.69			-
	Y79AA1001805	40.28	26.89	34.51	17.56	11.83	10.76	12.11	14.87	11.59	**	**	-
10	Y79AA1001807	42.38	40.49	41.45	39.87	44.56	37.42	30.19	22.76	22.12	**	-	-
	Y79AA1001827	9.32	11.28	9.81	8.01	8.55	6.68	5.41	8.86	5.83	*	*	-
	Y79AA1001846	22.14	19.33	18.59	11.82	17.37	13.61	12.56	15.77	9.7	*	*	-
	Y79AA1001848	8.04	9.99	9.11	5.33	6.98	5.01	6.65	6.63	5.92	*	*	-
	Y79AA1001853	10.87	10.1	9.06	5.77	8.29	4.56	4.63	5.75	4.91	*	**	-
	Y79AA1001863	24.97	27.27	22.17	17.04	22	11.97	13.95	21.02	18.07	*	-	-
15	Y79AA1001866	13.46	10.72	11.93	6.28	4.52	4.93	6.56	4.65	4.51	**	**	-
	Y79AA1001874	2.1	1.41	2.93	0.78	1.08	0.95	1.46	1.22	1.08			-
	Y79AA1001875	31.78	22.74	37.59	12.11	19.59	16.03	9.16	15	14.61	*	*	-
	Y79AA1001907	517.52	778.32	567.93	750.86	875.67	821.68	479.34	605.65	529.63			-
	Y79AA1001908	5.27	6.69	9.96	3.58	5.35	3.25	2.93	3.09	1.48	*	-	-
20	Y79AA1001923	8.48	16.75	14.8	9.28	7.65	6.34	6.48	6.75	5.36	*	-	-
	Y79AA1001927	18.05	21.6	19.1	12.29	16.25	12.12	14.45	14.01	14.79	*	**	-
	Y79AA1001930	12.23	24.48	15.86	10.91	18.16	6.72	4.54	5.11	5.37	*	-	-
	Y79AA1001932	61.74	56.58	52.19	37.44	49.06	33.54	58.52	51.29	51.59	*	-	-
	Y79AA1001933	9.52	6.51	10.88	6.04	6.05	6.44	4.27	11.51	4.91			-
	Y79AA1001942	10.76	6.66	7.93	7.97	5.94	4.4	3.29	2.7	3.99	*	-	-
25	Y79AA1001963	138.12	106.9	117.87	95.52	130.54	91.9	83.12	67.08	69.04	*	-	-
	Y79AA1001968	147.27	91.21	62.32	82.32	49.63	76.26	20.14	2.41	10.4	*	-	-
	Y79AA1001983	12.1	16.25	14.99	5.06	8.59	7.83	3.08	3.73	3.02	*	**	-
	Y79AA1002000	8.87	9.86	16.46	6.28	9.55	3.45	4.66	4.84	4.51	*	-	-
	Y79AA1002004	46.17	58.66	37.42	34.61	47	15.44	17.13	16.13	8.67	**	-	-
	Y79AA1002008	16.52	21.1	20.83	11.85	16.14	12.02	7.95	15.74	18.89	*	-	-
30	Y79AA1002012	13.85	12.54	10.41	5.85	6.84	6.65	8.76	11.21	9.52	**	-	-
	Y79AA1002017	15.21	10.94	15.42	6.73	12.23	8.22	1.29	15.64	2.06			-
	Y79AA1002022	42.57	32.77	37.11	21.13	22.85	16.91	21.09	21.59	19.22	**	**	-
	Y79AA1002027	10.35	8.04	15.25	2.11	4.6	4.84	5.16	2.67	4.2	*	*	-
	Y79AA1002050	13.21	11.11	14.39	7.26	8.9	5.9	6.9	7.16	7.33	*	**	-
	Y79AA1002058	167.29	130.21	156.91	193.04	186.39	149.35	127.37	93.56	137.15			-
35	Y79AA1002060	54.35	76.53	61.68	36.08	41.21	29.16	24.43	9.99	5.28	*	**	-
	Y79AA1002062	49.46	32.53	50.05	16.65	20.72	17.6	35.11	28.1	35.48	*	-	-
	Y79AA1002065	113.45	69.34	64.62	65.01	102.96	72.96	82.29	90.04	44.91			-
	Y79AA1002067	33.46	37.19	43.9	21.85	20.1	22.68	15.4	10.55	10.37	**	**	-
	Y79AA1002069	5.33	3.94	7.12	3.04	1.49	2.47	3.1	3.24	2.29	*	-	-
	Y79AA1002070	67.39	142.78	83.33	77.38	149.87	86.41	153.3	88.92	78.17			-
40	Y79AA1002074	1225	1102	498.16	721.59	1162.7	771.32	764.45	491.49	312.45			-
	Y79AA1002076	8.24	11.39	15.58	4.01	6.13	3.99	13	9.01	11.16	*	-	-
	Y79AA1002083	11.94	6.94	9.48	4.49	4.53	3.15	4.48	1.37	1.78	*	*	-
	Y79AA1002084	20.05	13.84	17.88	7.41	8.36	6.24	10.42	8.8	8.13	**	*	-
	Y79AA1002086	15.57	8.01	9.58	4.16	3.65	3.41	3.6	4.3	3.59	*	*	-
	Y79AA1002087	265.36	258.38	345.6	296.44	355.85	246.9	347.62	322.78	317.34			-
45	Y79AA1002089	15.8	12.04	15.08	6.67	9.17	6.14	12.29	9.32	9.91	**	-	-
	Y79AA1002093	13.66	12.64	9.33	5.35	6.21	4.47	3.01	2.8	2.57	**	**	-
	Y79AA1002101	6.58	7.04	8.08	3.07	2.77	1.96	3.3	4.71	1.2	**	*	-
	Y79AA1002103	11.98	11.79	10.9	4.11	5.96	4.92	4.54	2.99	2.4	**	**	-
	Y79AA1002115	15.51	18.46	14.58	9.3	11.82	8.45	4.13	9.04	5.86	*	**	-
	Y79AA1002121	6.93	5.28	6.92	6.7	3.27	4.36	3.68	3.01	3.29	**	-	-
50	Y79AA1002125	40.85	21.04	26.11	14.22	18.4	17.66	12.21	8.56	11.75	*	-	-
	Y79AA1002129	7.76	7.25	11.87	4.36	3.94	3.2	3.76	3.8	4.37	*	*	-
	Y79AA1002131	5.89	3.57	4.65	1.58	2.79	2.27	3.32	1.61	2.75	*	-	-
	Y79AA1002139	8.48	7.22	6.23	4.06	4.42	2.47	3.44	3.86	2.67	*	**	-
	Y79AA1002144	53.23	47.33	47.13	32.96	42.65	28.86	30.69	36.28	25.23	*	**	-
	Y79AA1002177	14.09	13.17	13.65	5.87	6.08	5.05	5.82	4.1	4.34	**	**	-
55	Y79AA1002183	76.21	99.47	69.64	24.87	40.12	25.67	26.7	15.32	11.38	**	**	-
	Y79AA1002202	29.69	18.4	18.04	8.22	10.65	9.82	13.41	13.22	16.71	*	-	-
	Y79AA1002204	4.17	2.23	3.23	5.04	1.05	2.68	3.28	2.4	2.69			-

Table 509

	Y79AA1002206	7.86	6.79	4.86	2.41	3.6	5.74	5.49	1.51	2.8				
	Y79AA1002208	21.91	17.64	15.14	5.6	4.07	5.57	6.81	5.17	2.55	**	**	-	-
5	Y79AA1002209	14.82	11.28	11.86	6.23	4.7	2.82	4.71	1.33	3.18	**	**	-	-
	Y79AA1002210	13.64	7.39	7.59	9.08	4.62	5.18	20.5	2.05	6.37				
	Y79AA1002211	11.76	19.59	13.47	10.43	6.65	6.52	12.32	8.42	11.25				
	Y79AA1002213	40.78	31.99	22.96	18.41	26.57	14.98	45.88	32.4	41.97				
	Y79AA1002215	54.92	41.69	39.55	24.88	24.36	11.25	37.49	23.6	35.98	*	*	-	-
10	Y79AA1002220	17.03	11.5	20.58	7.13	5.68	5.31	4.57	4.8	6.51	*	*	-	-
	Y79AA1002226	48.55	31.27	31.34	7.35	12.72	13.65	9.19	6.65	11.13	*	**	-	-
	Y79AA1002229	7.88	6.84	5.37	6.02	4.67	2.85	3.67	2.52	3.73	*	*	-	-
	Y79AA1002234	20.83	13.27	12.39	9.34	6.36	3.6	6.9	3.36	5.84	*	*	-	-
	Y79AA1002235	28.03	23.84	21.24	15.07	14.87	9.39	10.75	8.42	13.64	*	**	-	-
15	Y79AA1002246	9.72	14.9	10.35	5.25	6.99	4.12	8.31	3.82	6.69	*	*	-	-
	Y79AA1002258	12.35	12.02	7.88	7.82	11.57	8.55	9.77	4.5	4.81				
	Y79AA1002279	51.52	49.19	41.11	5.28	2.78	2.07	15.99	20.03	22.13	**	**	-	-
	Y79AA1002292	13.64	7.58	4.14	5.73	4.43	2.94	6.45	6.01	8.36				
	Y79AA1002298	9.43	8.29	4.77	3.29	5.48	4.2	4.42	4.85	3.79				
20	Y79AA1002307	9.31	8.07	6.62	3.9	4.4	2.44	5.17	1.76	2.58	*	*	-	-
	Y79AA1002309	8.88	7.96	8.79	3.32	4.26	2.83	4.23	2.88	3.97	**	**	-	-
	Y79AA1002311	16.51	9.27	11.76	6.9	6.2	3.45	7.45	3.09	6.4	*	*	-	-
	Y79AA1002334	13.05	8.36	7.7	5.13	4.89	3.36	5.91	4.32	5.92	*	*	-	-
	Y79AA1002351	13.61	12.49	9.42	7.1	4.15	6.19	7.95	4.93	5.8	*	*	-	-
	Y79AA1002355	31.74	30.6	21.85	12.21	15.81	9.74	20.54	18.29	18.48	*	*	-	-
25	Y79AA1002361	23.42	15.4	18.02	12.53	10.73	6.85	25.86	17.1	25.5	*	*	-	-
	Y79AA1002365	12.42	6.37	7.19	3.15	4.11	3.03	4.29	4.74	4.01				
	Y79AA1002373	8.95	6.89	5.46	5.13	4.81	3.4	9.6	4.57	7.84				
	Y79AA1002376	1550.5	2569.2	1680.8	462.62	827.86	616.71	1477.6	1040.3	1062.1	*	*	-	-
	Y79AA1002378	20.24	17.32	13.54	5.14	9.41	4.23	19.28	11.07	16.88	*	*	-	-
30	Y79AA1002381	116.11	128.86	74.48	110.66	141.78	92.68	155.95	123.08	170.94				
	Y79AA1002388	33.4	33.3	27.31	13.85	26.75	11.62	21.29	16.32	21.24	*	*	-	-
	Y79AA1002399	11.13	8.22	7.72	4.28	5.54	4.87	7.56	5.9	6.25	*	*	-	-
	Y79AA1002407	12.66	14.43	18.13	7.72	14.18	6.84	5.83	9.78	4.59	*	*	-	-
	Y79AA1002413	16.98	12.77	14.95	6.14	9.13	4.62	8.44	10.73	7.99	*	*	-	-
	Y79AA1002416	7.52	8.19	8.76	5.47	10.72	5.8	8.2	6.05	6.59				
35	Y79AA1002429	17.73	18.61	8.81	5.82	10.24	4.73	3.65	6.89	5.66	*	*	-	-
	Y79AA1002431	3.38	3.05	6.2	3.01	5.89	1.6	2.81	2.79	1.69				
	Y79AA1002433	9.94	11.67	9.29	5.11	5.57	3.18	3.49	4.6	3.87	**	**	-	-
	Y79AA1002445	33.47	25.62	23.49	15.99	10.67	7.02	18.92	25.26	13.87	*	*	-	-
	Y79AA1002461	7.94	6.22	7.84	3.36	7.35	4.7	3.49	2.25	3.85		**	-	-
40	Y79AA1002466	778.44	339.4	681.02	542.56	499.15	369	592.67	971	768.71				
	Y79AA1002471	11.38	8.13	15.35	12.81	13.4	11.43	4.94	6.06	4.47	*	*	-	-
	Y79AA1002472	31.22	33.06	31.17	18.15	21.85	9.34	16.29	20.14	20.03	*	**	-	-
	Y79AA1002474	10.68	12.29	10.71	6.77	7.3	7.75	3.17	7.37	4.86	**	*	-	-
	Y79AA1002482	30.09	33.68	36.63	19.02	23.45	17.38	21.9	25.81	23.08	**	*	-	-
	Y79AA1002487	8.33	8.29	7.43	7.28	8.45	6.44	5.34	3.78	3.86		**	-	-
45	Y79AA1002490	143.18	106.89	117.63	56.22	71.49	57.31	59.76	51.39	52.37	**	**	-	-
	Y79AA1002493	44.75	41.56	40.36	20.64	28.52	19.33	38.02	46.19	46.7	**	**	-	-
	ZRV6C1006278	5.26	7	5.52	3.16	2.97	2.19	2.99	2.6	2.72	**	**	-	-

## EXAMPLE 16

Selection of novel cDNA clones from cDNA libraries prepared by oligo-capping method

[0246] The following 54 clones were newly selected from cDNA libraries prepared by oligo-capping method, based on the criterion that the 5'-end sequence of a cDNA clone contained a coding region which was initiated with ATG codon and which encoded 50 amino acids or more:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBA1006812, HEMBB1000672, HEMBB1001197, HEMBB1001871, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657,

NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001282, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

Among them, the following 23 clones was predicted to contain a coding region encoding 100 amino acids or more: HEMBA1000497, HEMBA1003854, HEMBA1004193, HEMBA1006812, HEMBB1001871, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3001282, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218. This indicates that the clones encode proteins.

**[0247]** Table 510 shows maximal ATGprl value determined for each clone. Since the respective maximal ATGprl values for HEMBA1006812, HEMBB1001871 and NT2RRP3001282 are higher than 0.3, the clones would be full-length. Other clones indicated below have maximal ATGprl values of 0.3 or less, and this means that the fullness ratios of the clones are low.

However, the sequences can still be full-length: HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218

**[0248]** Table 511 (same as Table 2) shows SEQ ID NOs of the nucleotide sequences located at the 5'-end and 3'-end of each of the 54 clones and the corresponding plasmid clone, which was obtained herein, containing a polynucleotide as an insert. SEQ ID NO for a 5'-end sequence is indicated on the right side of the corresponding Sequence name of 5'-end sequence, and SEQ ID NO for a 3'-end sequence is indicated on the right side of the corresponding Sequence name of 3'-end sequence.

**[0249]** Swiss-Prot was searched for data homologous to the 5' -end sequences of the selected 54 clones, and GenBank and UniGene were searched for data homologous to the 5' -end and 3'-end sequences of the same clones. The search results are indicated as Homology search results 1-7 in the last part of this SPECIFICATION.

**[0250]** Based on the matching data obtained by the search, 7 clones presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoproteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, and protein synthesis- and/or protein transport-associated proteins. These were clones exhibiting relatively low homology to any of known proteins belonging to said categories. Here, the term "relatively low homology" means that a nucleotide sequence does not satisfy the conditions under which the nucleotide sequence exhibits "relatively high homology" (which means that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence identity is 60% or higher and the P value is  $10^{-10}$  or less) and that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence to be compared contains 55 nucleotides or more, the sequence identity is 25% or higher, and the P value is  $10^{-6}$  or less.

**[0251]** Among the 7 clones, clones presumably encoding proteins belonging to the category of secretory or membrane proteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); clones presumably encoding proteins belonging to the category of glycoproteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the category of signal transduction-associated proteins is PLACE1005549; clones presumably encoding proteins belonging to the category of transcription-associated proteins are the three clones, HEMBA1005572, NT2RP2001756, and NT2RP2005776; a clone presumably encoding a protein belonging to the category of disease-associated proteins is NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the category of protein synthesis- and/or protein transport-associated proteins is HEMBA1001750 (see Examples 12).

Table 510

The maximal ATGpr1 value of each clone selected in Example 16

clone name	name of sequence	maximal ATGpr1 score
HEMBA1000497	F-HEMBA1000497	0.25
HEMBA1001750	F-HEMBA1001750	0.08
HEMBA1003854	F-HEMBA1003854	0.23
HEMBA1004193	F-HEMBA1004193	0.22
HEMBA1004860	F-HEMBA1004860	0.29
HEMBA1005572	F-HEMBA1005572	0.24
HEMBA1006038	F-HEMBA1006038	0.29
HEMBA1006092	F-HEMBA1006092	0.28
HEMBA1006406	F-HEMBA1006406	0.26
HEMBA1006650	F-HEMBA1006650	0.22
HEMBA1006812	F-HEMBA1006812	0.71
HEMBB1000672	F-HEMBB1000672	0.24
HEMBB1001197	F-HEMBB1001197	0.22
HEMBB1001871	F-HEMBB1001871	0.94
MAMMA1001252	F-MAMMA1001252	0.29
MAMMA1002094	F-MAMMA1002094	0.28
NT2RM4000634	F-NT2RM4000634	0.07
NT2RM4000657	F-NT2RM4000657	0.24
NT2RM4000783	F-NT2RM4000783	0.22
NT2RM4000857	F-NT2RM4000857	0.12
NT2RM4001178	F-NT2RM4001178	0.27
NT2RM4002420	F-NT2RM4002420	0.06
NT2RP2000198	F-NT2RP2000198	0.15
NT2RP2000551	F-NT2RP2000551	0.07
NT2RP2000660	F-NT2RP2000660	0.22
NT2RP2001214	F-NT2RP2001214	0.26
NT2RP2001460	F-NT2RP2001460	0.07
NT2RP2001756	F-NT2RP2001756	0.17

	NT2RP2002056	F-NT2RP2002056	0.12
	NT2RP2002677	F-NT2RP2002677	0.14
5	NT2RP2002755	F-NT2RP2002755	0.12
	NT2RP2002843	F-NT2RP2002843	0.11
	NT2RP2003101	F-NT2RP2003101	0.13
	NT2RP2003799	F-NT2RP2003799	0.24
10	NT2RP2004095	F-NT2RP2004095	0.16
	NT2RP2004732	F-NT2RP2004732	0.18
	NT2RP2004920	F-NT2RP2004920	0.15
	NT2RP2005454	F-NT2RP2005454	0.09
15	NT2RP2005776	F-NT2RP2005776	0.19
	NT2RP2005806	F-NT2RP2005806	0.27
	NT2RP2005882	F-NT2RP2005882	0.11
20	NT2RP3001282	F-NT2RP3001282	0.39
	NT2RP3001723	F-NT2RP3001723	0.22
	NT2RP3002099	F-NT2RP3002099	0.20
	NT2RP3003155	F-NT2RP3003155	0.29
25	NT2RP3004028	F-NT2RP3004028	0.13
	OVARC1000008	F-OVARC1000008	0.23
	OVARC1000724	F-OVARC1000724	0.27
	OVARC1000751	F-OVARC1000751	0.28
30	OVARC1001029	F-OVARC1001029	0.25
	PLACE1000814	F-PLACE1000814	0.21
	PLACE1003030	F-PLACE1003030	0.26
	PLACE1005549	F-PLACE1005549	0.16
35	PLACE1007218	F-PLACE1007218	0.30

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Table 511

clone name	name of the 5'-end sequence	SEQ ID NO of the 5'-end sequence	name of the 3'-end sequence	SEQ ID NO of the 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175

	HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
	HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
	HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
5	MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
	MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
	NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
	NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
10	NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
	NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
	NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
	NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
15	NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
	NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
	NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
	NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
20	NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
	NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
	NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
	NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
25	NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
	NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
	NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
	NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
30	NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
	NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
	NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
	NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
35	NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
	NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
	NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
	NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
40	NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
	NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
	NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
	NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
45	OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
	OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
	OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
	OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
50	PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
	PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
	PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
55	PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

**EXAMPLE 17**

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

5 **[0252]** The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)]  
 10 (Mitsui Knowledge Industry Co., Ltd.) and Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a membrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). The functional domain search can be performed by using PROSITE instead of Pfam.

**[0253]** Search results obtained by using the respective software programs are indicated below.

**[0254]** Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

20 HEMBA1001052, HEMBA1001407, HEMBA1002486, HEMBA1002661, HEMBA1002818, HEMBA1002876,  
 HEMBA1003086, HEMBA1003711, HEMBA1004752, HEMBA1005991, HEMBA1006067, HEMBA1006173,  
 HEMBA1006198, HEMBA1006789, HEMBA1006921, HEMBB1000054, HEMBB1000175, HEMBB1002692,  
 MAMMA1000798, MAMMA1002427, MAMMA1002881, MAMMA1003035, NT2RM1000035, NT2RM1000742,  
 NT2RM1000811, NT2RM1000905, NT2RM1001008, NT2RM2000287, NT2RM2000609, NT2RM2001613,  
 25 NT2RM4000634, NT2RM4000778, NT2RM4002339, NT2RM4002460, NT2RP1000782, NT2RP1000856,  
 NT2RP1001247, NT2RP1001546, NT2RP1001569, NT2RP2001597, NT2RP2002537, NT2RP2004142,  
 NT2RP2005752, NT2RP2005812, NT2RP3001084, NT2RP3001589, NT2RP3002163, NT2RP3002650,  
 NT2RP3003145, NT2RP3003242, NT2RP3003621, NT2RP3004282, NT2RP3004503, NT2RP4000051,  
 NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000417, NT2RP4001064,  
 30 NT2RP4001117, NT2RP4001730, NT2RP4001739, NT2RP4002075, NT2RP5003500, OVARC1001154,  
 PLACE1000611, PLACE1003030, PLACE1003044, PLACE1003369, PLACE1003596, PLACE1004258,  
 PLACE1005086, PLACE1006239, PLACE1006754, PLACE1006829, PLACE1007954, PLACE1008424,  
 PLACE1008533, PLACE1008693, PLACE1010622, PLACE1010942, PLACE2000176, PLACE2000341,  
 PLACE2000379, PLACE2000427, PLACE2000477, PLACE4000431, PLACE4000593, THYRO1000156,  
 35 THYRO1001134, THYRO1001287, Y79AA1000258, Y79AA1001874, Y79AA1002399, HEMBB1001871,  
 HEMBB1001925, MAMMA1000778, MAMMA1000897, MAMMA1001080, NT2RP2004300, NT2RP3002985,  
 NT2RP3003059, OVARC1000689, OVARC1000890, PLACE1005162, PLACE3000399, PLACE3000455,  
 PLACE4000247, PLACE4000259, PLACE4000494

**[0255]** Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows:

40 HEMBA1000005, HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719,  
 HEMBA1000817, HEMBA1000822, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001085,  
 HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001510, HEMBA1001515,  
 HEMBA1001557, HEMBA1001746, HEMBA1002092, HEMBA1002125, HEMBA1002150, HEMBA1002166,  
 45 HEMBA1002462, HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661,  
 HEMBA1002780, HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003077, HEMBA1003079,  
 HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003711, HEMBA1003742,  
 HEMBA1003803, HEMBA1004143, HEMBA1004146, HEMBA1004341, HEMBA1004461, HEMBA1004577,  
 HEMBA1004637, HEMBA1004752, HEMBA1004756, HEMBA1004850, HEMBA1004889, HEMBA1004923,  
 50 HEMBA1004930, HEMBA1005029, HEMBA1005035, HEMBA1005050, HEMBA1005552, HEMBA1005588,  
 HEMBA1005616, HEMBA1005991, HEMBA1006036, HEMBA1006067, HEMBA1006293, HEMBA1006492,  
 HEMBA1006502, HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926,  
 HEMBA1007203, HEMBB1000050, HEMBB1000054, HEMBB1000556, HEMBB1000593, HEMBB1000631,  
 HEMBB1000763, HEMBB1000827, HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001177,  
 55 HEMBB1001302, HEMBB1001348, HEMBB1001962, HEMBB1002142, HEMBB1002190, HEMBB1002247,  
 HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692, MAMMA1000129, MAMMA1000133,  
 MAMMA1000277, MAMMA1000278, MAMMA1000410, MAMMA1000416, MAMMA1000472, MAMMA1000714,  
 MAMMA1000731, MAMMA1000734, MAMMA1000798, MAMMA1000842, MAMMA1000956, MAMMA1001008,



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	MAMMA1002769,	MAMMA1002890,	MAMMA1002938,	MAMMA1003146,	NT2RM1000035,	NT2RM1000037,
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5	NT2RM1000742,	NT2RM1000800,	NT2RM1000811,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
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25	NT2RP2003629,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004194,	NT2RP2004270,
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50	PLACE1000656,	PLACE1000712,	PLACE1000909,	PLACE1000948,	PLACE1001241,	PLACE1001257,
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 10 PLACE4000052, PLACE4000129, PLACE4000300, PLACE4000387, PLACE4000581, PLACE4000593,  
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 20 NT2RP3003828, NT2RP3003992, NT2RP3004051, NT2RP3004155, OVARC1000890, OVARC1001117,  
 OVARC1001329, PLACE1001761, PLACE1002437, PLACE1004793, PLACE1005611, PLACE1005898,  
 PLACE1009935, PLACE1011896, PLACE2000132, PLACE2000335, PLACE3000373, PLACE3000406,  
 PLACE4000250, PLACE4000487, PLACE4000494, THYRO1001320, THYRO1001537, THYRO1001828,  
 Y79AA1001384

25 **[0256]** Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam  
 search, and names of the matched functional domains are shown below.

When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash  
 mark, //.

30 HEMBA1000005//DnaJ, prokaryotic heat shock protein  
 HEMBA1000020//Tubulin  
 HEMBA1000129//Helicases conserved C-terminal domain  
 HEMBA1000156//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc finger, C2H2 type  
 35 HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING finger)  
 HEMBA1000411//Ank repeat  
 HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)  
 HEMBA1000531//Heat shock hsp70 proteins  
 HEMBA1000561//Zinc finger, C2H2 type  
 40 HEMBA1000608//Src homology domain 3  
 HEMBA1000919//WD domain, G-beta repeats  
 HEMBA1001043//Ank repeat  
 HEMBA1001088//LIM domain containing proteins  
 HEMBA1001137//Zinc finger, C2H2 type  
 45 HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)  
 HEMBA1001247//WW/rsp5/WWP domain containing proteins  
 HEMBA1001286//Sushi domain  
 HEMBA1001510//Basic region plus leucine zipper transcription factors  
 HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)  
 50 HEMBA1001661//Cadherin  
 HEMBA1001723//WD domain, G-beta repeats  
 HEMBA1001744//Eukaryotic protein kinase domain  
 HEMBA1001804//Zinc finger, C2H2 type  
 HEMBA1001819//Zinc finger, C2H2 type  
 55 HEMBA1001847//Zinc finger, C2H2 type  
 HEMBA1002035//Bromodomain  
 HEMBA1002102//Ank repeat  
 HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loop)

HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type  
 HEMBA1002212//Eukaryotic protein kinase domain  
 HEMBA1002215//LIM domain containing proteins  
 HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 5 HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)  
 HEMBA1002768//Src homology domain 3  
 HEMBA1002810//WW/rsp5/WWP domain containing proteins  
 HEMBA1002818//EGF-like domain  
 HEMBA1002935//Zinc finger, C2H2 type  
 10 HEMBA1002939//Ank repeat  
 HEMBA1002973//3'5'-cyclic nucleotide phosphodiesterases  
 HEMBA1003077//Fibronectin type III domain  
 HEMBA1003250//Eukaryotic protein kinase domain  
 HEMBA1003257//Zinc finger, C2H2 type  
 15 HEMBA1003281//IG superfamily  
 HEMBA1003291//Eukaryotic protein kinase domain  
 HEMBA1003433//Forkhead-associated (FHA) domain  
 HEMBA1003545//Homeobox domain //LIM domain containing proteins  
 HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 20 HEMBA1003684//Zinc finger, C2H2 type  
 HEMBA1003953//Zinc finger, C2H2 type  
 HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)  
 HEMBA1004227//Protein phosphatase 2C  
 HEMBA1004321//Zinc finger, C2H2 type  
 25 HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1004408//Peptidyl-prolyl cis-trans isomerases  
 HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1004734//Ubiquitin-conjugating enzymes  
 HEMBA1004973//Fibronectin type III domain  
 30 HEMBA1005009//Actins  
 HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1005581//EGF-like domain //Laminin G domain  
 HEMBA1005732//Polyprenyl synthetases  
 HEMBA1005737//EF hand  
 35 HEMBA1006248//Zinc finger, C2H2 type  
 HEMBA1006284//Ubiquitin family  
 HEMBA1006293//IG superfamily  
 HEMBA1006344//Band 4.1 family  
 HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)  
 40 HEMBA1006492//Ank repeat  
 HEMBA1006559//Zinc finger, C3HC4 type (RING finger)  
 HEMBA1006708//WD domain, G-beta repeats  
 HEMBA1006737//Ank repeat  
 HEMBA1006758//Cadherin  
 45 HEMBA1006941//Thioredoxins  
 HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases  
 HEMBA1007300//3'5'-cyclic nucleotide phosphodiesterases  
 HEMBB1000083//IG superfamily  
 HEMBB1000317//EGF-like domain //Thrombospondin type 1 domain  
 50 HEMBB1000556//Actinin-type actin-binding domain containing proteins //LIM domain containing proteins  
 HEMBB1000725//Ras family (contains ATP/GTP binding P-loop)  
 HEMBB1000781//Eukaryotic protein kinase domain  
 HEMBB1000915//Thrombospondin type 1 domain  
 HEMBB1000927//EF hand  
 55 HEMBB1000947//Double-stranded RNA binding motif  
 HEMBB1001112//eubacterial secY protein  
 HEMBB1001175//Ank repeat  
 HEMBB1001234//WW/rsp5/WWP domain containing proteins

HEMBB1001282//Ank repeat  
 HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)  
 HEMBB1001339//Forkhead-associated (FHA) domain  
 HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)  
 5 HEMBB1001802//Intermediate filament proteins  
 HEMBB1001839//Zinc finger, C2H2 type  
 HEMBB1002217//Zinc finger, C2H2 type  
 HEMBB1002342//Thioredoxins  
 HEMBB1002600//4 transmembrane segments integral membrane proteins  
 10 MAMMA1000173//Src homology domain 3  
 MAMMA1000388//Zinc finger, C2H2 type  
 MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)  
 MAMMA1000612//WD domain, G-beta repeats  
 MAMMA1000672//Serine carboxypeptidases  
 15 MAMMA1000731//SNF2 and others N-terminal domain  
 MAMMA1001008//Eukaryotic aspartyl proteases  
 MAMMA1001041//Actinin-type actin-binding domain containing proteins  
 MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 MAMMA1001105//Zinc finger, C2H2 type  
 20 MAMMA1001260//Zinc finger, C3HC4 type (RING finger)  
 MAMMA1001576//Tubulin  
 MAMMA1001735//Tubulin  
 MAMMA1001768//ATPases associated with various cellular activities (AAA)  
 MAMMA1001837//Zinc finger, C2H2 type  
 25 MAMMA1002170//Ribosomal protein S5  
 MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2  
 MAMMA1002637//Kinesin light chain repeat  
 MAMMA1002650//Zinc finger, C2H2 type  
 30 MAMMA1002671//AMP-binding enzymes  
 MAMMA1002869//LIM domain containing proteins  
 MAMMA1002881//SCP-like extracellular Proteins  
 MAMMA1002937//Zinc finger, C2H2 type  
 MAMMA1002938//Multicopper oxidases  
 35 MAMMA1003011//Core histones H2A, H2B, H3 and H4  
 MAMMA1003057//WD domain, G-beta repeats  
 MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)  
 NT2RM1000086//Zinc finger, C3HC4 type (RING finger)  
 NT2RM1000199//CUB domain //Sushi domain  
 40 NT2RM1000256//Glutamine amidotransferases class-II  
 NT2RM1000499//Ank repeat  
 NT2RM1000555//'Cold-shock' DNA-binding domain containing proteins  
 NT2RM1000666//'Cold-shock' DNA-binding domain containing proteins //Zinc finger, CCHC class  
 NT2RM1000772//WD domain, G-beta repeats  
 45 NT2RM1000826//'Cold-shock' DNA-binding domain containing proteins  
 NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain  
 NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases  
 NT2RM1000885//Zinc finger, C3HC4 type (RING finger)  
 50 NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RM2000101//Zinc finger, C3HC4 type (RING finger)  
 55 NT2RM2000191//3'5'-cyclic nucleotide phosphodiesterases  
 NT2RM2000422//Sodium:neurotransmitter symporter family  
 NT2RM2000490//C2 domain  
 NT2RM2000566//Integrins alpha chain

NT2RM2000577//tRNA synthetases class I  
 NT2RM2000594//C-5 cytosine-specific DNA methylases  
 NT2RM2000691//Actins  
 NT2RM2000735//Zinc finger, C2H2 type  
 5 NT2RM2000740//Helicases conserved C-terminal domain  
 NT2RM2000951//FGGY family of carbohydrate kinases  
 NT2RM2001324//LIM domain containing proteins  
 NT2RM2001499//Amino acid permeases  
 NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins  
 10 NT2RM2001613//eubacterial secY protein  
 NT2RM2001670//Zinc finger, C2H2 type  
 NT2RM2001700//Acyl-CoA dehydrogenases  
 NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RM2001813//WD domain, G-beta repeats  
 15 NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain  
 NT2RM2001896//Cytochrome C oxidase subunit II  
 NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RM2001997//Thioredoxins  
 NT2RM2002088//KH domain family of RNA binding proteins  
 20 NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RM2002109//IG superfamily  
 NT2RM4000046//Zinc finger, C3HC4 type (RING finger)  
 NT2RM4000104//Zinc finger, C2H2 type  
 NT2RM4000167//Kinesin motor domain  
 25 NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RM4000202//Zinc finger, C2H2 type  
 NT2RM4000229//PH (pleckstrin homology) domain  
 NT2RM4000344//ATPases associated with various cellular activities (AAA)  
 NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)  
 30 NT2RM4000471//Aminotransferases class-V  
 NT2RM4000496//ATPases associated with various cellular activities (AAA)  
 NT2RM4000611//WD domain, G-beta repeats  
 NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 35 NT2RM4000733//Forkhead-associated (FHA) domain  
 NT2RM4000734//Zinc finger, C2H2 type  
 NT2RM4000751//Zinc finger, C2H2 type  
 NT2RM4000795//Carboxylesterases  
 NT2RM4000996//Zinc finger, C2H2 type  
 40 NT2RM4001054//eubacterial secY protein  
 NT2RM4001140//Homeobox domain  
 NT2RM4001178//DEAD and DEAH box helicases  
 NT2RM4001200//Zinc finger, C2H2 type  
 NT2RM4001313//Phosphatidylinositol 3- and 4-kinases  
 45 NT2RM4001316//Acyl-CoA dehydrogenases  
 NT2RM4001320//Src homology domain 3  
 NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2  
 NT2RM4001454//PH (pleckstrin homology) domain  
 NT2RM4001483//Zinc finger, C2H2 type  
 50 NT2RM4001629//Src homology domain 3  
 NT2RM4001758//Eukaryotic protein kinase domain  
 NT2RM4001810//Zinc finger, C2H2 type  
 NT2RM4001813//Lectin C-type domain short and long forms  
 NT2RM4001823//Zinc finger, C2H2 type  
 55 NT2RM4001828//Zinc finger, C2H2 type  
 NT2RM4001979//Zinc finger, C2H2 type  
 NT2RM4001987//IG superfamily  
 NT2RM4002013//WD domain, G-beta repeats

NT2RM4002073//AMP-binding enzymes  
 NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RM4002145//IG superfamily  
 NT2RM4002287//Fibronectin type III domain  
 5 NT2RM4002527//WD domain, G-beta repeats  
 NT2RM4002623//tRNA synthetases class II  
 NT2RP1000101//Zinc finger, C2H2 type  
 NT2RP1000202//Ank repeat  
 NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 10 NT2RP1000363//PH (pleckstrin homology) domain  
 NT2RP1000376//Ank repeat  
 NT2RP1000470//DEAD and DEAH box helicases  
 NT2RP1000478//Tubulin  
 NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 15 NT2RP1000677//Kazal-type serine protease inhibitor domain  
 NT2RP1000701//WD domain, G-beta repeats  
 NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP1000782//4 transmembrane segments integral membrane proteins  
 NT2RP1000833//3'5'-cyclic nucleotide phosphodiesterases  
 20 NT2RP1000856//4 transmembrane segments integral membrane proteins  
 NT2RP1000947//Ubiquitin-conjugating enzymes  
 NT2RP1000959//60s Acidic ribosomal protein  
 NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP1001033//Tubulin  
 25 NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RP1001177//Core histones H2A, H2B, H3 and H4  
 NT2RP1001247//Transforming growth factor beta like domain  
 NT2RP1001294//WD domain, G-beta repeats  
 NT2RP1001302//WD domain, G-beta repeats  
 30 NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases  
 NT2RP1001457//WD domain, G-beta repeats  
 NT2RP1001546//4 transmembrane segments integral membrane proteins  
 NT2RP2000008//Zinc finger, C2H2 type  
 NT2RP2000040//C2 domain  
 35 NT2RP2000045//DnaJ, prokaryotic heat shock protein  
 NT2RP2000054//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2000070//Cadherin  
 NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain  
 NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 40 NT2RP2000224//PH (pleckstrin, homology) domain  
 NT2RP2000257//Mitochondrial carrier proteins  
 NT2RP2000329//Adenylate kinases  
 NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP2000448//PH (pleckstrin homology) domain  
 45 NT2RP2000660//ATPases associated with various cellular activities (AAA)  
 NT2RP2000668//Eukaryotic protein kinase domain  
 NT2RP2000710//tRNA synthetases class II  
 NT2RP2000764//Aminotransferases class-V  
 NT2RP2000842//7 transmembrane receptor (rhodopsin family)  
 50 NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP2000932//Ank repeat  
 NT2RP2001081//C2 domain  
 NT2RP2001174//Zinc finger, C2H2 type  
 55 NT2RP2001397//Cyclins  
 NT2RP2001520//Mitochondrial carrier proteins  
 NT2RP2001597//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2

NT2RP2001748//Polyprenyl synthetases  
 NT2RP2001756//Zinc finger, C2H2 type  
 NT2RP2001839//Eukaryotic protein kinase domain  
 NT2RP2001900//Actins  
 5 NT2RP2001991//Sodium:neurotransmitter symporter family  
 NT2RP2002058//WD domain, G-beta repeats  
 NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP2002185//Ubiquitin family  
 NT2RP2002208//Zinc finger, C3HC4 type (RING finger)  
 10 NT2RP2002256//Cytochrome P450  
 NT2RP2002479//ABC transporters  
 NT2RP2002503//Zinc finger, C2H2 type  
 NT2RP2002520//Ank repeat  
 NT2RP2002591//Zinc finger, C2H2 type  
 15 NT2RP2002741//Src homology domain 3  
 NT2RP2002929//WD domain, G-beta repeats  
 NT2RP2002939//Zinc finger, C2H2 type  
 NT2RP2002959//Ubiquitin-conjugating enzymes  
 NT2RP2002980//Ribosomal protein S10  
 20 NT2RP2003137//Ubiquitin family  
 NT2RP2003164//Eukaryotic protein kinase domain  
 NT2RP2003228//MCM2/3/5 family  
 NT2RP2003243//Fibronectin type III domain  
 NT2RP2003272//Ubiquitin family  
 25 NT2RP2003307//Kinesin light chain repeat  
 NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases, family 2  
 NT2RP2003433//eubacterial secY protein  
 NT2RP2003480//Zinc finger, C2H2 type  
 NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2  
 30 NT2RP2003737//Ubiquitin-conjugating enzymes  
 NT2RP2003777//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2003840//Ubiquitin-conjugating enzymes  
 NT2RP2003857//Ank repeat  
 NT2RP2003981//Zinc finger, C3HC4 type (RING finger)  
 35 NT2RP2004170//WD domain, G-beta repeats  
 NT2RP2004187//Zinc finger, C2H2 type  
 NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic  
 protein kinase domain  
 NT2RP2004389//Ribosomal protein S9  
 40 NT2RP2004538//PH (pleckstrin homology) domain  
 NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RP2004710//WW/rsp5/WWP domain containing proteins  
 NT2RP2004768//Eukaryotic protein kinase domain  
 NT2RP2004933//Eukaryotic protein kinase domain  
 45 NT2RP2004961//Zinc finger, C2H2 type  
 NT2RP2005003//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2005012//DnaJ, prokaryotic heat shock protein  
 NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RP2005139//Ank repeat  
 50 NT2RP2005140//PH (pleckstrin homology) domain  
 NT2RP2005239//Aminotransferases class-V  
 NT2RP2005288//Regulator of chromosome condensation (RCC1)  
 NT2RP2005293//PH (pleckstrin homology) domain  
 NT2RP2005325//Homeobox domain //LIM domain containing proteins  
 55 NT2RP2005344//E1-E2 ATPases  
 NT2RP2005465//Mitochondrial carrier proteins  
 NT2RP2005525//Forkhead-associated (FHA) domain  
 NT2RP2005531//Band 4.1 family

NT2RP2005557//Bacterial mutT protein  
 NT2RP2005654//DnaJ, prokaryotic heat shock protein  
 NT2RP2005701//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2005722//Zinc finger, C2H2 type  
 5 NT2RP2005752//TNFR/NGFR cysteine-rich region  
 NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RP2005767//HMG (high mobility group) box  
 NT2RP2006312//HMG (high mobility group) box  
 NT2RP2006464//HMG (high mobility group) box  
 10 NT2RP2006571//Cytochrome P450  
 NT2RP3000050//Zinc finger, C2H2 type  
 NT2RP3000068//PH (pleckstrin homology) domain  
 NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (CPSase)  
 NT2RP3000299//Src homology domain 3  
 15 NT2RP3000359//Adenylate kinases  
 NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)  
 NT2RP3000403//WW/rsp5/WWP domain containing proteins  
 NT2RP3000487//WW/rsp5/WWP domain containing proteins  
 NT2RP3000512//Homeobox domain  
 20 NT2RP3000527//Zinc finger, C2H2 type  
 NT2RP3000531//IG superfamily  
 NT2RP3000590//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3000603//Helix-loop-helix DNA-binding domain  
 NT2RP3000605//Zinc finger, C2H2 type  
 25 NT2RP3000632//Zinc finger, C2H2 type  
 NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)  
 NT2RP3000825//EGF-like domain  
 30 NT2RP3000869//ATPases associated with various cellular activities (AAA)  
 NT2RP3000994//Double-stranded RNA binding motif  
 NT2RP3001057//Zinc finger, C2H2 type  
 NT2RP3001084//PH (pleckstrin homology) domain  
 NT2RP3001120//Zinc finger, C2H2 type  
 35 NT2RP3001140//Thrombospondin type 1 domain  
 NT2RP3001150//Forkhead-associated (FHA) domain  
 NT2RP3001155//HMG (high mobility group) box  
 NT2RP3001214//Zinc finger, C2H2 type  
 NT2RP3001268//Zinc finger, C2H2 type  
 40 NT2RP3001338//Zinc finger, C2H2 type  
 NT2RP3001355//Mitochondrial carrier proteins  
 NT2RP3001398//Zinc finger, C2H2 type  
 NT2RP3001426//DnaJ, prokaryotic heat shock protein  
 NT2RP3001453//ABC transporters  
 45 NT2RP3001457//PH (pleckstrin homology) domain  
 NT2RP3001472//HMG (high mobility group) box  
 NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/WWP domain containing proteins  
 NT2RP3001497//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3001724//Helicases conserved C-terminal domain  
 50 NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP3001943//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3001944//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3002007//ATPases associated with various cellular activities (AAA)  
 NT2RP3002054//Low-density lipoprotein receptor domain class A  
 55 NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP3002399//MCM2/3/5 family  
 NT2RP3002501//Serine/threonine dehydratases  
 NT2RP3002602//Thioredoxins



NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins  
 NT2RP3002663//PH (pleckstrin homology) domain  
 NT2RP3002909//Ank repeat  
 NT2RP3002953//Cadherin  
 5 NT2RP3002969//AMP-binding enzymes  
 NT2RP3003061//Ank repeat  
 NT2RP3003145//Zinc carboxypeptidases  
 NT2RP3003230//WD domain, G-beta repeats  
 NT2RP3003251//Zinc finger, C3HC4 type (RING finger)  
 10 NT2RP3003278//Ank repeat //Zinc finger, C2H2 type  
 NT2RP3003282//PH (pleckstrin homology) domain  
 NT2RP3003311//PH (pleckstrin homology) domain  
 NT2RP3003385//Ank repeat //Chaperonins clpA/B  
 NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)  
 15 NT2RP3003621//CUB domain //Krigle domain  
 NT2RP3003701//Thrombospondin type 1 domain  
 NT2RP3003716//Fibronectin type III domain  
 NT2RP3003809//ATPases associated with various cellular activities (AAA)  
 NT2RP3004016//Zinc finger, C3HC4 type (RING finger)  
 20 NT2RP3004207//CUB domain //Sushi domain  
 NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP3004242//PH (pleckstrin homology) domain  
 NT2RP3004262//DnaJ, prokaryotic heat shock protein  
 NT2RP3004566//Zinc finger, C2H2 type  
 25 NT2RP3004569//Ank repeat  
 NT2RP3004594//HMG (high mobility group) box  
 NT2RP3004617//Zinc finger, C3HC4 type (RING finger)  
 NT2RP4000259//Glutathione peroxidases  
 NT2RP4000370//Prokaryotic-type class I peptide chain release factors  
 30 NT2RP4000376//WD domain, G-beta repeats  
 NT2RP4000398//Zinc finger, C2H2 type  
 NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)  
 NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 35 NT2RP4000588//Actinin-type actin-binding domain containing proteins  
 NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)  
 NT2RP4000837//Zinc finger, C2H2 type  
 NT2RP4000839//WD domain, G-beta repeats  
 40 NT2RP4000865//Zinc finger, C2H2 type  
 NT2RP4000907//Fibronectin type III domain //IG superfamily  
 NT2RP4000925//Fibronectin type III domain  
 NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins  
 45 NT2RP4001079//E1-E2 ATPases  
 NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP4001117//eubacterial secY protein  
 NT2RP4001150//Fibronectin type III domain  
 NT2RP4001213//Zinc finger, C2H2 type  
 50 NT2RP4001219//Thioredoxins  
 NT2RP4001235//Zinc finger, CCHC class  
 NT2RP4001433//Zinc finger, C2H2 type  
 NT2RP4001498//Ank repeat  
 NT2RP4001568//Ank repeat  
 55 NT2RP4001644//Eukaryotic protein kinase domain  
 NT2RP4001725//WD domain, G-beta repeats  
 NT2RP4001753//Zinc finger, C2H2 type  
 NT2RP4001790//Zinc finger, C2H2 type

NT2RP4001822//4 transmembrane segments integral membrane proteins  
 NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain  
 NT2RP4001893//Ank repeat  
 NT2RP4001896//WD domain, G-beta repeats  
 5 NT2RP4001927//WD domain, G-beta repeats  
 NT2RP4001938//Zinc finger, C2H2 type  
 NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP4002078//Zinc finger, C2H2 type  
 NT2RP4002408//Eukaryotic protein kinase domain  
 10 NT2RP4002905//Cyclins  
 NT2RP5003477//WD domain, G-beta repeats  
 OVARC1000006//Core histones H2A, H2B, H3 and H4  
 OVARC1000085//Proteasome A-type and B-type  
 OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 15 OVARC1000556//Eukaryotic protein kinase domain  
 OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2  
 OVARC1000746//Double-stranded RNA binding motif  
 OVARC1000885//Alcohol/other dehydrogenases, short chain type  
 OVARC1000937//Cyclins  
 20 OVARC1000999//Ank repeat  
 OVARC1001154//Granulins  
 OVARC1001180//Ubiquitin family  
 OVARC1001306//Helix-loop-helix DNA-binding domain  
 OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 25 OVARC1001731//Tropomyosins  
 OVARC1001943//Zinc finger, C2H2 type  
 OVARC1002050//Spectrin alpha chain, repeated domain  
 OVARC1002112//Core histones H2A, H2B, H3 and H4  
 OVARC1002138//ATPases associated with various cellular activities (AAA)  
 30 OVARC1002182//WD domain, G-beta repeats  
 PLACE1000014//Zinc finger, C3HC4 type (RING finger)  
 PLACE1000040//Ras family (contains ATP/GTP binding P-loop)  
 PLACE1000050//Zinc finger, C2H2 type  
 PLACE1000081//PH (pleckstrin homology) domain  
 35 PLACE1000142//Enoyl-CoA hydratase/isomerase  
 PLACE1000401//IG superfamily  
 PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1000420//Bacterial mutT protein  
 PLACE1000706//Bromodomain  
 40 PLACE1000769//KH domain family of RNA binding proteins  
 PLACE1000786//PH (pleckstrin homology) domain  
 PLACE1000863//Ribosomal protein S4  
 PLACE1000909//Ank repeat  
 PLACE1000972//Src homology domain 3  
 45 PLACE1000979//Zinc finger, C2H2 type  
 PLACE1001304//Zinc finger, C2H2 type  
 PLACE1001387//Src homology domain 3  
 PLACE1001632//Zinc finger, C2H2 type  
 PLACE1001672//Aminotransferases class-III pyridoxal-phosphate  
 50 PLACE1001716//Zinc finger, CCHC class  
 PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 PLACE1001781//Phosphoglucomutase and phosphomannomutase phosphoserine  
 PLACE1001869//FGGY family of carbohydrate kinases  
 PLACE1002438//Zinc finger, C2H2 type  
 55 PLACE1002450//Zinc finger, C2H2 type  
 PLACE1002474//EGF-like domain //von Willebrand factor type A domain  
 PLACE1002499//Zinc finger, C3HC4 type (RING finger)  
 PLACE1002532//Homeobox domain

PLACE1002571//Actins  
 PLACE1002685//Src homology domain 2  
 PLACE1002722//7 transmembrane receptor (rhodopsin family)  
 PLACE1002775//Bromodomain  
 5 PLACE1002834//Zinc finger, C2H2 type  
 PLACE1003100//Alcohol/other dehydrogenases, short chain type  
 PLACE1003174//Ubiquitin-conjugating enzymes  
 PLACE1003238//7 transmembrane receptor (rhodopsin family)  
 PLACE1003302//Zinc finger, C2H2 type  
 10 PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1003366//C2 domain  
 PLACE1003394//Ras family (contains ATP/GTP binding P-loop)  
 PLACE1003420//Mitochondrial carrier proteins  
 PLACE1003493//C1q domain  
 15 PLACE1003519//KH domain family of RNA binding-proteins  
 PLACE1003723//Src homology domain 2  
 PLACE1003738//Zinc finger, C2H2 type  
 PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 20 PLACE1004128//WD domain, G-beta repeats  
 PLACE1004358//PH (pleckstrin homology) domain  
 PLACE1004428//Acyl-CoA dehydrogenases  
 PLACE1004437//Isocitrate and isopropylmalate dehydrogenases  
 PLACE1004506//LIM domain containing proteins  
 25 PLACE1004674//EF hand  
 PLACE1004918//L-lactate dehydrogenases  
 PLACE1005243//Eukaryotic protein kinase domain  
 PLACE1005305//Adenylate kinases  
 PLACE1005327//Src homology domain 3  
 30 PLACE1005530//Zinc finger, C3HC4 type (RING finger)  
 PLACE1005646//Helicases conserved C-terminal domain  
 PLACE1005656//Ribonucleotide reductases  
 PLACE1005966//WD domain, G-beta repeats  
 PLACE1006157//Sushi domain  
 35 PLACE1006196//DEAH and DEAR box helicases //Helicases conserved C-terminal domain  
 PLACE1006438//Zinc finger, C2H2 type  
 PLACE1006626//Double-stranded RNA binding motif  
 PLACE1006754//IG superfamily  
 PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 40 PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1006956//ABC transporters  
 PLACE1006958//Heat shock hsp70 proteins  
 PLACE1007375//C2 domain  
 PLACE1007488//PH (pleckstrin homology) domain  
 45 PLACE1007511//Intermediate filament proteins  
 PLACE1007537//Ank repeat  
 PLACE1007544//Zinc finger, C2H2 type  
 PLACE1007547//Zinc finger, C3HC4 type (RING finger)  
 PLACE1007598//Zinc finger, C2H2 type  
 50 PLACE1007697//ABC transporters  
 PLACE1007958//3'5'-cyclic nucleotide phosphodiesterases  
 PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1008201//Zinc finger, C2H2 type  
 PLACE1008429//Ank repeat  
 55 PLACE1008465//Zinc finger, C2H2 type  
 PLACE1008650//WD domain, G-beta repeats  
 PLACE1009020//Aminotransferases class-V  
 PLACE1009094//von Willebrand factor type C domain

PLACE1009099//Zinc finger, C2H2 type  
 PLACE1009246//LIM domain containing proteins  
 PLACE1009468//WD domain, G-beta repeats  
 PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 5 PLACE1009524//PH (pleckstrin homology) domain  
 PLACE1009596//WD domain, G-beta repeats  
 PLACE1009622//Double-stranded RNA binding motif  
 PLACE1009861//Cysteine proteases  
 PLACE1009925//Helicases conserved C-terminal domain  
 10 PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin  
 PLACE1010053//Double-stranded RNA binding motif  
 PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2  
 PLACE1010702//Zinc finger, C2H2 type  
 PLACE1010833//EF hand  
 15 PLACE1010926//Src homology domain 3  
 PLACE1010960//Actins  
 PLACE1011041//Src homology domain 3  
 PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-spe-  
 cific phospholipase C, Y domain  
 20 PLACE1011114//Helicases conserved C-terminal domain  
 PLACE1011160//Zinc finger, C3HC4 type (RING finger)  
 PLACE1011263//Ank repeat  
 PLACE1011433//Zinc finger, C2H2 type  
 PLACE1011576//Zinc finger, C2H2 type  
 25 PLACE1011923//Eukaryotic protein kinase domain  
 PLACE2000034//Fibronectin type III domain //IG superfamily  
 PLACE2000072//Zinc finger, C2H2 type  
 PLACE2000111//IG superfamily  
 PLACE2000164//WD domain, G-beta repeats  
 30 PLACE2000216//PH (pleckstrin homology) domain  
 PLACE2000341//Sodium:solute symporter family  
 PLACE2000371//Src homology domain 2  
 PLACE2000373//Thrombospondin type 1 domain  
 PLACE2000398//IG superfamily  
 35 PLACE2000427//Helicases conserved C-terminal domain  
 PLACE2000458//Cadherin  
 PLACE3000020//Guanylate cyclases  
 PLACE3000169//Zinc finger, C2H2 type  
 PLACE4000014//Helicases conserved C-terminal domain  
 40 PLACE4000052//ABC transporters  
 PLACE4000192//Zinc finger, C2H2 type  
 PLACE4000211//Bromodomain  
 PLACE4000431//Helicases conserved C-terminal domain  
 PLACE4000522//Ank repeat  
 45 PLACE4000581//EGF-like domain //Sushi domain  
 PLACE4000654//Ubiquitin-conjugating enzymes  
 THYRO1000072//IG superfamily  
 THYRO1000242//Zinc finger, C2H2 type  
 THYRO1000288//Zinc-binding metalloprotease domain  
 50 THYRO1000488//Zinc finger, C3HC4 type (RING finger)  
 THYRO1000501//Zinc finger, C3HC4 type (RING finger)  
 THYRO1000666//Kinesin motor domain  
 THYRO1000748//Src homology domain 3  
 THYRO1000926//3' 5'-cyclic nucleotide phosphodiesterases  
 55 THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 THYRO1001671//Ubiquitin family  
 Y79AA1000037//Zinc finger, C3HC4 type (RING finger)  
 Y79AA1000214//Core histones H2A, H2B, H3 and H4

Y79AA1000342//Zinc finger, C2H2 type  
 Y79AA1000349//Double-stranded RNA binding motif  
 Y79AA1000627//Zinc finger, C2H2 type  
 Y79AA1000705//Helicases conserved C-terminal domain  
 5 Y79AA1000752//KH domain family of RNA binding proteins  
 Y79AA1000833//Tubulin  
 Y79AA1001048//Acyl-CoA dehydrogenases  
 Y79AA1001391//Homeobox domain  
 Y79AA1001394//ATPases associated with various cellular activities (AAA)  
 10 Y79AA1001493//Ubiquitin-conjugating enzymes  
 Y79AA1001613//Zinc finger, C2H2 type  
 Y79AA1001874//TNFR/NGFR cysteine-rich region  
 Y79AA1002027//Ubiquitin-conjugating enzymes  
 Y79AA1002139//DnaJ, prokaryotic heat shock protein  
 15 Y79AA1002208//Ank repeat  
 Y79AA1002246//C2 domain  
 Y79AA1002307//Fibronectin type III domain  
 Y79AA1002472//Zinc finger, C2H2 type  
 HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3  
 20 HEMBA1005206//Glutathione S-transferases.  
 HEMBA1006521//Alcohol/other dehydrogenases, short chain type  
 HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type  
 MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG  
 25 superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type  
 NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type  
 NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type  
 NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family)  
 NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type  
 30 NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain  
 NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif  
 NT2RP3004125//Zinc finger, C2H2 type  
 OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases  
 35 PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2  
 PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases  
 PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC  
 40 transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//  
 Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain  
 PLACE4000156//Zinc finger, C2H2 type

#### 45 EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

[0257] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based  
 50 on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, Swiss-Prot and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target 4997 clones are listed below:

55 HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000042, HEMBA1000046,  
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 HEMBA1000158, HEMBA1000168, HEMBA1000185, HEMBA1000193, HEMBA1000201, HEMBA1000213,  
 HEMBA1000216, HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251,  
 HEMBA1000264, HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302,

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Y79AA1001581, Y79AA1001585, Y79AA1001594, Y79AA1001603, Y79AA1001613, Y79AA1001647,  
10 Y79AA1001665, Y79AA1001679, Y79AA1001692, Y79AA1001696, Y79AA1001705, Y79AA1001711,  
Y79AA1001781, Y79AA1001805, Y79AA1001827, Y79AA1001846, Y79AA1001866, Y79AA1001874,  
Y79AA1001875, Y79AA1001923, Y79AA1001963, Y79AA1002027, Y79AA1002083, Y79AA1002089,  
Y79AA1002103, Y79AA1002115, Y79AA1002125, Y79AA1002139, Y79AA1002204, Y79AA1002208,  
Y79AA1002209, Y79AA1002210, Y79AA1002211, Y79AA1002220, Y79AA1002229, Y79AA1002234,  
15 Y79AA1002246, Y79AA1002258, Y79AA1002298, Y79AA1002307, Y79AA1002311, Y79AA1002351,  
Y79AA1002361, Y79AA1002399, Y79AA1002407, Y79AA1002416, Y79AA1002431, Y79AA1002433,  
Y79AA1002472, Y79AA1002482, Y79AA1002487,

[0258] Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins, nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

25 [0259] The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which  
30 matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0260] The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those  
35 which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0261] The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins  
40 are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0262] The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated  
45 proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0263] The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched  
50 sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.

[0264] The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms "metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

55 [0265] The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins are those which matched the data with the terms "ATP-binding" or "GTP-binding".

[0266] The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein".

**[0267]** The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

**[0268]** The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

**[0269]** The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

**[0270]** The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

**[0271]** The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis".

**[0272]** The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

**[0273]** The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

**[0274]** When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

**[0275]** The following 796 clones are categorized into secretory or membrane proteins.

HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,	HEMBA1000817,
HEMBA1000822,	HEMBA1000852,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001071,
HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,
HEMBA1001557,	HEMBA1001569,	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,
HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,	HEMBA1002780,
HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,	HEMBA1003077,	HEMBA1003079,
HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,
HEMBA1003742,	HEMBA1003803,	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,
HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,
HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,	HEMBA1005588,	HEMBA1005616,
HEMBA1005699,	HEMBA1005991,	HEMBA1006036,	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,
HEMBA1006198,	HEMBA1006293,	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,
HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,	HEMBA1000175,
HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,
HEMBA1001348,	HEMBA1001564,	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,
HEMBA1001962,	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,
MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,
MAMMA1000416,	MAMMA1000472,	MAMMA1000672,	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,
MAMMA1000778,	MAMMA1000798,	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,
MAMMA1001008,	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,	MAMMA1002428,	MAMMA1002461,
MAMMA1002524,	MAMMA1002573,	MAMMA1002598,	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,
MAMMA1002844,	MAMMA1002881,	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,
MAMMA1003089,	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,	NT2RM1000260,
NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,	NT2RM1000742,	NT2RM1000770,
NT2RM1000800,	NT2RM1000811,	NT2RM1000833,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
NT2RM1000905,	NT2RM1001008,				
NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000260,	NT2RM2000287,	NT2RM2000395,
NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2000522,	NT2RM2000566,

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	NT2RM2000581,	NT2RM2000609,	NT2RM2000821,	NT2RM2001370,	NT2RM2001393,	NT2RM2001499,
	NT2RM2001547,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,	NT2RM2001688,
	NT2RM2001698,	NT2RM2001718,	NT2RM2001753,	NT2RM2001760,	NT2RM2001785,	NT2RM2001930,
	NT2RM2001950,	NT2RM2001997,	NT2RM2001998,	NT2RM2002049,	NT2RM2002145,	NT2RM4000233,
5	NT2RM4000433,	NT2RM4000457,	NT2RM4000486,	NT2RM4000496,	NT2RM4000520,	NT2RM4000634,
	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000778,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001116,	NT2RM4001455,	NT2RM4001666,
	NT2RM4001810,	NT2RM4001813,	NT2RM4001930,	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,
10	NT2RM4002145,	NT2RM4002146,	NT2RM4002189,	NT2RM4002194,	NT2RM4002251,	NT2RM4002339,
	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,	NT2RM4002558,
	NT2RM4002565,	NT2RM4002571,	NT2RM4002594,	NT2RP1000130,	NT2RP1000191,	NT2RP1000326,
	NT2RP1000358,	NT2RP1000413,	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,
	NT2RP1000767,	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,	NT2RP1001286,
15	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,	NT2RP1001546,
	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000056,	NT2RP2000070,	NT2RP2000091,
	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,	NT2RP2000175,	NT2RP2000195,	NT2RP2000257,
	NT2RP2000270,	NT2RP2000283,	NT2RP2000288,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,
	NT2RP2000660,	NT2RP2000842,	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,
20	NT2RP2001366,	NT2RP2001378,	NT2RP2001576,	NT2RP2001581,	NT2RP2001597,	NT2RP2001613,
	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002066,	NT2RP2002078,	NT2RP2002105,
	NT2RP2002312,	NT2RP2002325,	NT2RP2002385,	NT2RP2002479,	NT2RP2002537,	NT2RP2002643,
	NT2RP2002701,	NT2RP2002740,	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,	NT2RP2003433,
	NT2RP2003446,	NT2RP2003466,	NT2RP2003506,	NT2RP2003513,	NT2RP2003629,	NT2RP2003668,
25	NT2RP2003760,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004142,	NT2RP2004194,
	NT2RP2004270,	NT2RP2004300,	NT2RP2004392,	NT2RP2004655,	NT2RP2004681,	NT2RP2004775,
	NT2RP2004799,	NT2RP2004936,	NT2RP2004959,	NT2RP2005012,	NT2RP2005159,	NT2RP2005227,
	NT2RP2005270,	NT2RP2005344,	NT2RP2005465,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,
	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006184,
30	NT2RP2006261,	NT2RP2006565,	NT2RP2006571,	NT2RP2006573,	NT2RP3000092,	NT2RP3000109,
	NT2RP3000134,	NT2RP3000207,	NT2RP3000333,	NT2RP3000341,	NT2RP3000393,	NT2RP3000439,
	NT2RP3000441,	NT2RP3000531,	NT2RP3000685,	NT2RP3000825,	NT2RP3000826,	NT2RP3000852,
	NT2RP3000919,	NT2RP3001084,	NT2RP3001096,	NT2RP3001126,	NT2RP3001140,	NT2RP3001176,
	NT2RP3001260,	NT2RP3001282,	NT2RP3001355,	NT2RP3001383,	NT2RP3001426,	NT2RP3001453,
35	NT2RP3001497,	NT2RP3001538,	NT2RP3001589,	NT2RP3001642,	NT2RP3001708,	NT2RP3001716,
	NT2RP3001727,	NT2RP3001739,	NT2RP3001799,	NT2RP3001943,	NT2RP3001944,	NT2RP3002002,
	NT2RP3002007,	NT2RP3002014,	NT2RP3002054,	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,
	NT2RP3002455,	NT2RP3002549,	NT2RP3002602,	NT2RP3002628,	NT2RP3002650,	NT2RP3002687,
	NT2RP3002701,	NT2RP3002810,	NT2RP3002869,	NT2RP3002969,	NT2RP3002985,	NT2RP3003008,
40	NT2RP3003059,	NT2RP3003071,	NT2RP3003101,	NT2RP3003145,	NT2RP3003197,	NT2RP3003203,
	NT2RP3003242,	NT2RP3003302,	NT2RP3003353,	NT2RP3003409,	NT2RP3003576,	NT2RP3003621,
	NT2RP3003665,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003799,	NT2RP3003828,
	NT2RP3003914,	NT2RP3003918,	NT2RP3003992,	NT2RP3004051,	NT2RP3004148,	NT2RP3004155,
	NT2RP3004207,	NT2RP3004282,	NT2RP3004454,	NT2RP3004480,	NT2RP3004503,	NT2RP4000008,
45	NT2RP4000051,	NT2RP4000151,	NT2RP4000212,	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,
	NT2RP4000417,	NT2RP4000500,	NT2RP4000524,	NT2RP4000556,	NT2RP4000560,	NT2RP4000588,
	NT2RP4000713,	NT2RP4000724,	NT2RP4000817,	NT2RP4000833,	NT2RP4000878,	NT2RP4000907,
	NT2RP4000925,	NT2RP4000928,	NT2RP4000973,	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,
	NT2RP4001079,	NT2RP4001117,	NT2RP4001138,	NT2RP4001149,	NT2RP4001150,	NT2RP4001174,
50	NT2RP4001219,	NT2RP4001274,	NT2RP4001313,	NT2RP4001345,	NT2RP4001372,	NT2RP4001373,
	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,	NT2RP4001571,	NT2RP4001574,	NT2RP4001644,
	NT2RP4001656,	NT2RP4001677,	NT2RP4001730,	NT2RP4001739,	NT2RP4001803,	NT2RP4001822,
	NT2RP4001823,	NT2RP4001950,	NT2RP4001975,	NT2RP4002052,	NT2RP4002075,	NT2RP5003500,
	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000060,	OVARC1000335,	OVARC1000682,
	OVARC1000689,	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,	OVARC1000890,
55	OVARC1000924,	OVARC1000936,	OVARC1000959,	OVARC1000984,	OVARC1000999,	OVARC1001034,
	OVARC1001055,	OVARC1001117,	OVARC1001129,	OVARC1001154,	OVARC1001329,	OVARC1001381,
	OVARC1001391,	OVARC1001453,	OVARC1001476,	OVARC1001506,	OVARC1001610,	OVARC1001702,
	OVARC1001703,	OVARC1001713,	OVARC1001745,	OVARC1001767,	OVARC1002127,	OVARC1002138,

5 OVARC1002158, OVARC1002165, PLACE1000014, PLACE1000213, PLACE1000401, PLACE1000562,  
 PLACE1000611, PLACE1000656, PLACE1000712, PLACE1 000793, PLACE1000909, PLACE1000948,  
 PLACE1000977, PLACE1001241, PLACE1001257, PLACE1001377, PLACE1001517, PLACE1001610,  
 PLACE1001761, PLACE1001771, PLACE1001817, PLACE1001983, PLACE1002046, PLACE1002140,  
 PLACE1002213, PLACE1002395, PLACE1002437, PLACE1002500, PLACE1002583, PLACE1002714,  
 PLACE1002722, PLACE1002782, PLACE1002794, PLACE1002851, PLACE1002908, PLACE1003030,  
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 PLACE1003493, PLACE1003537, PLACE1003553, PLACE1003596, PLACE1003760, PLACE1003768,  
 PLACE1003771, PLACE1003903, PLACE1004149, PLACE1004197, PLACE1004203, PLACE1004258,  
 10 PLACE1004270, PLACE1004277, PLACE1004289, PLACE1004473, PLACE1004629, PLACE1004646,  
 PLACE1004743, PLACE1004751, PLACE1004793, PLACE1004840, PLACE1004969, PLACE1005086,  
 PLACE1005162, PLACE1005206, PLACE1005313, PLACE1005467, PLACE1005530, PLACE1005595,  
 PLACE1005611, PLACE1005623, PLACE1005763, PLACE1005884, PLACE1005890, PLACE1005898,  
 PLACE1005934, PLACE1005953, PLACE1006157, PLACE1006225, PLACE1006239, PLACE1006288,  
 15 PLACE1006492, PLACE1006534, PLACE1006678, PLACE1006754, PLACE1006901, PLACE1006935,  
 PLACE1006956, PLACE1007111, PLACE1007243, PLACE1007274, PLACE1007282, PLACE1007317,  
 PLACE1007375, PLACE1007386, PLACE1007409, PLACE1007416, PLACE1007484, PLACE1007583,  
 PLACE1007632, PLACE1007645, PLACE1007649, PLACE1007852, PLACE1007877, PLACE1007954,  
 PLACE1008273, PLACE1008309, PLACE1008331, PLACE1008402, PLACE1008424, PLACE1008429,  
 20 PLACE1008531, PLACE1008532, PLACE1008533, PLACE1008568, PLACE1008643, PLACE1008693,  
 PLACE1008715, PLACE1009045, PLACE1009094, PLACE1009298, PLACE1009319, PLACE1009338,  
 PLACE1009368, PLACE1009493, PLACE1009639, PLACE1009659, PLACE1009708, PLACE1009731,  
 PLACE1009845, PLACE1009861, PLACE1009935, PLACE1009992, PLACE1010089, PLACE1010231,  
 PLACE1010321, PLACE1010362, PLACE1010599, PLACE1010622, PLACE1010662, PLACE1010811,  
 25 PLACE1010917, PLACE1010942, PLACE10110954, PLACE1011090, PLACE1011214, PLACE1011221,  
 PLACE1011371, PLACE1011399, PLACE1011492, PLACE1011646, PLACE1011749, PLACE1011896,  
 PLACE2000034, PLACE2000062, PLACE2000111, PLACE2000132, PLACE2000176, PLACE2000187,  
 PLACE2000216, PLACE2000335, PLACE2000341, PLACE2000373, PLACE2000379, PLACE2000398,  
 PLACE2000399, PLACE2000425, PLACE2000438, PLACE2000458, PLACE2000477, PLACE3000020,  
 30 PLACE3000218, PLACE3000226, PLACE3000242, PLACE3000244, PLACE3000339, PLACE3000373,  
 PLACE3000399, PLACE3000406, PLACE3000413, PLACE3000455, PLACE4000052, PLACE4000063,  
 PLACE4000129, PLACE4000247, PLACE4000250, PLACE4000259, PLACE4000300, PLACE4000387,  
 PLACE4000431, PLACE4000487, PLACE4000494, PLACE4000522, PLACE4000548, PLACE4000581,  
 PLACE4000593, PLACE4000650, THYRO1000156, THYRO1000327, THYRO1000394, THYRO1000395,  
 35 THYRO1000570, THYRO1000748, THYRO1000756, THYRO1000783, THYRO1001134, THYRO1001271,  
 THYRO1001287, THYRO1001320, THYRO1001401, THYRO1001534, THYRO1001537, THYRO1001541,  
 THYRO1001828, Y79AA1000258, Y79AA1000420, Y79AA1000469, Y79AA1000734, Y79AA1000800,  
 Y79AA1000976, Y79AA1001023, Y79AA1001177, Y79AA1001384, Y79AA1001394, Y79AA1001603,  
 Y79AA1001647, Y79AA1001846, Y79AA1001874, Y79AA1002139, Y79AA1002246, Y79AA1002351,  
 40 Y79AA1002399, Y79AA1002416,

**[0276]** The following 141 clones are categorized into glycoproteins-associated proteins.

45 HEMBA1000156, HEMBA1000518, HEMBA1000852, HEMBA1001071, HEMBA1001286, HEMBA1001661,  
 HEMBA1001734, HEMBA1001866, HEMBA1003071, HEMBA1003077, HEMBA1003281, HEMBA1003538,  
 HEMBA1003679, HEMBA1003866, HEMBA1005576, HEMBA1005581, HEMBA1005699, HEMBA1006038,  
 HEMBA1006976, HEMBA1007301, HEMBB1000317, HEMBB1000915, HEMBB1001871, HEMBB1001872,  
 HEMBB1002193, MAMMA1000672, MAMMA1000897, MAMMA1001030, MAMMA1001388, MAMMA1002329,  
 MAMMA1002428, MAMMA1002573, MAMMA1003150, NT2RM1000648, NT2RM1001115, NT2RM2000260,  
 NT2RM2000407, NT2RM2000422, NT2RM2000490, NT2RM2001499, NT2RM2001659, NT2RM2001930,  
 NT2RM4000820, NT2RM4000857, NT2RM4001810, NT2RM4001813, NT2RM4001987, NT2RM4002145,  
 50 NT2RM4002189, NT2RM4002251, NT2RM4002460, NT2RM4002558, NT2RP1000677, NT2RP1000782,  
 NT2RP1000856, NT2RP1001546, NT2RP2000056, NT2RP2000070, NT2RP2001295, NT2RP2001378,  
 NT2RP2001597, NT2RP2001991, NT2RP2002025, NT2RP2002078, NT2RP2002385, NT2RP2004587,  
 NT2RP2004732, NT2RP2005531, NT2RP3000207, NT2RP3000531, NT2RP3000825, NT2RP3001140,  
 NT2RP3002810, NT2RP3003672, NT2RP3003701, NT2RP3003716, NT2RP3003914, NT2RP3004148,  
 55 NT2RP4000212, NT2RP4000417, NT2RP4000724, NT2RP4000817, NT2RP4000925, NT2RP4001150,  
 NT2RP4001372, NT2RP4001730, NT2RP4001822, NT2RP4001823, NT2RP5003522, OVARC1000091,  
 OVARC1000288, OVARC1000682, OVARC1001055, OVARC1001506, OVARC1001713, OVARC1002127,  
 PLACE1000213, PLACE1000401, PLACE1002437, PLACE1002583,



PLACE1002722, PLACE1003045, PLACE1003238, PLACE1003258, PLACE1003493, PLACE1004197,  
 PLACE1004793, PLACE1005953, PLACE1005955, PLACE1006157, PLACE1006239, PLACE1006368,  
 PLACE1006534, PLACE1006754, PLACE1006956, PLACE1007416, PLACE1007632, PLACE1007649,  
 PLACE1008643, PLACE1009094, PLACE1009992, PLACE1010231, PLACE1010662, PLACE1011371,  
 5 PLACE2000034, PLACE2000373, PLACE2000398, PLACE2000399, PLACE2000438, PLACE2000458,  
 PLACE3000339, PLACE4000063, PLACE4000230, PLACE4000522, PLACE4000548, PLACE4000581,  
 THYRO1000327, THYRO1000756, THYRO1001287, Y79AA1001603, Y79AA1001874

**[0277]** The following 129 clones are categorized into signal transduction-associated proteins.

10 HEMBA1000303, HEMBA1000369, HEMBA1000608, HEMBA1000657, HEMBA1000919, HEMBA1001019,  
 HEMBA1001174, HEMBA1001822, HEMBA1001921, HEMBA1002139, HEMBA1002212, HEMBA1002341,  
 HEMBA1002417, HEMBA1002768, HEMBA1003250, HEMBA1003291, HEMBA1003645, HEMBA1004286,  
 HEMBA1005737, HEMBA1006130, HEMBA1006708, HEMBB1000083, HEMBB1000266, HEMBB1000632,  
 HEMBB1000781, HEMBB1000831, HEMBB1002193, MAMMA1000173, MAMMA1001038, MAMMA1001198,  
 MAMMA1002842, MAMMA1003057, NT2RM1000702, NT2RM1000772, NT2RM1001072, NT2RM2000030,  
 15 NT2RM2000469, NT2RM2000612, NT2RM2001221, NT2RM2001345, NT2RM2002128, NT2RM4000229,  
 NT2RM4000354, NT2RM4000611, NT2RM4000798, NT2RM4001411, NT2RM4001412, NT2RM4001629,  
 NT2RM4001758, NT2RM4002013, NT2RM4002527, NT2RP1000018, NT2RP1000701, NT2RP1001294,  
 NT2RP1001302, NT2RP2000668, NT2RP2001440, NT2RP2001560, NT2RP2002058, NT2RP2002193,  
 NT2RP2002408, NT2RP2002710, NT2RP2002929, NT2RP2003164, NT2RP2003912, NT2RP2004232,  
 20 NT2RP2004768, NT2RP2006071, NT2RP2006534, NT2RP3000759, NT2RP3000845, NT2RP3001646,  
 NT2RP3001857, NT2RP3001938, NT2RP3002004, NT2RP3002785, NT2RP3002909, NT2RP3002988,  
 NT2RP3003800, NT2RP3004189, NT2RP3004544, NT2RP4000147, NT2RP4000839, NT2RP4001122,  
 NT2RP4001148, NT2RP4001336, NT2RP4001375, NT2RP4001644, NT2RP4001725, NT2RP4001849,  
 NT2RP4001896, NT2RP4001927, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000437,  
 25 OVARC1000556, OVARC1000649, OVARC 1000945, OVARC1001200, OVARC1002182, PLACE1000977,  
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 PLACE1004302, PLACE1004937, PLACE1005243, PLACE1008000, PLACE1008244, PLACE1008650,  
 PLACE1009468, PLACE1009596, PLACE1009708, PLACE1009845, PLACE1010926, PLACE1011041,  
 PLACE2000164, PLACE2000371, PLACE3000145, PLACE3000350, THYRO1000072, THYRO1000748,  
 30 THYRO1001120, Y79AA1000328, Y79AA1002431

**[0278]** The following 309 clones are categorized into transcription -associated proteins.

HEMBA1000158, HEMBA1000201, HEMBA1000216, HEMBA1000555, HEMBA1000561, HEMBA1000851,  
 HEMBA1001077, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001635, HEMBA1001804,  
 HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1001869, HEMBA1002035, HEMBA1002092,  
 35 HEMBA1002177, HEMBA1002770, HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568,  
 HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003953, HEMBA1004097, HEMBA1004321,  
 HEMBA1004353, HEMBA1004389, HEMBA1004479, HEMBA1004758, HEMBA1004973, HEMBA1005219,  
 HEMBA1005359, HEMBA1005513, HEMBA1005528, HEMBA1005548, HEMBA1005558, HEMBA1005931,  
 HEMBA1006158, HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006347, HEMBA1006359,  
 40 HEMBA1006559, HEMBA1006941, HEMBB1000789, HEMBB1001011, HEMBB1001314, HEMBB1001482,  
 HEMBB1001673, HEMBB1001749, HEMBB1001839, HEMBB1001908, HEMBB1002134, HEMBB1002217,  
 HEMBB1002342, HEMBB1002607, MAMMA1000183, MAMMA1000388, MAMMA1001105, MAMMA1001222,  
 MAMMA1001260, MAMMA1001627, MAMMA1001633, MAMMA1001743, MAMMA1001820, MAMMA1001837,  
 MAMMA1002617, MAMMA1002650, MAMMA1002937, NT2RM1000055, NT2RM1000086, NT2RM1000746,  
 45 NT2RM1000885, NT2RM1000894, NT2RM1001092, NT2RM2000013, NT2RM2000452, NT2RM2000735,  
 NT2RM2000740, NT2RM2001035, NT2RM2001105, NT2RM2001575, NT2RM2001670, NT2RM2001716,  
 NT2RM2001771, NT2RM2002091, NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202,  
 NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000734,  
 NT2RM4000741, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001200,  
 50 NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858,  
 NT2RM4001979, NT2RM4002066, NT2RP1000086, NT2RP1000111, NT2RP1000574, NT2RP1000902,  
 NT2RP1001013, NT2RP2000008, NT2RP2000126, NT2RP2000297, NT2RP2000420, NT2RP2001174,  
 NT2RP2001233, NT2RP2001756, NT2RP2001869, NT2RP2002046, NT2RP2002252, NT2RP2002270,  
 NT2RP2002464, NT2RP2002503, NT2RP2002520, NT2RP2002591, NT2RP2002880, NT2RP2002939,  
 55 NT2RP2002993, NT2RP2003243, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522,  
 NT2RP2003564, NT2RP2003714, NT2RP2004013, NT2RP2004066, NT2RP2004187, NT2RP2004920,  
 NT2RP2004961, NT2RP2005003, NT2RP2005139, NT2RP2005325, NT2RP2005496, NT2RP2005701,  
 NT2RP2005722, NT2RP2005776, NT2RP2005942, NT2RP2006238, NT2RP2006436, NT2RP3000050,



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	NT2RP3000320,	NT2RP3000512,	NT2RP3000527,	NT2RP3000590,	NT2RP3000603,	NT2RP3000605,
	NT2RP3000632,	NT2RP3001057,	NT2RP3001107,	NT2RP3001111,	NT2RP3001120,	NT2RP3001150,
	NT2RP3001268,	NT2RP3001338,	NT2RP3001398,	NT2RP3001527,	NT2RP3001688,	NT2RP3001855,
	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003133,	NT2RP3003193,	NT2RP3003251,
5	NT2RP3003313,	NT2RP3003327,	NT2RP3003555,	NT2RP3004016,	NT2RP3004125,	NT2RP3004242,
	NT2RP3004428,	NT2RP3004498,	NT2RP3004566,	NT2RP3004617,	NT2RP4000210,	NT2RP4000398,
	NT2RP4000455,	NT2RP4000648,	NT2RP4000837,	NT2RP4000865,	NT2RP4000997,	NT2RP4001029,
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10	NT2RP4002078,	NT2RP4002081,	NT2RP5003461,	OVARC1000151,	OVARC1000241,	OVARC1000479,
	OVARC1001271,	OVARC1001417,	OVARC1001436,	PLACE1000133,	PLACE1000583,	PLACE1000706,
	PLACE1000786,	PLACE1000979,	PLACE1001118,	PLACE1001238,	PLACE1001294,	PLACE1001304,
	PLACE1001383,	PLACE1001602,	PLACE1001632,	PLACE1002171,	PLACE1002438,	PLACE1002450,
	PLACE1002532,	PLACE1002775,	PLACE1002834,	PLACE1003302,	PLACE1003605,	PLACE1003738,
15	PLACE1003885,	PLACE1004471,	PLACE1005584,	PLACE1005803,	PLACE1005966,	PLACE1006167,
	PLACE1006318,	PLACE1006438,	PLACE1006482,	PLACE1007239,	PLACE1007346,	PLACE1007488,
	PLACE1007547,	PLACE1007598,	PLACE1007955,	PLACE1008132,	PLACE1008201,	PLACE1009099,
	PLACE1009246,	PLACE1009308,	PLACE1009398,	PLACE1009798,	PLACE1010134,	PLACE1010702,
	PLACE1010771,	PLACE1010870,	PLACE1011160,	PLACE1011433,	PLACE1011576,	PLACE3000009,
20	PLACE3000169,	PLACE3000254,	PLACE4000128,	PLACE4000156,	PLACE4000192,	PLACE4000211,
	PLACE4000261,	PLACE4000450,	PLACE4000489,	THYRO1000085,	THYRO1000121,	THYRO1000242,
	THYRO1000488,	THYRO1000501,	THYRO1000569,	THYRO 1001100,	THYRO1001189,	THYRO1001809,
	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,	Y79AA1000342,	Y79AA1000627,	Y79AA1000705,
	Y79AA1001299,	Y79AA1001312,	Y79AA1001391,	Y79AA1001533,	Y79AA1001613,	Y79AA1001866,
25	Y79AA1002103, Y79AA1002229, Y79AA1002433, Y79AA1002472, Y79AA1002482,					
	<b>[0279]</b> The following 392 clones are categorized into disease-associated proteins.					
	HEMBA1000020,	HEMBA1000216,	HEMBA1000304,	HEMBA1000561,	HEMBA1000569,	HEMBA1000910,
	HEMBA1001043,	HEMBA1001059,	HEMBA1001071,	HEMBA1001088,	HEMBA1001569,	HEMBA1001661,
	HEMBA1001672,	HEMBA1001819,	HEMBA1001921,	HEMBA1002267,	HEMBA1002419,	HEMBA1002469,
30	HEMBA1002547,	HEMBA1002555,	HEMBA1002810,	HEMBA1002939,	HEMBA1002997,	HEMBA1003148,
	HEMBA1003369,	HEMBA1003417,	HEMBA1003418,	HEMBA1003433,	HEMBA1003538,	HEMBA1003555,
	HEMBA1003568,	HEMBA1003569,	HEMBA1003581,	HEMBA1004168,	HEMBA1004202,	HEMBA1004248,
	HEMBA1004275,	HEMBA1004321,	HEMBA1004353,	HEMBA1004356,	HEMBA1004479,	HEMBA1004509,
	HEMBA1004669,	HEMBA1005009,	HEMBA1005338,	HEMBA1005367,	HEMBA1005423,	HEMBA1005528,
35	HEMBA1005581,	HEMBA1005621,	HEMBA1005699,	HEMBA1006507,	HEMBA1006650,	HEMBA1006652,
	HEMBA1006737,	HEMBA1006807,	HEMBA1006877,	HEMBA1007121,	HEMBA1007243,	HEMBA1007243,
	HEMBA100693,	HEMBA1006927,	HEMBA1006985,	HEMBA1007068,	HEMBA1007282,	HEMBA1007339,
	HEMBA1001482,	HEMBA1001564,	HEMBA1001802,	HEMBA1001905,	HEMBA1001908,	HEMBA1002217,
	HEMBA1002477,	MAMMA1000388,	MAMMA1000731,	MAMMA1001305,	MAMMA1001633,	MAMMA1001868,
40	MAMMA1002170,	MAMMA1002198,	MAMMA1002268,	MAMMA1002485,	MAMMA1002530,	MAMMA1002858,
	MAMMA1002869,	MAMMA1002881,	MAMMA1003047,	MAMMA1003146,	MAMMA1003166,	NT2RM1000001,
	NT2RM1000153,	NT2RM1000252,	NT2RM1000555,	NT2RM1000770,	NT2RM1000826,	NT2RM1000850,
	NT2RM1001003,	NT2RM1001092,	NT2RM1001102,	NT2RM2000191,		
	NT2RM2000363,	NT2RM2000594,	NT2RM2000624,	NT2RM2000714,	NT2RM2000821,	NT2RM2001035,
45	NT2RM2001575,	NT2RM2001652,	NT2RM2001664,	NT2RM2001668,	NT2RM2001698,	NT2RM2001803,
	NT2RM2001839,	NT2RM4000155,	NT2RM4000471,	NT2RM4000486,	NT2RM4000657,	NT2RM4000751,
	NT2RM4000996,	NT2RM4001629,	NT2RM4001810,	NT2RM4001819,	NT2RM4001865,	NT2RM4001876,
	NT2RM4001940,	NT2RM4002066,	NT2RM4002093,	NT2RM4002146,	NT2RM4002161,	NT2RM4002323,
	NT2RM4002558,	NT2RM4002571,	NT2RP1000086,	NT2RP1000574,	NT2RP1000738,	NT2RP1000825,
50	NT2RP1000833,	NT2RP1000959,	NT2RP1000966,	NT2RP1001013,	NT2RP1001185,	NT2RP1001482,
	NT2RP1001665,	NT2RP2000070,	NT2RP2000147,	NT2RP2000224,	NT2RP2000248,	NT2RP2000297,
	NT2RP2000310,	NT2RP2000414,	NT2RP2000420,	NT2RP2000523,	NT2RP2000809,	NT2RP2000812,
	NT2RP2001233,	NT2RP2001327,	NT2RP2001378,	NT2RP2001394,	NT2RP2001397,	NT2RP2001460,
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55	NT2RP2002124,	NT2RP2002325,	NT2RP2002503,	NT2RP2002959,	NT2RP2003000,	NT2RP2003157,
	NT2RP2003164,	NT2RP2003228,	NT2RP2003295,	NT2RP2003517,	NT2RP2003564,	NT2RP2003604,
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 5 NT2RP3000875, NT2RP3001057, NT2RP3001081, NT2RP3001216, NT2RP3001307, NT2RP3001338,  
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 10 NT2RP3004209, NT2RP3004258, NT2RP3004490, NT2RP3004534, NT2RP3004569, NT2RP3004572,  
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 NT2RP4001407, NT2RP4001433, NT2RP4001483, NT2RP4001575, NT2RP4001760, NT2RP4001861,  
 NT2RP4002078, NT2RP4002791, OVARC1000014, OVARC1000139, OVARC1000520, OVARC1000722,  
 15 OVARC1000771, OVARC1000834, OVARC1001051, OVARC1001113, OVARC1001244, OVARC1001372,  
 OVARC1001417, OVARC1001496, OVARC1001506, OVARC1001577, OVARC1001726, OVARC1001766,  
 OVARC1001809, OVARC1002165, PLACE1000133, PLACE1000383, PLACE1000420, PLACE1000583,  
 PLACE1000588, PLACE1001171, PLACE1001387, PLACE1001602, PLACE1002046, PLACE1002140,  
 PLACE1002437, PLACE1002474, PLACE1002685, PLACE1002782, PLACE1002834, PLACE1002908,  
 20 PLACE1003045, PLACE1003302, PLACE1003353, PLACE1003366, PLACE1003493, PLACE1003669,  
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 25 PLACE1008177, PLACE1008356, PLACE1008402, PLACE1008696, PLACE1009027, PLACE1009113,  
 PLACE1009158, PLACE1009444, PLACE1009524, PLACE1010529, PLACE1010870, PLACE1010896,  
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 PLACE2000399, PLACE2000438, PLACE2000458, PLACE3000242, PLACE4000009, PLACE4000014,  
 PLACE4000156, PLACE4000369, SKNMC1000046, SKNMC1000050, THYRO1000034, THYRO1000327,  
 30 THYRO1000343, THYRO1000358, THYRO1000501, THYRO1000662, THYRO1000684, THYRO1000748,  
 THYRO1000934, THYRO1001120, THYRO1001189, THYRO1001204, THYRO1001458, THYRO1001617,  
 THYRO1001671, Y79AA1000346, Y79AA1000469, Y79AA1000560, Y79AA1000734, Y79AA1000782,  
 Y79AA1001391, Y79AA1001548, Y79AA1001594, Y79AA1001711, Y79AA1001874, Y79AA1002204,  
 Y79AA1002210, Y79AA1002258, Y79AA1002472, Y79AA1002482,  
 35 **[0280]** Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the fol-  
 lowing 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian  
 Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.  
 (The corresponding OMIM numbers are parenthetically indicated following the clone names.)  
 HEMBB1000985(147485), HEMBB1001068(603142), HEMBB1001282(182900), HEMBB1001339(300080),  
 40 HEMBB1001482(603971), HEMBB1001564(603931), HEMBB1001802(125660), HEMBB1001905(190370),  
 HEMBB1001908(601408), HEMBB1002217(603971), HEMBB1002477(604439), MAMMA1000388(604865),  
 MAMMA1000731(602118), MAMMA1001305(602732), MAMMA1001633(600834), MAMMA1001868(190370),  
 MAMMA1002170(603624), MAMMA1002198(600538), MAMMA1002268(603730), MAMMA1002485(603665),  
 MAMMA1002530(603602), MAMMA1002858(601064), MAMMA1002869(602567), MAMMA1002881(602692),  
 45 MAMMA1003047(603566), MAMMA1003146(603094), MAMMA1003166(604061), NT2RM1000001(601169),  
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 NT2RM1000826(191510), NT2RM1000850(182900), NT2RM1001003(604785), NT2RM1001092(603971),  
 NT2RM1001102(604533), NT2RM2000191(602973), NT2RM2000363(151410), NT2RM2000594(602900),  
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 50 NT2RM2001575(109092), NT2RM2001652(604141), NT2RM2001664(603722), NT2RM2001668(602952),  
 NT2RM2001698(604327), NT2RM2001803(603722), NT2RM2001839(603420), NT2RM4000155(187790),  
 NT2RM4000471(603485), NT2RM4000486(168730), NT2RM4000657(602142), NT2RM4000751(602277),  
 NT2RM4000996(603971), NT2RM4001629(601114), NT2RM4001810(155760), NT2RM4001819(176873),  
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 55 NT2RM4002146(602603), NT2RM4002161(254780), NT2RM4002558(604194), NT2RM4002571(602274),  
 NT2RP1000086(602219), NT2RP1000574(601740), NT2RP1000825(602732), NT2RP1000833(602973),  
 NT2RP1000959(180510), NT2RP1000966(164035), NT2RP1001013(194558), NT2RP1001185(243500),  
 NT2RP1001482(600586), NT2RP1001665(114180), NT2RP2000070(600976), NT2RP2000147(603535),

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	NT2RP2000248(603367);	NT2RP2000297(602277),	NT2RP2000310(239500),	NT2RP2000414(601037),
	NT2RP2000420(600834),	NT2RP2000523(600130),	NT2RP2000809(603885),	NT2RP2000812(160777),
	NT2RP2001233(603971),	NT2RP2001327(191161),	NT2RP2001378(158370),	NT2RP2001394(300208),
	NT2RP2001397(602755),	NT2RP2001460(190370),	NT2RP2001520(603667),	NT2RP2001536(600675),
5	NT2RP2001876(601833),	NT2RP2001898(147264),	NT2RP2002025(601581),	NT2RP2002058(604737),
	NT2RP2002124(603486),	NT2RP2002325(603866),	NT2RP2002503(601781),	NT2RP2002959(602962),
	NT2RP2003000(191161),	NT2RP2003157(601940),	NT2RP2003164(604746),	NT2RP2003228(602638),
	NT2RP2003295(603494),	NT2RP2003517(190040),	NT2RP2003564(109092),	NT2RP2003604(604785),
	NT2RP2003714(603971),	NT2RP2003737(602962),	NT2RP2003952(602675),	NT2RP2004013(602542),
10	NT2RP2004170(300196),	NT2RP2004587(162250),	NT2RP2004732(162250),	NT2RP2004933(603289),
	NT2RP2005003(109092),	NT2RP2005144(604730),	NT2RP2005239(603485),	NT2RP2005276(602371),
	NT2RP2005288(603524),	NT2RP2005315(604039),	NT2RP2005325(603759),	NT2RP2005336(190370),
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	NT2RP2005525(602655),	NT2RP2005719(601178),	NT2RP2006043(601940),	NT2RP2006071(604299),
15	NT2RP2006219(601279),	NT2RP2006312(603111),	NT2RP2006456(604619),	NT2RP3000050(603971),
	NT2RP3000068(182530),	NT2RP3000085(300032),	NT2RP3000299(602941),	NT2RP3000403(604981),
	NT2RP3000596(190370),	NT2RP3000739(125370),	NT2RP3000753(162230),	NT2RP3001057(603971),
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	NT2RP3001428(189940),	NT2RP3001723(604569),	NT2RP3001855(602100),	NT2RP3001898(604561),
20	NT2RP3001969(190370),	NT2RP3002056(180201),	NT2RP3002062(603885),	NT2RP3002151(139259),
	NT2RP3002351(604887),	NT2RP3002399(602638),	NT2RP3002953(604967),	NT2RP3002988(603258),
	NT2RP3003251(109092),	NT2RP3003282(602378),	NT2RP3003313(603810),	NT2RP3003409(604533),
	NT2RP3003672(313470),	NT2RP3003831(604051),	NT2RP3004016(601742),	NT2RP3004078(142765),
	NT2RP3004209(125255),	NT2RP3004258(604347),	NT2RP3004490(603328),	NT2RP3004534(600586),
25	NT2RP3004569(106410),	NT2RP3004572(604912),	NT2RP4000109(603745),	NT2RP4000367(603722),
	NT2RP4000376(603873),	NT2RP4000449(604479),	NT2RP4000855(602675),	NT2RP4000879(314370),
	NT2RP4000925(600245),	NT2RP4001086(162230),	NT2RP4001126(190370),	NT2RP4001150(601581),
	NT2RP4001213(602277),	NT2RP4001276(190370),	NT2RP4001407(190370),	NT2RP4001433(602277),
	NT2RP4001483(203740),	NT2RP4001575(603443),	NT2RP4001760(305400),	NT2RP4001861(190370),
30	NT2RP4002078(603971),	NT2RP4002791(189940),	OVARC1000014(603371),	OVARC1000139(603486),
	OVARC1000520(604126),	OVARC1000722(604014),	OVARC1000771(179509),	OVARC1001051(600051),
	OVARC1001113(602121),	OVARC1001244(601540),	OVARC1001372(603145),	OVARC1001417(300182),
	OVARC1001496(602619),	OVARC1001506(601313),	OVARC1001577(603269),	OVARC1001726(300103),
	OVARC1001766(603910),	OVARC1001809(603730),	PLACE1000133(602542),	PLACE1000383(300171),
35	PLACE1000420(600312),	PLACE1000583(194558),	PLACE1000588(600411),	PLACE1001171(310400),
	PLACE1001387(600206),	PLACE1001602(604913),	PLACE1002046(151625),	PLACE1002140(603748),
	PLACE1002437(600046),	PLACE1002474(602108),	PLACE1002685(604515),	PLACE1002782(602095),
	PLACE1002834(194558),	PLACE1002908(604327),	PLACE1003045(173910),	PLACE1003302(194558),
	PLACE1003353(604704),	PLACE1003366(603681),	PLACE1003493(601456),	PLACE1003669(190370),
40	PLACE1003704(601940),	PLACE1003903(123860),	PLACE1003968(602742),	PLACE1004183(604701),
	PLACE1004197(601610),	PLACE1004277(603493),	PLACE1004316(604261),	PLACE1004358(603272),
	PLACE1004471(194558),	PLACE1004506(603450),	PLACE1004510(604912),	PLACE1004674(601057),
	PLACE1004777(118423),	PLACE1004814(601940),	PLACE1005494(603652),	PLACE1006040(603061),
	PLACE1006170(601026),	PLACE1006438(600834),	PLACE1006615(603910),	PLACE1007140(190370),
45	PLACE1007239(604784),	PLACE1007257(300108),	PLACE1007511(148020),	PLACE1007598(602277),
	PLACE1008177(190370),	PLACE1008356(604039),	PLACE1008402(603344),	PLACE1008696(602141),
	PLACE1009027(300121),	PLACE1009113(600675),	PLACE1009158(604140),	PLACE1009444(600286),
	PLACE1009524(602488),	PLACE1010529(604834),	PLACE1010870(603971),	PLACE1010896(160776),
	PLACE1011635(604058),	PLACE1011858(603882),	PLACE1011922(160776),	PLACE2000015(600051),
50	PLACE2000072(603430),	PLACE2000216(182790),	PLACE2000399(313470),	PLACE2000438(602273),
	PLACE2000458(600976),	PLACE3000242(300132),	PLACE4000009(160776),	PLACE4000014(300032),
	PLACE4000156(603971),	PLACE4000369(603808),	SKNMC1000046(603144),	SKNMC1000050(114230),
	THYRO1000034(190370),	THYRO1000327(603243),	THYRO1000343(125370),	THYRO1000358(604188),
	THYRO1000501(109092),	THYRO1000662(278750),	THYRO1000684(603885),	THYRO1000748(300023),
55	THYRO1000934(179035),	THYRO1001120(602582),	THYRO1001189(603971),	THYRO1001204(603169),
	THYRO1001458(160776),	THYRO1001617(602744),	THYRO1001671(603281),	Y79AA1000346(604355),
	Y79AA1000469(602434),	Y79AA1000560(601026),	Y79AA1000734(603867),	Y79AA1000782(600417),
	Y79AA1001391(142959),	Y79AA1001548(600286),	Y79AA1001594(600936),	Y79AA1001711(600063),

Y79AA1001874(600315), Y79AA1002204(605033), Y79AA1002210(191161), Y79AA1002472(603971),  
Y79AA1002482(603971),

**[0281]** The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

	HEMBA1000012,	HEMBA1000129,	HEMBA1000141,	HEMBA1000150,	HEMBA1000542,	HEMBA1000852,
5	HEMBA1001019,	HEMBA1001257,	HEMBA1001526,	HEMBA1001620,	HEMBA1001866,	HEMBA1001896,
	HEMBA1002212,	HEMBA1002513,	HEMBA1002746,	HEMBA1002973,	HEMBA1003046,	HEMBA1003136,
	HEMBA1003179,	HEMBA1003250,	HEMBA1003291,	HEMBA1003408,	HEMBA1003538,	HEMBA1003679,
	HEMBA1003680,	HEMBA1004199,	HEMBA1004227,	HEMBA1004408,	HEMBA1004509,	HEMBA1004734,
	HEMBA1004768,	HEMBA1005394,	HEMBA1005513,	HEMBA1005737,	HEMBA1005815,	HEMBA1006031,
10	HEMBA1006272,	HEMBA1006278,	HEMBA1006291,	HEMBA1006309,	HEMBA1006347,	HEMBA1006485,
	HEMBA1006521,	HEMBA1006624,	HEMBA1006885,	HEMBA1006976,	HEMBA1007121,	HEMBA1007224,
	HEMBA1007243,	HEMBA1007300,	HEMBB1000083,	HEMBB1000217,	HEMBB1000915,	HEMBB1000947,
	HEMBB1001137,	HEMBB1001346,	HEMBB1001429,	HEMBB1001443,	HEMBB1001915,	HEMBB1001950,
	HEMBB1002042,	MAMMA1000020,	MAMMA1000085,	MAMMA1000672,	MAMMA1000713,	MAMMA1000841,
15	MAMMA1000897,	MAMMA1001008,	MAMMA1001038,	MAMMA1001059,	MAMMA1001476,	MAMMA1001501,
	MAMMA1002268,	MAMMA1002470,	MAMMA1002530,	MAMMA1002573,	MAMMA1002619,	MAMMA1002655,
	MAMMA1002671,	MAMMA1003013,	MAMMA1003035,	NT2RM1000039,	NT2RM1000132,	NT2RM1000153,
	NT2RM1000256,	NT2RM1000280,	NT2RM1000377,	NT2RM1000553,	NT2RM1000648,	NT2RM1000702,
	NT2RM1000894,	NT2RM1001072,	NT2RM1001115,	NT2RM2000013,	NT2RM2000092,	NT2RM2000322,
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	NT2RM2000951,	NT2RM2001238,	NT2RM2001547,	NT2RM2001632,	NT2RM2001664,	NT2RM2001698,
	NT2RM2001700,	NT2RM2001730,	NT2RM2001782,	NT2RM2001803,	NT2RM2001886,	NT2RM2001935,
	NT2RM2001997,	NT2RM2002030,	NT2RM2002128,	NT2RM4000024,	NT2RM4000155,	NT2RM4000344,
	NT2RM4000471,	NT2RM4000616,	NT2RM4000657,	NT2RM4000712,	NT2RM4000820,	NT2RM4001313,
25	NT2RM4001316,	NT2RM4001444,	NT2RM4001592,	NT2RM4001758,	NT2RM4001819,	NT2RM4001880,
	NT2RM4002062,	NT2RM4002063,	NT2RM4002189,	NT2RM4002213,	NT2RM4002251,	NT2RM4002409,
	NT2RM4002532,	NT2RM4002623,	NT2RP1000376,	NT2RP1000443,	NT2RP1000522,	NT2RP1000834,
	NT2RP1000947,	NT2RP1001079,	NT2RP1001185,	NT2RP1001253,	NT2RP1001361,	NT2RP1001543,
	NT2RP2000056,	NT2RP2000114,	NT2RP2000183,	NT2RP2000248,	NT2RP2000329,	NT2RP2000422,
30	NT2RP2000448,	NT2RP2000668,	NT2RP2000710,	NT2RP2000816,	NT2RP2001070,	NT2RP2001392,
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	NT2RP2002256,	NT2RP2002609,	NT2RP2002618,	NT2RP2002959,	NT2RP2002993,	NT2RP2003230,
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	NT2RP3000742,	NT2RP3000845,	NT2RP3000875,	NT2RP3000917,	NT2RP3001055,	NT2RP3001221,
	NT2RP3001495,	NT2RP3001898,	NT2RP3001938,	NT2RP3002303,	NT2RP3002351,	NT2RP3002501,
	NT2RP3002602,	NT2RP3002628,	NT2RP3002663,	NT2RP3003301,	NT2RP3003385,	NT2RP3003490,
	NT2RP3003659,	NT2RP3003825,	NT2RP3003831,	NT2RP3003846,	NT2RP3003914,	NT2RP3004148,
45	NT2RP3004209,	NT2RP3004378,	NT2RP3004669,	NT2RP3004670,	NT2RP4000259,	NT2RP4000312,
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	NT2RP4000879,	NT2RP4000927,	NT2RP4000973,	NT2RP4000997,	NT2RP4001041,	NT2RP4001079,
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50	NT2RP5003500,	NT2RP5003522,	OVARC1000013,	OVARC1000060,	OVARC1000139,	OVARC1000288,
	OVARC1000309,	OVARC1000473,	OVARC1000556,	OVARC1000682,	OVARC1000722,	OVARC1000751,
	OVARC1000885,	OVARC1000915,	OVARC1001107,	OVARC1001713,	OVARC1001762,	OVARC1001809,
	OVARC1001942,	OVARC1002156,	OVARC1002165,	PLACE1000007,	PLACE1000142,	PLACE1000185,
	PLACE1000213,	PLACE1000383,	PLACE1000420,	PLACE1000547,	PLACE1000653,	PLACE1000755,
55	PLACE1001054,	PLACE1001062,	PLACE1001672,	PLACE1001692,	PLACE1001748,	PLACE1001781,
	PLACE1001817,	PLACE1001869,	PLACE1001989,	PLACE1002073,	PLACE1002598,	PLACE1002908,
	PLACE1002991,	PLACE1003174,	PLACE1003176,	PLACE1003709,	PLACE1003885,	PLACE1003888,
	PLACE1003903,	PLACE1003915,	PLACE1004270,	PLACE1004428,	PLACE1004437,	PLACE1004751,

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 10 PLACE3000147, PLACE3000339, PLACE3000350, PLACE4000063, PLACE4000100, PLACE4000401,  
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 THYRO1000605, THYRO1000662, THYRO1000756, THYRO1000852, THYRO1000926, THYRO 1000934,  
 THYRO1000951, THYRO 1000983, THYRO1001003, THYRO1001287, THYRO1001374, THYRO1001406,  
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 15 Y79AA1001394, Y79AA1001493, Y79AA1001548, Y79AA1001581, Y79AA1001603, Y79AA1001827,  
 Y79AA1002027, Y79AA1002209, Y79AA1002211, Y79AA1002361, Y79AA1002416,

**[0282]** The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.

HEMBA1000012, HEMBA1000129, HEMBA1000185, HEMBA1000491, HEMBA1000531, HEMBA1001019,  
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 20 HEMBA1002212, HEMBA1002876, HEMBA1002997, HEMBA1003250, HEMBA1003291, HEMBA1003369,  
 HEMBA1003555, HEMBA1003560, HEMBA1004131, HEMBA1004199, HEMBA1004202, HEMBA1004354,  
 HEMBA1004697, HEMBA1005047, HEMBA1005595, HEMBA1007018, HEMBA1007151, HEMBB1000083,  
 HEMBB1000226, HEMBB1000264, HEMBB1000632, HEMBB1000725, HEMBB1001294, HEMBB1002193,  
 MAMMA1000085, MAMMA1000612, MAMMA1000731, MAMMA1000738, MAMMA1001038, MAMMA1001735,  
 25 MAMMA1001768, MAMMA1003127, NT2RM1000187, NT2RM1000388, NT2RM1000702, NT2RM1000772,  
 NT2RM1000924, NT2RM2000469, NT2RM2000577, NT2RM2000740, NT2RM2001100, NT2RM2001201,  
 NT2RM2001345, NT2RM2001823, NT2RM2002128, NT2RM4000155, NT2RM4000191, NT2RM4000356,  
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 30 NT2RM4002062, NT2RM4002174, NT2RM4002205, NT2RM4002527, NT2RM4002594, NT2RM4002623,  
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 NT2RP4001592, NT2RP4001634, NT2RP4001644, NT2RP4001656, NT2RP4001896, NT2RP4002047,  
 NT2RP4002058, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000304, OVARC1000556,  
 45 OVARC1000771, OVARC1000800, OVARC1001068, OVARC1002138, PLACE1000040, PLACE1000588,  
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 PLACE1003521, PLACE1003915, PLACE1004902, PLACE1005243, PLACE1005305, PLACE1005549,  
 PLACE1005739, PLACE1005921, PLACE1006119, PLACE1006196, PLACE1006552, PLACE1006956,  
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 PLACE2000404, PLACE2000427, PLACE3000350, PLACE4000009, PLACE4000014, PLACE4000326,  
 SKNMC1000013, THYRO1000072, THYRO1001458, Y79AA1000833, Y79AA1000962, Y79AA1001394,  
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**[0283]** The following 320 clones presumably belong to nuclear proteins.

HEMBA1000005, HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1001088,  
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 HEMBA1001824, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002241, HEMBA1002495,

HEMBA1002569, HEMBA1002935, HEMBA1002951, HEMBA1002999, HEMBA1003408, HEMBA1003545,  
 HEMBA1003662, HEMBA1003684, HEMBA1003690, HEMBA1003760, HEMBA1004203, HEMBA1004321,  
 HEMBA1004353, HEMBA1004479, HEMBA1004973, HEMBA1005219, HEMBA1005359, HEMBA1005558,  
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 5 HEMBB1000226, HEMBB1000789, HEMBB1001011, HEMBB1001056, HEMBB1001242, HEMBB1001482,  
 HEMBB1001915, HEMBB1002134, HEMBB1002217, MAMMA1000183, MAMMA1000731, MAMMA1001105,  
 MAMMA1001222, MAMMA1001260, MAMMA1001633, MAMMA1001743, MAMMA1001837, MAMMA1002617,  
 MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000187, NT2RM1000666,  
 NT2RM1000885, NT2RM1000894, NT2RM1001059, NT2RM1001092, NT2RM2000013, NT2RM2000588,  
 10 NT2RM2000624, NT2RM2000735, NT2RM2000740, NT2RM2001105, NT2RM2001635, NT2RM2001670,  
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 NT2RM2002091, NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202, NT2RM4000215,  
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 NT2RP1000035, NT2RP1000111, NT2RP1000493, NT2RP1000574, NT2RP1000630, NT2RP1000902,  
 NT2RP1000915, NT2RP1000958, NT2RP1000966, NT2RP1001013, NT2RP1001177, NT2RP2000008,  
 NT2RP2000076, NT2RP2000126, NT2RP2000153, NT2RP2000161, NT2RP2000248, NT2RP2000258,  
 NT2RP2000297, NT2RP2000420, NT2RP2000931, NT2RP2001233, NT2RP2001420, NT2RP2001756,  
 20 NT2RP2001869, NT2RP2002079, NT2RP2002270, NT2RP2002503, NT2RP2002591, NT2RP2002880,  
 NT2RP2002939, NT2RP2002993, NT2RP2003137, NT2RP2003157, NT2RP2003277, NT2RP2003286,  
 NT2RP2003308, NT2RP2003347, NT2RP2003714, NT2RP2003912, NT2RP2004013, NT2RP2004187,  
 NT2RP2004689, NT2RP2004920, NT2RP2005393, NT2RP2005436, NT2RP2005496, NT2RP2005539,  
 NT2RP2005701, NT2RP2005767, NT2RP2005776, NT2RP2005933, NT2RP2005942, NT2RP2006043,  
 25 NT2RP2006436, NT2RP3000031, NT2RP3000050, NT2RP3000397, NT2RP3000512, NT2RP3000527,  
 NT2RP3000590, NT2RP3000603, NT2RP3000632, NT2RP3000917, NT2RP3001057, NT2RP3001107,  
 NT2RP3001120, NT2RP3001253, NT2RP3001338, NT2RP3001384, NT2RP3001398, NT2RP3001427,  
 NT2RP3001428, NT2RP3001472, NT2RP3001646, NT2RP3001671, NT2RP3001792, NT2RP3001855,  
 NT2RP3002056, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003193, NT2RP3003212,  
 30 NT2RP3003555, NT2RP3004016, NT2RP3004206, NT2RP3004424, NT2RP3004428, NT2RP3004566,  
 NT2RP3004617, NT2RP4000078, NT2RP4000111, NT2RP4000210, NT2RP4000398, NT2RP4000481,  
 NT2RP4000518, NT2RP4000997, NT2RP4001148, NT2RP4001206, NT2RP4001213, NT2RP4001433,  
 NT2RP4001568, NT2RP4001638, NT2RP4001696, NT2RP4001753, NT2RP4001938, NT2RP4002058,  
 NT2RP4002078, NT2RP4002081, NT2RP4002791, OVARC1000006, OVARC1000087, OVARC1000091,  
 35 OVARC1000241, OVARC1000326, OVARC1000556, OVARC1000846, OVARC1001038, OVARC1001180,  
 OVARC1001232, OVARC1001271, OVARC1001306, OVARC1001436, OVARC1002112, PLACE1000133,  
 PLACE1000184, PLACE1000406, PLACE1000583, PLACE1000596, PLACE1000979, PLACE1001118,  
 PLACE1001383, PLACE1001632, PLACE1002171, PLACE1002433, PLACE1002438, PLACE1002532,  
 PLACE1002775, PLACE1002816, PLACE1002834, PLACE1003100, PLACE1003190, PLACE1003302,  
 40 PLACE1003519, PLACE1003521, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885,  
 PLACE1003923, PLACE1004302, PLACE1004471, PLACE1004564, PLACE1004814, PLACE1004902,  
 PLACE1005287, PLACE1005876, PLACE1005966, PLACE1006167, PLACE1006438, PLACE1006482,  
 PLACE1006829, PLACE1006878, PLACE1006917, PLACE1007014, PLACE1007547, PLACE1007598,  
 PLACE1007688, PLACE1007969, PLACE1008044, PLACE1008132, PLACE1008603, PLACE1009099,  
 45 PLACE1009130, PLACE1009308, PLACE1009398, PLACE1010134, PLACE1010194, PLACE1010702,  
 PLACE1010720, PLACE1010870, PLACE1011056, PLACE1011433, PLACE1011664, PLACE2000014,  
 PLACE2000427, PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192,  
 PLACE4000261, PLACE4000326, PLACE4000489, SKNMC1000011, THYRO1000085, THYRO1000242,  
 THYRO1000585, THYRO1001100, THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000214,  
 50 Y79AA1000231, Y79AA1000589, Y79AA1000752, Y79AA1001391, Y79AA1001613, Y79AA1001705,  
 Y79AA1001963, Y79AA1002431, Y79AA1002472, Y79AA1002482

**[0284]** The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1000851, HEMBA1001088,  
 HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001804, HEMBA1001809, HEMBA1001819,  
 55 HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002935, HEMBA1003408, HEMBA1003545,  
 HEMBA1003568, HEMBA1003591, HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003783,  
 HEMBA1003805, HEMBA1003953, HEMBA1004321, HEMBA1004354, HEMBA1004389, HEMBA1004479,  
 HEMBA1004669, HEMBA1004847, HEMBA1004973, HEMBA1005202, HEMBA1005359, HEMBA1005931,

HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006652, HEMBA1007087,  
 HEMBA1007194, HEMBB1000264, HEMBB1000789, HEMBB1001011, HEMBB1001482, HEMBB1001736,  
 HEMBB1001749, HEMBB1001839, HEMBB1002217, MAMMA1000183, MAMMA1000284, MAMMA1000731,  
 MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001743, MAMMA1001837, MAMMA1002385,  
 5 MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000539,  
 NT2RM1000555, NT2RM1000666, NT2RM1000691, NT2RM1000826, NT2RM1000885, NT2RM1001059,  
 NT2RM1001092, NT2RM2000371, NT2RM2000624, NT2RM2000735, NT2RM2001105, NT2RM2001424,  
 NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989,  
 NT2RM2002004, NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104,  
 10 NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595, NT2RM4000733,  
 NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140,  
 NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823,  
 NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979, NT2RM4002093, NT2RM4002109,  
 NT2RP1000470, NT2RP1000493, NT2RP1000574, NT2RP1000902, NT2RP1000966, NT2RP1001013,  
 15 NT2RP1001073, NT2RP1001080, NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297,  
 NT2RP2001127, NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869,  
 NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939, NT2RP2003157,  
 NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522, NT2RP2003564, NT2RP2003714,  
 NT2RP2004187, NT2RP2004568, NT2RP2004920, NT2RP2005003, NT2RP2005139, NT2RP2005168,  
 20 NT2RP2005436, NT2RP2005496, NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942,  
 NT2RP2006043, NT2RP2006436, NT2RP2006464, NT2RP3000050, NT2RP3000512, NT2RP3000527,  
 NT2RP3000562, NT2RP3000590, NT2RP3000603, NT2RP3000624, NT2RP3000632, NT2RP3000994,  
 NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001150, NT2RP3001155, NT2RP3001338,  
 NT2RP3001398, NT2RP3001472, NT2RP3001672, NT2RP3001688, NT2RP3001724, NT2RP3001792,  
 25 NT2RP3001855, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003138, NT2RP3003193,  
 NT2RP3003251, NT2RP3003327, NT2RP3003555, NT2RP3004013, NT2RP3004078, NT2RP3004428,  
 NT2RP3004490, NT2RP3004566, NT2RP3004594, NT2RP3004617, NT2RP3004618, NT2RP4000111,  
 NT2RP4000398, NT2RP4000455, NT2RP4000518, NT2RP4000648, NT2RP4000865, NT2RP4000929,  
 NT2RP4001080, NT2RP4001095, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001696,  
 30 NT2RP4001753, NT2RP4001838, NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1000087,  
 OVARC1000241, OVARC1000746, OVARC1000846, OVARC1001232, OVARC1001271, OVARC1001306,  
 OVARC1001987, OVARC1002112, PLACE1000406, PLACE1000583, PLACE1000979, PLACE1001118,  
 PLACE1001632, PLACE1001739, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002834,  
 PLACE1003302, PLACE1003519, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885,  
 35 PLACE1004471, PLACE1004564, PLACE1004814, PLACE1005584, PLACE1005876, PLACE1005951,  
 PLACE1006196, PLACE1006482, PLACE1006488, PLACE1006531, PLACE1006917, PLACE1007346,  
 PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008132, PLACE1009099,  
 PLACE1009246, PLACE1009398, PLACE1009476, PLACE1009622, PLACE1010053, PLACE1010194,  
 PLACE1010702, PLACE1010870, PLACE1011056, PLACE1011114, PLACE1011433, PLACE2000427,  
 40 PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261,  
 PLACE4000489, SKNMC1000091, THYRO1000085, THYRO1000242, THYRO1000501, THYRO1001100,  
 THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000752, Y79AA1001211,  
 Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103, Y79AA1002472, Y79AA1002482,

**[0285]** The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.

45 HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278, HEMBB1000226,  
 NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989, NT2RM2002100, NT2RM4000191,  
 NT2RM4001178, NT2RM4002093, NT2RP1000035, NT2RP1000272, NT2RP1000470, NT2RP1001080,  
 NT2RP2000153, NT2RP2002928, NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436,  
 NT2RP2005539, NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238,  
 50 NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078, NT2RP4000111,  
 NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929, NT2RP4001696, NT2RP4002058,  
 OVARC1001232, OVARC1001577, PLACE1000406, PLACE1000596, PLACE1000755, PLACE1001739,  
 PLACE1003704, PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373,  
 PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878, PLACE1006917,  
 55 PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114, THYRO1000121, Y79AA1001963,

**[0286]** The following 183 clones presumably belong to protein synthesis-associated and/or protein transport-associated proteins.

HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773, HEMBA1004202,



	HEMBA1004276,	HEMBA1004734,	HEMBA1004847,	HEMBA1004929,	HEMBA1004930,	HEMBA1005047,
	HEMBA1005202,	HEMBA1006031,	HEMBA1006272,	HEMBA1006474,	HEMBA1006652,	HEMBA1006914,
	HEMBA1006973,	HEMBA1007224,	HEMBA1000915,	HEMBA1001112,	HEMBA1001137,	HEMBA1001736,
	HEMBA1001831,	HEMBA1001915,	MAMMA1000085,	MAMMA1000734,	MAMMA1001008,	MAMMA1002170,
5	MAMMA1002219,	MAMMA1002236,	MAMMA1002619,	NT2RM1000661,	NT2RM1000833,	NT2RM2000092,
	NT2RM2000504,	NT2RM2000577,	NT2RM2000821,	NT2RM2001201,	NT2RM2001592,	NT2RM2001613,
	NT2RM2001648,	NT2RM2001730,	NT2RM2001760,	NT2RM2002055,	NT2RM4000155,	NT2RM4000169,
	NT2RM4000344,	NT2RM4000356,	NT2RM4000421,	NT2RM4000712,	NT2RM4001054,	NT2RM4001203,
	NT2RM4001382,	NT2RM4001444,	NT2RM4002062,	NT2RM4002205,	NT2RM4002623,	NT2RP1000326,
10	NT2RP1000522,	NT2RP1000547,	NT2RP1000746,	NT2RP1000947,	NT2RP1001569,	NT2RP2000147,
	NT2RP2000710,	NT2RP2000880,	NT2RP2000943,	NT2RP2001290,	NT2RP2001392,	NT2RP2001601,
	NT2RP2001613,	NT2RP2001660,	NT2RP2001740,	NT2RP2002124,	NT2RP2002606,	NT2RP2002862,
	NT2RP2002959,	NT2RP2002980,	NT2RP2003137,	NT2RP2003158,	NT2RP2003391,	NT2RP2003394,
	NT2RP2003401,	NT2RP2003433,	NT2RP2003704,	NT2RP2003713,	NT2RP2003737,	NT2RP2003760,
15	NT2RP2003981,	NT2RP2004366,	NT2RP2004389,	NT2RP2004791,	NT2RP2005012,	NT2RP2005116,
	NT2RP2005360,	NT2RP2005763,	NT2RP2005784,	NT2RP3000366,		
	NT2RP3000759,	NT2RP3000968,	NT2RP3001113,	NT2RP3001690,	NT2RP3002045,	NT2RP3002151,
	NT2RP3002529,	NT2RP3002671,	NT2RP3003301,	NT2RP3003846,	NT2RP3003876,	NT2RP3004209,
	NT2RP4000370,	NT2RP4000457,	NT2RP4000879,	NT2RP4000927,	NT2RP4001041,	NT2RP4001117,
20	NT2RP4001313,	NT2RP4001315,	NT2RP4001574,	NT2RP4001592,	OVARC1000013,	OVARC1000071,
	OVARC1000085,	OVARC1000465,	OVARC1000564,	OVARC1000771,	OVARC1000862,	OVARC1001171,
	OVARC1001180,	OVARC1001342,	PLACE1000007,	PLACE1000061,	PLACE1000081,	PLACE1000492,
	PLACE1000863,	PLACE1001092,	PLACE1001748,	PLACE1002090,	PLACE1003174,	PLACE1003915,
	PLACE1004104,	PLACE1004270,	PLACE1004743,	PLACE1005557,	PLACE1005813,	PLACE1006170,
25	PLACE1006488,	PLACE1006829,	PLACE1007706,	PLACE1007729,	PLACE1008273,	PLACE1008402,
	PLACE1008790,	PLACE1008813,	PLACE1009094,	PLACE1009130,	PLACE1009477,	PLACE1009721,
	PLACE1009845,	PLACE1010074,	PLACE1010547,	PLACE1011109,	PLACE1011229,	PLACE1011477,
	PLACE1012031,	PLACE2000404,	PLACE3000059,	PLACE3000121,	PLACE4000269,	PLACE4000654,
	SKNMC1000011,	THYRO1000983,	THYRO1001003,	THYRO1001313,	Y79AA1000560,	Y79AA1000784,
30	Y79AA1000968,	Y79AA1001493,	Y79AA1001875,	Y79AA1002027,	Y79AA1002209,	
	[0287] The following 130 clones presumably belong to cytoskeletal-associated proteins.					
	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA1001041,	MAMMA1001576,	MAMMA1001679,	MAMMA1001735,
	MAMMA1002297,	MAMMA1002351,	MAMMA1002622,	MAMMA1002637,	MAMMA1003127,	NT2RM1000850,
	NT2RM1000898,	NT2RM2000030,	NT2RM2000260,	NT2RM2000691,	NT2RM2001324,	NT2RM4000169,
	NT2RM4000229,	NT2RM4000515,	NT2RM4001217,	NT2RP1000202,	NT2RP1000348,	NT2RP1000460,
40	NT2RP1000478,	NT2RP1001033,	NT2RP1001294,	NT2RP1001302,	NT2RP2000070,	NT2RP2000812,
	NT2RP2000814,	NT2RP2001168,	NT2RP2001245,	NT2RP2001634,	NT2RP2001900,	NT2RP2003307,
	NT2RP2003394,	NT2RP2004041,	NT2RP2004242,	NT2RP2004538,	NT2RP2004587,	NT2RP2004681,
	NT2RP2004732,	NT2RP2004978,	NT2RP2005491,	NT2RP2005531,	NT2RP2005712,	NT2RP2006275,
	NT2RP3000753,	NT2RP3001113,	NT2RP3001216,	NT2RP3001239,	NT2RP3001272,	NT2RP3001554,
45	NT2RP3001690,	NT2RP3001799,	NT2RP3002688,	NT2RP3003061,	NT2RP3003185,	NT2RP3003230,
	NT2RP3004569,	NT2RP3004578,	NT2RP4001004,	NT2RP4001086,	NT2RP4001256,	NT2RP4001567,
	NT2RP4001927,	OVARC1000001,	OVARC1000106,	OVARC1000437,	OVARC1000520,	OVARC1000679,
	OVARC1001731,	OVARC1002050,	PLACE1001104,	PLACE1002571,		
	PLACE1002591,	PLACE1002655,	PLACE1002714,	PLACE1003625,	PLACE1005287,	PLACE1006552,
50	PLACE1007946,	PLACE1008426,	PLACE1010148,	PLACE1010547,	PLACE1010743,	PLACE1010896,
	PLACE1010960,	PLACE1011310,	PLACE1011922,	PLACE2000216,	PLACE2000274,	PLACE2000371,
	PLACE2000458,	PLACE3000145,	PLACE3000416,	PLACE4000009,	THYRO1000132,	THYRO1001405,
	THYRO1001458,	Y79AA1000368,	Y79AA1000794,	Y79AA1000833,	Y79AA1000962,	Y79AA1002208,
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.					
55	HEMBA1001019,	HEMBA1001595,	HEMBA1002363,	HEMBA1002997,	HEMBA1003136,	HEMBA1003369,
	HEMBA1004131,	HEMBA1004354,	HEMBA1005621,	HEMBA1000037,	HEMBA1000264,	MAMMA1001768,
	MAMMA1002769,	NT2RM1000354,	NT2RM1000430,	NT2RM1000874,	NT2RM2001256,	NT2RM2001743,



NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333,  
 NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596,  
 NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835,  
 NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634,  
 5 OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287,  
 PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

**[0289]** The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442,  
 10 MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858,  
 NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580,  
 NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567,  
 OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625,  
 PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692,

15 **[0290]** The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880,  
 NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536,  
 NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062,  
 NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,  
 20 PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229,

**[0291]** Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

25 HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

30 HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.

HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).

HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.

HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.

HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.

35 HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.

HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.

HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.

HEMBA1001744//SCY1 PROTEIN.

HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.

40 HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.

HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].

HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.

HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.

HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.

45 HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.

HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).

HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.

HEMBA1004573//Homo sapiens mRNA for HELG protein.

50 HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.

HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).

HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.

HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.

HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.

55 HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.

HEMBA1005666//Homo sapiens mRNA for DIPB protein.

HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds.

HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.

HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.  
 HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds.  
 HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.  
 5 HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds. HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.  
 HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).  
 HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.  
 HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds  
 10 HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).  
 HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.  
 HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.  
 HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
 HEMBB1002266//NEURONAL PROTEIN.  
 15 HEMBB1002510//GYP7 PROTEIN.  
 HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.  
 MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].  
 MAMMA1000625//GYP7 PROTEIN.  
 MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.  
 20 MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.  
 MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.  
 MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.  
 MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.  
 25 MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.  
 MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.  
 MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.  
 NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).  
 30 NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).  
 NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.  
 NT2RM1000421//RIBONUCLEASE INHIBITOR.  
 NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.  
 35 NT2RM1000623//RIBONUCLEASE INHIBITOR.  
 NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.  
 NT2RM2000502//Rattus norvegicus W3O7 mRNA, complete cds.  
 NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.  
 NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.  
 40 NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
 NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
 NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.  
 NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.  
 NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.  
 45 NT2RM4000030//LAS1 PROTEIN.  
 NT2RM4000139//R. norvegicus trg mRNA.  
 NT2RM4000156//H. sapiens HPBR11-7 gene.  
 NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
 NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).  
 50 NT2RM4001047//MO25 PROTEIN.  
 NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.  
 NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.  
 NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.  
 NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).  
 55 NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.  
 NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.  
 NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.  
 NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).

NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.  
 NT2RM4001969//R.norvegicus mRNA for IP63 protein.  
 NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.  
 NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).  
 5 NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.  
 NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.  
 NT2RP1000363//R.norvegicus LL5 mRNA.  
 NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.  
 NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.  
 10 NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.  
 NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.  
 NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.  
 NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.  
 15 NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).  
 NT2RP1001494//MALE STERILITY PROTEIN 2.  
 NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.  
 NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
 NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.  
 20 NT2RP2000157//MLO2 PROTEIN.  
 NT2RP2000764//NIFS PROTEIN.  
 NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.  
 NT2RP2001839//SCY1 PROTEIN.  
 NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.  
 25 NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.  
 NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.  
 NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.  
 NT2RP2002442//HESA PROTEIN.  
 30 NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.  
 NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.  
 NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.  
 NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.  
 NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.  
 35 NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.  
 NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).  
 NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.  
 NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.  
 NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.  
 40 NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.  
 NT2RP2004816//H58 PROTEIN.  
 NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.  
 NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.  
 NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.  
 45 NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).  
 NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.  
 NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.  
 NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.  
 NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.  
 50 NT2RP3000047//NPL4 PROTEIN.  
 NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.  
 NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.  
 55 NT2RP3001399//SSU72 PROTEIN.  
 NT2RP3001407//SCY1 PROTEIN.  
 NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.  
 NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.

NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.  
 NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.  
 NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.  
 5 NT2RP3002273//SCD6 PROTEIN.  
 NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.  
 NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.  
 NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.  
 NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.  
 10 NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.  
 NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.  
 NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.  
 15 NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.  
 NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.  
 NT2RP3003500//SCY1 PROTEIN.  
 NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.  
 NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.  
 20 NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).  
 NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.  
 NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).  
 NT2RP4000528//NPL4 PROTEIN.  
 NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.  
 25 NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.  
 NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.  
 NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.  
 NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.  
 30 NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.  
 NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.  
 NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.  
 NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
 35 NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).  
 OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.  
 OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).  
 OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.  
 OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).  
 40 OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.  
 OVARC1001555//NGG1-INTERACTING FACTOR 3.  
 OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).  
 OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.  
 45 PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.  
 PLACE1000066//SSU72 PROTEIN.  
 PLACE1000610//MSN5 PROTEIN.  
 PLACE1000636//MALE STERILITY PROTEIN 2.  
 PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.  
 50 PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.  
 PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.  
 PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.  
 PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.  
 PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.  
 55 PLACE1003602//Homo sapiens mRNA expressed in placenta.  
 PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.  
 PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.  
 PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.

PLACE1004868//MALE STERILITY PROTEIN 2.  
 PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.  
 PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.  
 PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).  
 5 PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.  
 PLACE1005187//APAG PROTEIN.  
 PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.  
 PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.  
 PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.  
 10 PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.  
 PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.  
 PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.  
 PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.  
 PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.  
 15 PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.  
 PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.  
 PLACE1007897//Homo sapiens FLASH mRNA, complete cds.  
 PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.  
 PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).  
 20 PLACE1008398//GENE 33 POLYPEPTIDE.  
 PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).  
 PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.  
 PLACE1009020//NIFS PROTEIN.  
 PLACE1009060//BRO1 PROTEIN.  
 25 PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.  
 PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.  
 PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.  
 PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.  
 PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).  
 30 PLACE1010261//SEGREGATION DISTORTER PROTEIN.  
 PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).  
 PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.  
 PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.  
 PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and  
 35 S171 gene, partial cds.  
 PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.  
 PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.  
 PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.  
 PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.  
 40 PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.  
 PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).  
 PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.  
 PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.  
 THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.  
 45 THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.  
 THYRO1000666//Mus musculus mRNA for kinesin like protein 9.  
 THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.  
 THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.  
 THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.  
 50 THYRO1001703//NIFR3-LIKE PROTEIN.  
 THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).  
 Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.  
 Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.  
 Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.  
 55 Y79AA1000313//CALPHOTIN.  
 Y79AA1000540//CELL POLARITY PROTEIN TEA1.  
 Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
 Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.

Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.

Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.

Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.

Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.

Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

**[0292]** Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

**[0293]** Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

**[0294]** So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

**[0295]** So far, useful information for presuming the functions are unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042, HEMBA1000046, HEMBA1000050, HEMBA1000076, HEMBA1000193, HEMBA1000213,  
 HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251, HEMBA1000264,  
 HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302, HEMBA1000327,  
 HEMBA1000338, HEMBA1000351, HEMBA1000357, HEMBA1000376, HEMBA1000387, HEMBA1000392,  
 HEMBA1000396, HEMBA1000428, HEMBA1000442, HEMBA1000456, HEMBA1000459, HEMBA1000460,  
 HEMBA1000469, HEMBA1000497, HEMBA1000501, HEMBA1000504, HEMBA1000505, HEMBA1000508,  
 HEMBA1000519, HEMBA1000520, HEMBA1000534, HEMBA1000545, HEMBA1000557, HEMBA1000568,  
 HEMBA1000575, HEMBA1000594, HEMBA1000604, HEMBA1000622, HEMBA1000636, HEMBA1000655,  
 HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000702, HEMBA1000722, HEMBA1000726,  
 HEMBA1000727, HEMBA1000749, HEMBA1000752, HEMBA1000769, HEMBA1000773, HEMBA1000774,  
 HEMBA1000843, HEMBA1000867, HEMBA1000869, HEMBA1000872, HEMBA1000876, HEMBA1000908,  
 HEMBA1000918, HEMBA1000934, HEMBA1000942, HEMBA1000943, HEMBA1000946, HEMBA1000960,  
 HEMBA1000968, HEMBA1000971, HEMBA1000972, HEMBA1000975, HEMBA1000985, HEMBA1000986,  
 HEMBA1001008, HEMBA1001009, HEMBA1001020, HEMBA1001022, HEMBA1001024, HEMBA1001026,  
 HEMBA1001051, HEMBA1001060, HEMBA1001080, HEMBA1001094, HEMBA1001099, HEMBA1001109,  
 HEMBA1001121, HEMBA1001122, HEMBA1001123, HEMBA1001133, HEMBA1001140, HEMBA1001208,  
 HEMBA1001213, HEMBA1001226, HEMBA1001235, HEMBA1001281, HEMBA1001299, HEMBA1001303,  
 HEMBA1001310, HEMBA1001319, HEMBA1001323, HEMBA1001326, HEMBA1001327, HEMBA1001330,  
 HEMBA1001361, HEMBA1001375, HEMBA1001377, HEMBA1001383, HEMBA1001388, HEMBA1001391,  
 HEMBA1001398, HEMBA1001411, HEMBA1001413, HEMBA1001415, HEMBA1001432, HEMBA1001433,  
 HEMBA1001435, HEMBA1001442, HEMBA1001450, HEMBA1001463, HEMBA1001497, HEMBA1001522,  
 HEMBA1001533, HEMBA1001566, HEMBA1001570, HEMBA1001581, HEMBA1001589, HEMBA1001608,  
 HEMBA1001636, HEMBA1001640, HEMBA1001647, HEMBA1001655, HEMBA1001658, HEMBA1001702,  
 HEMBA1001711, HEMBA1001712, HEMBA1001731, HEMBA1001745, HEMBA1001750, HEMBA1001781,  
 HEMBA1001784, HEMBA1001791, HEMBA1001803, HEMBA1001815, HEMBA1001820, HEMBA1001835,  
 HEMBA1001864, HEMBA1001888, HEMBA1001910, HEMBA1001912, HEMBA1001915, HEMBA1001918,  
 HEMBA1001939, HEMBA1001940, HEMBA1001942, HEMBA1001950, HEMBA1001964, HEMBA1001987,  
 HEMBA1002018, HEMBA1002022, HEMBA1002039, HEMBA1002049, HEMBA1002084, HEMBA1002100,  
 HEMBA1002113, HEMBA1002119, HEMBA1002160, HEMBA1002162, HEMBA1002185, HEMBA1002189,  
 HEMBA1002191, HEMBA1002199, HEMBA1002204, HEMBA1002229, HEMBA1002237, HEMBA1002265,

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	HEMBA1002328,	HEMBA1002337,	HEMBA1002348,	HEMBA1002349,	HEMBA1002381,	HEMBA1002430,
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	HEMBA1002538,	HEMBA1002542,	HEMBA1002552,	HEMBA1002558,	HEMBA1002583,	HEMBA1002621,
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	PLACE1010364,	PLACE1010383,	PLACE1010401,	PLACE1010491,	PLACE1010492,	PLACE1010562,

	PLACE1010616,	PLACE1010624,	PLACE1010629,	PLACE1010630,	PLACE1010714,	PLACE1010786,
	PLACE1010800,	PLACE1010802,	PLACE1010856,	PLACE1010857,	PLACE1010877,	PLACE1010900,
	PLACE1010916,	PLACE1010925,	PLACE1010944,	PLACE1010947,	PLACE1010965,	PLACE1011026,
	PLACE1011032,	PLACE1011054,	PLACE1011057,	PLACE1011133,	PLACE1011143,	PLACE1011165,
5	PLACE1011273,	PLACE1011291,	PLACE1011325,	PLACE1011452,	PLACE1011465,	PLACE1011472,
	PLACE1011503,	PLACE1011520,	PLACE1011563,	PLACE1011567,	PLACE1011643,	PLACE1011649,
	PLACE1011650,	PLACE1011675,	PLACE1011682,	PLACE1011719,	PLACE1011725,	PLACE1011729,
	PLACE1011874,	PLACE1011875,	PLACE1011891,	PLACE1011982,	PLACE2000003,	PLACE2000006,
	PLACE2000007,	PLACE2000017,	PLACE2000047,	PLACE2000050,	PLACE2000061,	PLACE2000097,
10	PLACE2000100,	PLACE2000103,	PLACE2000115,	PLACE2000124,	PLACE2000140,	PLACE2000170,
	PLACE2000172,	PLACE2000223,	PLACE2000235,	PLACE2000302,	PLACE2000317,	PLACE2000347,
	PLACE2000359,	PLACE2000366,	PLACE2000394,	PLACE2000433,	PLACE2000450,	PLACE2000455,
	PLACE3000070,	PLACE3000103,	PLACE3000119,	PLACE3000136,	PLACE3000142,	PLACE3000148,
	PLACE3000155,	PLACE3000156,	PLACE3000157,	PLACE3000158,	PLACE3000160,	PLACE3000194,
15	PLACE3000197,	PLACE3000199,	PLACE3000207,	PLACE3000208,	PLACE3000221,	PLACE3000230,
	PLACE3000271,	PLACE3000276,	PLACE3000304,	PLACE3000310,	PLACE3000320,	PLACE3000322,
	PLACE3000331,	PLACE3000341,	PLACE3000352,	PLACE3000353,	PLACE3000362,	PLACE3000363,
	PLACE3000365,	PLACE3000388,	PLACE3000401,	PLACE3000402,	PLACE3000405,	PLACE3000425,
	PLACE3000475,	PLACE4000089,	PLACE4000093,	PLACE4000106,	PLACE4000131,	PLACE4000147,
20	PLACE4000222,	PLACE4000252,	PLACE4000270,	PLACE4000320,	PLACE4000323,	PLACE4000344,
	PLACE4000367,	PLACE4000392,	PLACE4000411,	PLACE4000445,	PLACE4000465,	PLACE4000521,
	PLACE4000590,	PLACE4000612,	PLACE4000638,	PLACE4000670,	THYRO1000026,	THYRO1000070,
	THYRO1000092,	THYRO1000107,	THYRO1000111,	THYRO1000124,	THYRO1000186,	THYRO1000187,
	THYRO1000199,	THYRO1000206,	THYRO1000241,	THYRO1000253,	THYRO1000270,	THYRO1000279,
25	THYRO1000320,	THYRO1000368,	THYRO1000381,	THYRO1000387,	THYRO1000452,	THYRO1000471,
	THYRO1000484,	THYRO1000502,	THYRO1000505,	THYRO1000558,	THYRO1000596,	THYRO1000625,
	THYRO1000637,	THYRO 1000676,	THYRO1000712,	THYRO1000715,	THYRO1000734,	THYRO1000777,
	THYRO1000787,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,	THYRO1000843,
	THYRO1000855,	THYRO1000865,	THYRO1000895,	THYRO1000916,	THYRO1000952,	THYRO1000988,
30	THYRO1001031,	THYRO1001062,	THYRO1001133,	THYRO1001142,	THYRO1001173,	THYRO1001213,
	THYRO1001262,	THYRO1001321,	THYRO1001322,	THYRO1001363,	THYRO1001365,	THYRO1001403,
	THYRO1001411,	THYRO1001426,	THYRO1001434,	THYRO1001480,	THYRO1001487,	THYRO1001559,
	THYRO1001570,	THYRO1001584,	THYRO1001595,	THYRO1001602,	THYRO1001605,	THYRO1001637,
	THYRO1001673,	THYRO1001706,	THYRO1001745,	THYRO1001746,	THYRO1001772,	THYRO1001793,
35	THYRO1001854,	THYRO1001895,	THYRO1001907,	VESEN1000122,	Y79AA1000065,	Y79AA1000131,
	Y79AA1000202,	Y79AA1000230,	Y79AA1000355,	Y79AA1000410,	Y79AA1000480,	Y79AA1000539,
	Y79AA1000574,	Y79AA1000774,	Y79AA1000802,	Y79AA1000805,	Y79AA1000824,	Y79AA1000827,
	Y79AA1000850,	Y79AA1000969,	Y79AA1001041,	Y79AA1001061,	Y79AA1001068,	Y79AA1001077,
	Y79AA1001078,	Y79AA1001145,	Y79AA1001167,	Y79AA1001185,	Y79AA1001216,	Y79AA1001228,
40	Y79AA1001281,	Y79AA1001511,	Y79AA1001541,	Y79AA1001555,	Y79AA1001585,	Y79AA1001665,
	Y79AA1001696,	Y79AA1001781,	Y79AA1001805,	Y79AA1002089,	Y79AA1002115,	Y79AA1002125,
	Y79AA1002220,	Y79AA1002234,	Y79AA1002298,	Y79AA1002407,	MAMMA1002215,	MAMMA1002721,
	NT2RP2002070,					

45 Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

50 the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the organism and the Accession No. of the top hit data, as in the order separated by //.

55 [0298] Data are not shown for the clones in which the P-value was higher than 1.

[0299] The P-value is a score obtained statistically by taking into account the possible similarity between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. &

States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

5 F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712  
 F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE)  
 (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996  
 F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA  
 CAPSULATUM).//P41742  
 10 F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM  
 KNOWLESI (STRAIN NURI).//P04922  
 F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//  
 P80247  
 F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P80355  
 15 F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86:41:41//HOMO SAPIENS  
 (HUMAN).//P56385  
 F-HEMBA1000111  
 F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE T4.//P20703  
 F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 20 P38374  
 F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/8.4e-16:47:70//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11).//  
 Q01042  
 25 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:40//HOMO SAPIENS  
 (HUMAN).//Q93074  
 F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:36//MUS MUSCULUS  
 (MOUSE).//P81122  
 F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VI-  
 30 RUS (SIV(CPZ)) (CIV).//P17286  
 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P22126  
 F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814  
 F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS  
 (MOUSE).//P05142  
 35 F-HEMBA1000213  
 F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221  
 F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P32583  
 40 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264  
 F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:  
 45 149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40480  
 F-HEMBA1000251  
 F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552  
 F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED  
 COBRA) (NAJA NAJA SIAMENSIS).//P14613  
 50 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.14:26:65//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1000288  
 F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO  
 SAPIENS (HUMAN).//P10516  
 55 F-HEMBA1000302  
 F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//  
 CAENORHABDITIS ELEGANS.//Q03601  
 F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.021:18:83//HOMO SAPIENS (HUMAN).//

P39194

F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235:25//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922

F-HEMBA1000327

5 F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10193

F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.8e-26:36:83//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000351

10 F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.99:22:50//HOMO SAPIENS (HUMAN).//P02811

F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

15 F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-35:105:74//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:42//ARCHAEOGLOBUS FULGIDUS.//O28646

F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//HOMO SAPIENS (HUMAN).//P78352

20 F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.8e-08:66:42//MUS MUSCULUS (MOUSE).//P11369

F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P20962

25 F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-30:92:69//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000411

30 F-HEMBA1000418

F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.3e-10:90:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HOMO SAPIENS (HUMAN).//P08547

35 F-HEMBA1000434

F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87048

40 F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT).//P33279

F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHAGE ALPHA-3.//P31280

F-HEMBA1000464

F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P43502

45 F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38//HOMO SAPIENS (HUMAN).//Q13105

F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427

F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVEGICUS (RAT).//P97538

50 F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-20:81:54//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000504

F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32//HOMO SAPIENS (HUMAN).//Q02410

55 F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P29465

F-HEMBA1000518

F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.8e-37:68:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.2e-09:75:49//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSCULUS (MOUSE).//  
 Q01755  
 5 F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBIMANUS (NEW WORLD  
 MALARIA MOSQUITO).//P41827  
 F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/9.7e-32:96:78//HOMO SAPIENS (HUMAN).//  
 P39193  
 10 F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.0:12:75//LACTOCOCCUS  
 LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36499  
 F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089:79:31//MUS  
 MUSCULUS (MOUSE).//P15265  
 F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//HOMO SAPIENS (HU-  
 MAN).//P08547  
 15 F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P39730  
 F-HEMBA1000557  
 F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1 e-18:200:28//HOMO SAPIENS (HUMAN).//  
 P51508  
 20 F-HEMBA1000563  
 F-HEMBA1000568  
 F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS (HUMAN).//Q14444  
 F-HEMBA1000575  
 F-HEMBA1000588  
 25 F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:41:92//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HOMO SAPIENS (HU-  
 MAN).//Q02224  
 F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.93:24:54//  
 30 CAENORHABDITIS ELEGANS.//P41997  
 F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00010:49:55//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:61//HOMO SAPIENS  
 (HUMAN).//Q43295  
 35 F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-21:94:62//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36//VOLVOX CARTERI.//  
 P21997  
 F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAPIENS (HUMAN).//P04281  
 40 F-HEMBA1000655  
 F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P35197  
 F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRISEUS (CHINESE HAM-  
 STER).//P02799  
 45 F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-17:86:59//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//3.0e-13:45:44//MUS MUSCULUS (MOUSE).//P11369  
 F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4.5e-07:79:34//  
 50 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13873  
 F-HEMBA1000702  
 F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//  
 P10569  
 55 F-HEMBA1000722  
 F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.4e-32:83:77//HOMO SAPIENS (HU-  
 MAN).//P39191  
 F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN).//0.73:26:46//SACCHAROMYCES CER-



EVISIAE (BAKER'S YEAST).//P47977  
 F-HEMBA1000747  
 F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44211  
 F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO SAPIENS (HU-  
 5 MAN).//P10267  
 F-HEMBA1000769  
 F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUMAN).//O43316  
 F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.3e-23:92:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 10 F-HEMBA1000791  
 F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R).//0.079:87:29//CERVUS ELAPHUS (RED  
 DEER).//Q28235  
 F-HEMBA1000822  
 F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS (STRAIN COPENHA-  
 15 GEN).//P20546  
 F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//0.92:46:34//  
 CAENORHABDITIS ELEGANS.//P41953  
 F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX  
 PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951  
 20 F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:29:100//HOMO SAPIENS  
 (HUMAN).//P51689  
 F-HEMBA1000867  
 F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792  
 F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALUS DURISSUS TER-  
 25 RIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333  
 F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//  
 P41891  
 F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745  
 F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.69:43:37//HO-  
 30 MO SAPIENS (HUMAN).//P30808  
 F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-08:44:38//HOMO  
 SAPIENS (HUMAN).//O15480  
 F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:52//SCHIZOSACCHARO-  
 MYCES POMBE (FISSION YEAST).//P22667  
 35 F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-A/PFR-B).//0.29:  
 116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225  
 F-HEMBA1000934  
 F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.85:27:59//HOMO SAPIENS (HUMAN).//  
 P39188  
 40 F-HEMBA1000943  
 F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19958  
 F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.0097:29:72//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-III A AND MT-20-III B).//0.047:45:37//  
 45 MYTILUS EDULIS (BLUE MUSSEL).//P80253  
 F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR VIRUS (STRAIN  
 B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBA1000972  
 F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA GENITALIUM.//P47679  
 50 F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.028:57:  
 36//HOMO SAPIENS (HUMAN).//P25067  
 F-HEMBA1000985  
 F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECURSOR (GRP-  
 CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:34//RATTUS NORVEGICUS (RAT).//P08462  
 55 F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-  
 MOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q18964  
 F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS (HUMAN).//Q14684  
 F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.4e-25:61:70//HOMO SAPIENS (HU-

MAN).//P39194

F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS ELEGANS.//P34687

F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-85:191:84//RATTUS NORVEGICUS (RAT).//P33671

F-HEMBA1001019

F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.7e-24:49:73//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001022

F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51100

F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).//P24712

F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES HYGROSCOPICUS.//P16961

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4) (N- ACETYL GALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFATASE) (GALNAC6S SULFATASE) (CHONDROITIN SULFATASE) (CHONDROITINASE).//3.2e-132:249:94//HOMO SAPIENS (HUMAN).//P34059

F-HEMBA1001060

F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:96//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//HOMO SAPIENS (HUMAN).//O43918

F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAW MGH-10).//P37319

F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PPS) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULUS (MOUSE).//Q60676

F-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5e-50:176:57//HOMO SAPIENS (HUMAN).//P48059

F-HEMBA1001094

F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EHA-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:60//ECTOTHIORHODOSPIRA HALOPHILA.//P80101

F-HEMBA1001109//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.7e-37:102:82//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001122

F-HEMBA1001123

F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV).//P19033

F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e-22:103:52//HOMO SAPIENS (HUMAN).//P51523

F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO SAPIENS (HUMAN).//P53420

F-HEMBA1001172

F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:79//RATTUS NORVEGICUS (RAT).//P51646

F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (FRAGMENT).//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (BARBARY APE).//Q95145

F-HEMBA1001208

F-HEMBA1001213

F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.99.46) (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91//HOMO SAPIENS (HUMAN).//P25788

F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS CUNICULUS (RABBIT).//

Q28749

F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00052:16:81//VOLVOX CART-ERI.//P21997

F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-).//1.6e-68:178:77//RATTUS NORVEGI-CUS (RAT).//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.78) (BETA- MAN-NANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A).//0.67:23:60//PIROMYCES SP.//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76).//0.83:48:35//PORPHYRA PURPU-REA.//P51229

F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//1.3e-07:185:29//CAVIA PORCELLUS (GUINEA PIG).//Q60401

F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.//0.00018:159:30//RATTUS NORVEGICUS (RAT).//P31422

F-HEMBA1001294

F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.3e-07:27:77//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DERIVED FACTOR 4) (SDF-4).//3.3e-61:150:76//MUS MUSCULUS (MOUSE).//Q61112

F-HEMBA1001303

F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161.//2.7e-10:170:27//HOMO SAPIENS (HUMAN).//P50876

F-HEMBA1001319

F-HEMBA1001323

F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601

F-HEMBA1001327

F-HEMBA1001330

F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943

F-HEMBA1001361//RUBREDOXIN (RD).//0.95:44:29//ALCALIGENES EUTROPHUS.//P31912

F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN.//0.013:45:33//AEROMONAS SOBRIA.//P09165

F-HEMBA1001377//SPERM PROTAMINE P1.//1.0:22:40//PLANIGALE MACULATA SINUALIS (COMMON PLAN-IGALE).//O18746

F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.60:37:29//HUMAN IM-MUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506

F-HEMBA1001387//GTP-BINDING PROTEIN TC10.//6.6e-43:83:92//HOMO SAPIENS (HUMAN).//P17081

F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).//0.00088:46:45//HOMO SAPIENS (HUMAN).//Q14149

F-HEMBA1001391

F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE).//1.0:59:37//ESCHERICHIA COLI.//P00645

F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.25:41:34//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.0e-09:129:40//HOMO SAPIENS (HUMAN).//P04280

F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (O313).//0.95:88:31//ESCHERICHIA COLI.//P55140

F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT).//0.95:46:32//MUS MUSCULUS (MOUSE).//Q04890

F-HEMBA1001415//HISTONE H5.//0.43:95:29//GALLUS GALLUS (CHICKEN).//P02259

F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR.//0.77:46:32//LACTOCOCCUS LACTIS (SUBSP. LAC-TIS) (STREPTOCOCCUS LACTIS).//P13068

F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.8e-09:132:31//NYCTICEBUS COU-CANG (SLOW LORIS).//P08548

F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-31:84:77//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001442

F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.71:41:39//PSEUDOPLEURONECTA AMERI-CANUS (WINTER FLOUNDER).//P02734

F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17.//0.13:127:27//SACCHAROMYCES CEREVISIAE (BAK-

ER'S YEAST).//Q12446

F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.57:38:47//HANSENULA WINGEI (YEAST).//P48882

F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-).//0.98:124:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44737

F-HEMBA1001463//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-32:62:67//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159).//6.8e-09:252:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40477

F-HEMBA1001478

F-HEMBA1001497//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-33:105:72//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1001510//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.3e-37:54:81//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-63:223:57//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1001517

F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P49437

F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:130:29//CLOSTRIDIUM PASTEURIANUM.//P29166

F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS TYPE 6A.//Q84296

F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//1.5e-07:99:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51635

F-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.2e-50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P19065

F-HEMBA1001570//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.3e-33:107:72//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-HEMBA1001581

F-HEMBA1001585

F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33//HUMAN ADENOVIRUS TYPE 2.//P03263

F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPIENS (HUMAN).//Q14141

F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28615

F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4.3e-45:222:46//SPIRODELA POLYRRHIZA.//P42803

F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q22053

F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//HOMO SAPIENS (HUMAN).//Q09155

F-HEMBA1001640//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//14.7e-06:80:41//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS (HUMAN).//O00268

F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO-SAPIENS (HUMAN).//Q08379

F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446

F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD SUBUNIT (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M METHYLTRANSFERASE 12 KD SUBUNIT).//1.0:29:44//METHANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133).//Q50773

F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTER XYLINUM (ACETOBACTER PASTEURIANUS).//P37697

F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:35//PLASMODIUM  
 CYNOMOLGI (STRAIN BEROK).//P08672  
 F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX (SOYBEAN).//P08960  
 F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.2e-13:62:64//HOMO SAPIENS (HUMAN).//  
 5 P39195  
 F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REGION (P40) (ORF3)  
 (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//  
 P24653  
 F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:54:37//TRYPANOSOMA BRU-  
 10 CEI BRUCEI.//P24499  
 F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.59:109:35//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042  
 F-HEMBA1001711  
 F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0.54:44:34//HUMAN AD-  
 15 ENOVIRUS TYPE 41.//P23690  
 F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:75//RATTUS NOR-  
 VEGICUS (RAT).//Q03344  
 F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN  
 AD169).//P16820  
 20 F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2  
 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318  
 F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE  
 VIRUS (STRAIN 52/70) (IBDV).//P25221  
 F-HEMBA1001734  
 25 F-HEMBA1001744//SCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53009  
 F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECUR-  
 SOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116  
 F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTE-  
 30 RIUM LEPRAE.//P38388  
 F-HEMBA1001761  
 F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40//  
 HOMO SAPIENS (HUMAN).//P17023  
 F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46//  
 35 CAENORHABDITIS ELEGANS.//Q11116  
 F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216  
 F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:  
 48//MUS MUSCULUS (MOUSE).//P16372  
 F-HEMBA1001803  
 40 F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//9.3e-17:56:57//  
 ORYZA SATIVA (RICE).//P25074  
 F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU-ANTIGEN  
 D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//O09032  
 F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORABIES VIRUS (STRAIN  
 45 INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
 F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:30//SCHIZOSACCHA-  
 ROMYCES POMBE (FISSION YEAST).//P05733  
 F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS (HUMAN).//P52742  
 F-HEMBA1001820  
 50 F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567  
 F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//4.7e-11:124:37//  
 OVIS ARIES (SHEEP).//P26372  
 F-HEMBA1001835  
 55 F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-14:36:63//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MUSCULUS (MOUSE).//  
 Q07230

F-HEMBA1001861

F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//1.0:31:38//ESCHERICHIA COLI.//P07965

F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I.//5.3e-13:65.47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362

F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:37//STREPTOMYCES FRADIAE.//P26800

F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.8e-20:250:29//RATTUS NORVEGICUS (RAT).//Q63342

F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAENORHABDITIS ELEGANS.//O61955

F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-07:53:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43535

F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA COLI.//Q52280

F-HEMBA1001918

F-HEMBA1001921

F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONTELLA SINENSIS.//P49560

F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0017:31:77//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (HIBERNATOR-SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS ASIATICUS (CHIPMUNK).//Q06577

F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGION (ORF E).//1.0:35:37//BACTERIOPHAGE T4.//P32269

F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933

F-HEMBA1001960//HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HOMO SAPIENS (HUMAN).//Q00444

F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.//1.0:30:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53056

F-HEMBA1001964

F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-HEMBA1001979

F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10356

F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I).//0.99:31:45//ANEMONIA SULCATA (SNAKE-LOCKS SEA ANEMONE).//P01533

F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (EC 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467

F-HEMBA1002008

F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377

F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH).//P12704

F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//HOMO SAPIENS (HUMAN).//Q92794

F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:40//HOMO SAPIENS (HUMAN).//Q92558

F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:37:75//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002084

F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35210

F-HEMBA1002100

F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357  
 F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICAGO TRUNCATULA  
 (BARREL MEDIC).//P93329  
 5 F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01643  
 F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.35:111:33//FELINE  
 SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338  
 F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION.//0.88:72:25//  
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192  
 F-HEMBA1002144  
 F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:65:46//BOS TAURUS  
 (BOVINE).//P06579  
 F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:28//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 15 F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.93:58:25//APIS MEL-  
 LIFERA (HONEYBEE).//P34859  
 F-HEMBA1002160/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.1e-21:94:65//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-51:180:56//SUS  
 20 SCROFA (PIG).//P79293  
 F-HEMBA1002162/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-40:102:75//HOMO SAPIENS (HU-  
 MAN).//P39193  
 F-HEMBA1002166/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-13:133:45//HOMO SAPIENS (HUMAN).//  
 25 P39188  
 F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153:26//HOMO SAPIENS (HU-  
 MAN).//P52746  
 F-HEMBA1002185  
 F-HEMBA1002189/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.86:46:45//HOMO SAPIENS (HUMAN).//  
 30 P39194  
 F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:57//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01644  
 F-HEMBA1002199  
 F-HEMBA1002204  
 F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE  
 35 KINASE DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:30//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q24324  
 F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:147:84//MUS MUSCULUS  
 (MOUSE).//P47226  
 F-HEMBA1002226/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-26:168:44//HOMO SAPIENS (HUMAN).//  
 40 P39188  
 F-HEMBA1002229/////ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.8e-18:68:72//HOMO SAPIENS (HU-  
 MAN).//P39190  
 F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA ACERVULINA.//P21959  
 F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS (COMMON SEA UR-  
 45 CHIN).//P80367  
 F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AURATUS (GOLDEN HAM-  
 STER).//P17808  
 F-HEMBA1002257  
 F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOPHILA MELA-  
 50 NOGASTER (FRUIT FLY).//Q01644  
 F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS GALLUS (CHICKEN).//  
 Q90667  
 F-HEMBA1002270  
 F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:40//BACTERIOPHAGE PHI-  
 55 105.//P10437  
 F-HEMBA1002328  
 F-HEMBA1002337  
 F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//MUS MUSCULUS

(MOUSE).//Q62415

F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226

F-HEMBA1002349

F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:71//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-24:69:73//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//2.6e-51:187:56//MUS MUSCULUS (MOUSE).//P39447

F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMAN).//P02814

F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.042:41:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:47:29//CALYPTROSPHAERA SPHAEROIDEA.//P41548

F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:109:55//HOMO SAPIENS (HUMAN).//Q00994

F-HEMBA1002460

F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:80:30//HOMO SAPIENS (HUMAN).//P81489

F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO SAPIENS (HUMAN).//P52756

F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS MUSCULUS (MOUSE).//P05143

F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-34:96:71//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1002486

F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P48732

F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38166

F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.0e-06:49:63//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-22:169:44//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//0.00017:79:35//CAENORHABDITIS ELEGANS.//Q20296

F-HEMBA1002515

F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//1.0:53:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P81449

F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.7e-32:96:75//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002547//AGRIN PRECURSOR.//2.5e-100:218:80//RATTUS NORVEGICUS (RAT).//P25304

F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D).//9.5e-12:29:82//HOMO SAPIENS (HUMAN).//Q13268

F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN.//2.4e-15:207:36//BOS TAURUS (BOVINE).//P04258

F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0:34:50//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-05:49:46//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12.//0.97:60:33//BACTERIOPHAGE PRD1.//P17637

F-HEMBA1002583

F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-15:54:55//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002592//HISTIDINE-RICH PROTEIN.//0.99:39:28//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586

F-HEMBA1002609//SSM4 PROTEIN.//1.9e-12:135:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//



P40318

F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F COMPLEX SUB-UNIT 6).//1.0:20:55//ZEA MAYS (MAIZE).//P19445

F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-HEMBA1002628

F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES VIRUS (STRAIN KAP-LAN) (PRV).//P33479

F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-16:57:68//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1002651

F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS ELEGANS.//P17656

F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//HOMO SAPIENS (HU-MAN).//P08547

F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN).//P49152

F-HEMBA1002678

F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:27//PLASMODIUM FALCI-PARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-07:198:32//NEPHILA CLA-VIPES (ORB SPIDER).//P46804

F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLA-GEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388

F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1002712//11.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE PF1.//P25133

F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS SUBTILIS.//P37807

F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-18:56:75//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS JANNASCHII.//Q57764

F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//SUS SCROFA (PIG).//P27917

F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910

F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA) (GPIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400

F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-15:49:75//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746

F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//023:88:27//ORYCTOLAGUS CUNICU-LUS (RABBIT).//P02779

F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43//MUS MUSCULUS (MOUSE).//P06798

F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REGION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880

F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS MUSCULUS (MOUSE).//Q60879

F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0044:66:37//GLYCINE MAX (SOYBEAN).//Q10370

F-HEMBA1002801

F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.0033:116:31//CAENORHABDITIS ELEGANS.//Q09202

F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14308

F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE).//P37889

F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:34//BACTERIOPHAGE T4.//P16012

F-HEMBA1002833

F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:27:37//METRIDIVM SENILE  
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493  
 F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 8.1 KD PROTEIN)  
 (P30 PROTEIN) (PSI-E)//0.84:37:43//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P12975  
 5 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2//0.74:58:34//MUS MUSCULUS (MOUSE)//Q06666  
 F-HEMBA1002886  
 F-HEMBA1002896//HOMEODOMAIN PROTEIN HOX-B3 (HOX-2G) (HOX-2.7)//4.7e-05:84:35//HOMO SAPIENS  
 (HUMAN)//P14651  
 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.21:42:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1)//P05908  
 10 F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.85:75:22//ARABIDOPSIS THALIANA  
 (MOUSE-EAR CRESS)//Q42377  
 F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-31:92:72//HOMO SAPIENS (HUMAN)//  
 P39188  
 15 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT)//7.7e-06:187:29//XENOPUS  
 LAEVIS (AFRICAN CLAWED FROG)//P18730  
 F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40//0.00031:150:24//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST)//P32583  
 F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//5.2e-25:225:33//HOMO  
 20 SAPIENS (HUMAN)//P16157  
 F-HEMBA1002944  
 F-HEMBA1002951//TRICHOHYALIN//0.0011:220:24//HOMO SAPIENS (HUMAN)//Q07283  
 F-HEMBA1002954//PROBABLE E8 PROTEIN//0.98:49:32//BOVINE PAPILLOMAVIRUS TYPE 4//P08352  
 F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//0.93:41:34//  
 25 DROSOPHILA SECHELLIA (FRUIT FLY)//O18417  
 F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.00010:35:62//HOMO SAPIENS (HUMAN)//  
 P39193  
 F-HEMBA1002971//INSULIN//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH) (PACIFIC RATFISH),  
 AND CHIMAERA MONSTROSA (RABBIT FISH)//P09536 F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC  
 30 PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//3.0e-29:63:100//RATTUS NORVEGICUS (RAT)//  
 P14646  
 F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION//1.0e-08:  
 211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53253  
 F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40//0.026:175:23//SACCHAROMYCES CEREVISIAE (BAKER'S  
 35 YEAST)//P32583  
 F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:102:70//HOMO SAPIENS (HUMAN)//  
 P39194  
 F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C//0.029:75:29//MYCOBACTERIUM TUBERCULOSIS//  
 P71779  
 40 F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.3e-23:144:46//HOMO SAPIENS (HUMAN)//  
 P39192  
 F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION//0.99:55:  
 30//BACILLUS SUBTILIS//P54457  
 F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4//0.17:42:40//HOMO SAPIENS (HUMAN)//  
 45 P47928  
 F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.69:28:46//HOMO  
 SAPIENS (HUMAN)//P30808  
 F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC  
 3.4.24.64) (BETA-MPP) (P-52)//7.9e-124:253:96//HOMO SAPIENS (HUMAN)//O75439  
 50 F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)//0.25:263:22//TRYPANOSOMA  
 BRUCEI BRUCEI//P04540  
 F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//4.1e-05:  
 189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214  
 F-HEMBA1003071//CUTICLE COLLAGEN 40//6.0e-07:126:38//CAENORHABDITIS ELEGANS//P34804  
 55 F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)//2.4e-12:  
 139:34//HOMO SAPIENS (HUMAN)//Q06828  
 F-HEMBA1003078//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE]//7.2e-05:60:40//MUS MUSCULUS (MOUSE)//P11369

F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.3e-32:95:75//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBA1003086  
 5 F-HEMBA1003096//PROTAMINE IA (IRIDINE IA).//0.36:20:40//SALMO IRIDEUS (RAINBOW TROUT).//P02328  
 F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-09:43:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHABDITIS ELEGANS.//  
 Q09456  
 10 F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MEL-  
 LIFERA (HONEYBEE).//P34859  
 F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:  
 37//HOMO SAPIENS (HUMAN).//P25067  
 F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-  
 15 PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940  
 F-HEMBA1003142  
 F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECUR-  
 SOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189  
 20 F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-13:54:66//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:  
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-  
 25 FERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//O35020  
 F-HEMBA1003197  
 F-HEMBA1003199//HOMEBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:38//HOMO SAPIENS  
 (HUMAN).//Q00056  
 F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILES (FLAT-SKULLED MARSUPIAL  
 30 MOUSE).//O18747  
 F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.2e-22:42:80//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.6e-18:74:71//HOMO SAPIENS (HUMAN).//  
 P39193  
 35 F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-18:56:78//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION.//0.0018:159:  
 27//BACILLUS SUBTILIS.//P46327  
 F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPS).//1.0:85:28//  
 40 TRITICUM AESTIVUM (WHEAT).//P24846  
 F-HEMBA1003235//TROPOMYOSIN.//8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION  
 YEAST).//Q02088  
 F-HEMBA1003250  
 F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSI-  
 45 FORMIS.//P21260  
 F-HEMBA1003273  
 F-HEMBA1003276  
 F-HEMBA1003278  
 F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALLUS GALLUS (CHICK-  
 50 EN).//P17277  
 F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.96:37:35//SULFOLOBUS  
 ACIDOCALDARIUS.//P39472  
 F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK  
 ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROFA (PIG).//Q28948  
 55 F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN) (PULMO-  
 NARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49:28//BOS TAURUS (BOVINE).//P15781  
 F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:30//PROTOTHECA WICKER-  
 HAMII.//P46750

F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN.//0.69:54:37//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306

F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06:143:22//HOMO SAPIENS (HUMAN).//Q02779

5 F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-30:53:77//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003327

F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

10 F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667

F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.5e-09:56:66//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

15 F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-18:99:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003373

F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-16:60:75//HOMO SAPIENS (HUMAN).//P39189

20 F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-10:50:68//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003384

F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927

25 F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04521

F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

30 F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481

F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170

35 F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33301

F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-09:239:33//NEPHILA CLAVIPES (ORB SPIDER).//P19837

40 F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497

F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127.

45 F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451

F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-18:56:78//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e-28:136:47//HOMO SAPIENS (HUMAN).//P00736

50 F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105:217:85//RATTUS NORVEGICUS (RAT).//P50480

F-HEMBA1003548

F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558

55 F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGION (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706

F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-

MA-I).//1.8e-32:71:100//BOS TAURUS (BOVINE).//P16874  
 F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//4.1e-19:126:31//HOMO SAPIENS (HUMAN).//P14373  
 5 F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//3.9e-83:143:74//HOMO SAPIENS (HUMAN).//Q13330  
 F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D).//1.0:64:25//STAPHYLOCOCCUS AUREUS.//P03860  
 F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1).//1.0:41:29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01448  
 10 F-HEMBA1003581//TALIN.//3.7e-36:52:98//MUS MUSCULUS (MOUSE).//P26039  
 F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P19682  
 F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182  
 15 F-HEMBA1003597  
 F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//4.9e-10:85:41//ORYZOLAGUS CUNICULUS (RABBIT).//P06333  
 F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43).//0.086:10:70//BACTERIOPHAGE PHI-LF//Q07482  
 20 F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I.//4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10169  
 F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A).//0.096:40:37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P01387  
 F-HEMBA1003622  
 25 F-HEMBA1003630  
 F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:47:74//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.87:25:64//HOMO SAPIENS (HUMAN).//P39193  
 30 F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.8e-10:157:26//CAENORHABDITIS ELEGANS.//Q17963  
 F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED) (52-KD BRACKETING PROTEIN) (B52 PROTEIN).//4.9e-05:207:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26686  
 F-HEMBA1003656  
 35 F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B.//0.57:17:52//HOMO SAPIENS (HUMAN).//P02814  
 F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.0e-16:43:72//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1003679  
 F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//3.9e-08:137:27//CAENORHABDITIS ELEGANS.//P34629  
 40 F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//2.1e-20:127:40//MUS MUSCULUS (MOUSE).//Q60821  
 F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//3.0e-85:201:78//HOMO SAPIENS (HUMAN).//P56524  
 45 F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1.//0.13:69:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986  
 F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN).//0.021:153:26//HOMO SAPIENS (HUMAN).//P06731  
 F-HEMBA1003714//ABAECIN.//0.99:34:32//BOMBUS PASCUORUM.//P81463  
 50 F-HEMBA1003715  
 F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4e-34:155:56//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-27:181:41//HOMO SAPIENS (HUMAN).//P08547  
 55 F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.0037:103:33//HOMO SAPIENS (HUMAN).//P23246  
 F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-54:210:58//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1003758

F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.5e-51:220:52//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1003773

F-HEMBA1003783

F-HEMBA1003784

F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C).//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER).//P01434

F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338

F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.019:30:50//HOMO SAPIENS (HUMAN).//P30808

F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III.//1.8e-20:109:47//CAENORHABDITIS ELEGANS.//P42083

F-HEMBA1003807

F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.1e-09:23:78//OWENIA FUSIFORMIS.//P21260

F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484

F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.9e-22:39:76//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1003856

F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151

F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062

F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161

F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIS CATUS (CAT).//P48896

F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215

F-HEMBA1003902

F-HEMBA1003908

F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-10:60:63//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.1e-29:68:64//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637

F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//0.95:26:34//ESCHERICHIA COLI.//P46878

F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1003959

F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOMO SAPIENS (HUMAN).//Q14999

F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.98:19:57//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS) (FRAGMENT).//1.0:40:32//MYCOBACTERIUM LEPRAE.//P46861

F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66.//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN

AD169).//P16822

F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB.//5.2e-05:64:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-HEMBA1004000//PROTEIN Q300.//0.00042:17:82//MUS MUSCULUS (MOUSE).//Q02722

5 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1).//0.47:106:32//HOMO SAPIENS (HUMAN).//P06881

F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.96:36:33//PARAMECIUM TETRAURELIA.//P16001

10 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.00018:90:34//CAENORHABDITIS ELEGANS.//P41997

F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-34:75:80//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1004038

F-HEMBA1004042

15 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A.//1.0:20:55//ASPARAGUS OFFICINALIS (GARDEN ASPARAGUS).//P31753

F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3e-06:158:35//MUS MUSCULUS (MOUSE).//P05143

20 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN).//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54658

F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259.//0.87:133:23//HAEMOPHILUS INFLUENZAE.//P43974

F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.3e-25:39:64//HOMO SAPIENS (HUMAN).//P39191

25 F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-08:35:68//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004086

F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT).//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379

30 F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-26:84:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIENS (HUMAN).//Q14141

F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736.//1.0:44:34//HAEMOPHILUS INFLUENZAE.//P44300

35 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS.//Q10826

F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:41//MEDICAGO SATIVA (ALFALFA).//P11728

40 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039

F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO SAPIENS (HUMAN).//P02811

F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MOUSE).//P02798

45 F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-13:57:71//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE.//P43437

F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-14:115:31//CAENORHABDITIS ELEGANS.//P34529

50 F-HEMBA1004200

F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P11620

F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-09:48:64//HOMO SAPIENS (HUMAN).//P39193

55 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

F-HEMBA1004225//METALLOTHIONEIN-II.//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114

F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015).//5.9e-06:109:  
 33//HOMO SAPIENS (HUMAN).//P49593  
 F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN.//0.98:39:38//ESCHERICHIA COLI.//P05056  
 F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT).//0.66:36:38//MUS MUSCULUS (MOUSE).//Q04891  
 5 F-HEMBA1004246  
 F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN  
 CL-6).//1.0e-43:98:84//RATTUS NORVEGICUS (RAT).//Q08755  
 F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.014:160:28//NEPHILA CLA-  
 VIPES (ORB SPIDER).//P46804  
 10 F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-52:56:83//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBA1004272  
 F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III.//0.00084:33:54//  
 CAENORHABDITIS ELEGANS.//P34485  
 15 F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION)/9.3e-06:125:  
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40034  
 F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT)  
 (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A).//3.7e-30:239:32//HOMO SA-  
 PIENS (HUMAN).//Q10567  
 20 F-HEMBA1004286//CUTICLE COLLAGEN 34.//0.0027:71:38//CAENORHABDITIS ELEGANS.//P34687  
 F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN).//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P43606  
 F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.075:58:39//HO-  
 MO SAPIENS (HUMAN).//P30808  
 25 F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORGYIA PSEUDOTSUGATA  
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)  
 (ASFV).//P27946  
 30 F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//4.3e-43:133:44//  
 MUS MUSCULUS (MOUSE).//Q61967  
 F-HEMBA1004323  
 F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIENS (HUMAN).//P35326  
 F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOMO SAPIENS (HU-  
 MAN).//Q05925  
 35 F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-24:41:80//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//MUS MUSCULUS  
 40 (MOUSE).//P05143  
 F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-29:57:80//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P22516  
 45 F-HEMBA1004356  
 F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//1.0:125:28//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263  
 50 F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION.//0.76:170:25//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893  
 F-HEMBA1004394  
 F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HOMO SAPIENS (HU-  
 MAN).//P08547  
 55 F-HEMBA1004405  
 F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-  
 CLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGANS.//P52017  
 F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0019:47:59//HOMO SAPIENS (HU-



MAN).//P39191  
 F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-20:47:68//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.2e-64:134:69//HOMO SAPIENS (HU-  
 5 MAN).//P39193  
 F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVUM (GARDEN PEA).//  
 P20830  
 F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221  
 10 F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDIDA GLABRATA (YEAST)  
 (TORULOPSIS GLABRATA).//P05040  
 F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGANS.//P52275  
 F-HEMBA1004502  
 F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3-11:119:35//MUS MUSCULUS (MOUSE).//  
 15 P11260  
 F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00072:90:37//HOMO  
 SAPIENS (HUMAN).//Q15428  
 F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION.//6.3e-28:169:  
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589  
 20 F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN  
 1).//1.3e-80:226:66//HOMO SAPIENS (HUMAN).//P21333  
 F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS JANNASCHII.//  
 Q58174  
 F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTIC COD).//P51902  
 25 F-HEMBA1004554  
 F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//HOMO SAPIENS (HU-  
 MAN).//Q92556  
 F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PLASMODIUM  
 BERGHEI.//P06915  
 30 F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-08:35:80//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.6e-08:64:54//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE  
 35 PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT).//P17132  
 F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:37:45//MUS MUSCU-  
 LUS (MOUSE).//Q64739  
 F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-11:73:54//HOMO SAPIENS (HUMAN).//  
 P39188  
 40 F-HEMBA1004617  
 F-HEMBA1004629  
 F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION.//1.0:36:38//BA-  
 CILLUS SUBTILIS.//P42303  
 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING  
 45 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI.//P20453  
 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.7e-32:159:42//  
 CAENORHABDITIS ELEGANS.//P34535  
 F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:50:46//OWENIA FUSI-  
 FORMIS.//P21260  
 50 F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S  
 MAMBA).//P25682  
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170  
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//HOMO SAPIENS (HU-  
 55 MAN).//P02452  
 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS JANNASCHII.//  
 Q57879  
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,

TYPE B) (NMMHC-B).//0.00035:217:23//HOMO SAPIENS (HUMAN).//P35580  
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H).//0.058:118:30//  
 STREPTOCOCCUS PYOGENES.//P50470  
 F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-09:43:72//HOMO SAPIENS (HUMAN).//  
 5 P39188  
 F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/8.8e-18:50:84//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//0.0027:148:30//HOMO  
 SAPIENS (HUMAN).//000321  
 10 F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS ELEGANS.//P17656  
 F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-07:50:62//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR  
 CRESS).//P42743  
 F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.1e-60:210:61//HOMO SAPIENS (HU-  
 MAN).//P08547  
 20 F-HEMBA1004748  
 F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.8e-20:88:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0043:126:34//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 25 F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-28:47:78//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.22:77:27//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981  
 F-HEMBA1004758  
 30 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:58:43//OWENIA FUSI-  
 FORMIS.//P21260  
 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:298:53//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1004770  
 35 F-HEMBA1004771  
 F-HEMBA1004776//GRANULIN 1.//0.78:28:42//CYPRINUS CARPIO (COMMON CARP).//P81013  
 F-HEMBA1004778  
 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//6.9e-20:74:63//HOMO SAPIENS (HUMAN).//P50851  
 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:58:86//HOMO SAPIENS (HU-  
 MAN).//P08547  
 40 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182).//  
 0.72:75:33//CYANOPHORA PARADOXA.//P48324  
 F-HEMBA1004807  
 F-HEMBA1004816  
 45 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT).//1.0:50:38//MANDUCA  
 SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).//P26226  
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e-76:171:91//CANIS FA-  
 MILIARIS (DOG).//Q00004  
 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.0e-05:64:43//BOS TAURUS (BO-  
 VINE).//P25508  
 50 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR.//0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN  
 GREEN MAMBA).//P18329  
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.89:24:50//  
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612  
 55 F-HEMBA1004865  
 F-HEMBA1004880  
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.66:23:47//HOMO SAPIENS  
 (HUMAN).//P22532

F-HEMBA1004900

F-HEMBA1004909

F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:37:32//SPINACIA OL-  
ERACEA (SPINACH).//P09597

5 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3,5e-24:44:68//HOMO SAPIENS (HUMAN).//  
P39188

F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38//STRONGYLOCENTROTUS  
PURPURATUS (PURPLE SEA URCHIN).//P15997

10 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HOMO SAPIENS (HU-  
MAN).//P08547

F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:41//HOMO SAPIENS  
(HUMAN).//P50552

F-HEMBA1004934

F-HEMBA1004944

15 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.58:78:30//PARA-  
MECIUM TETRAURELIA.//P15579

F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM TETRAURELIA.//  
P15605

20 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA  
COLI.//P21324

F-HEMBA1004972

F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS  
(HUMAN).//P22531

F-HEMBA1004977

25 F-HEMBA1004978

F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811

F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA  
APHIDICOLA.//Q59176

30 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-  
TEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080

F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYS-  
TER).//P23038

F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P14235

F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS INFLUENZAE.//P44129

35 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).//0.76:72:31//GALLUS  
GALLUS (CHICKEN).//P32250

F-HEMBA1005035//HOMEBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN).//P50219

F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.47:49:32//HOMO SAPIENS  
(HUMAN).//P22532

40 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MUS MUSCULUS  
(MOUSE).//P35290

F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//BOS TAURUS (BOVINE).//  
P25508

F-HEMBA1005062

45 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//HOMO SAPIENS (HU-  
MAN).//P08547

F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAK-  
ER'S YEAST).//P32583

50 F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.6e-20:75:64//HOMO SAPIENS (HU-  
MAN).//P39191

F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34//BOS TAURUS (BO-  
VINE).//P25508

F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1).//  
4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809

55 F-HEMBA1005113

F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-24:99:60//HOMO SAPIENS (HU-  
MAN).//P39194

F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.11:22:54//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-HEMBA1005149/////ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-16:59:71//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN].//1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV).//Q01207

F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.40:53:33//APIS MEL-LIFERA (HONEYBEE).//P34859

F-HEMBA1005185//MYOSIN IB HEAVY CHAIN.//0.011:58:48//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34092

F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I.//3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09817

F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.8e-124:257:95//CANIS FAMILIARIS (DOG).//Q00004

F-HEMBA1005206//CUTICLE COLLAGEN 1.//0.010:118:33//CAENORHABDITIS ELEGANS.//P08124

F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40//HOMO SAPIENS (HUMAN).//P23246

F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN.//0.31:75:28//BACTERIOPHAGE T3.//P07715

F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN.//0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P20544

F-HEMBA1005241/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-28:138:55//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.014:39:41//HOMO SAPIENS (HUMAN).//P22531

F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362

F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.088:33:42//ZEA MAYS (MAIZE).//P43401

F-HEMBA1005274

F-HEMBA1005275/////ALU SUBFAMILY J WARNING ENTRY !!!!!/0.96:42:45//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168

F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:34//HOMO SAPIENS (HUMAN).//Q02817

F-HEMBA1005304/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-33:103:74//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY).//Q04536

F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III.//0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009

F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:51//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT).//0.57:44:38//GALLUS GALLUS (CHICKEN).//Q98913

F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//1.8e-55:199:59//GALLUS GALLUS (CHICKEN).//P05099

F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:36//PORPHYRA PURPUREA.//P51305

F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.1e-68:255:48//HOMO SAPIENS (HUMAN).//P51522

F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER).//P80403

F-HEMBA1005372

F-HEMBA1005374/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-34:92:75//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII)//0.99:39:33//BOS TAURUS (BOVINE)//P19034  
 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3'REGION (ORF4)//0.82:164:31//LACTO-  
 COCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P42377  
 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.98:44:38//  
 5 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703  
 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.066:64:29//MUS MUSCULUS  
 (MOUSE)//P07978  
 F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33//0.77:32:25//BACILLUS SUBTILIS//Q06798  
 F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 10 (EC 2.7.7.49); ENDONUCLEASE]//0.0065:38:52//MUS MUSCULUS (MOUSE)//P11369  
 F-HEMBA1005411//TOXIN S4C8//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMES-  
 ON'S MAMBA)//P25683  
 F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE  
 4 INHIBITOR C) (P18-INK4C)//4.3e-09:29:96//HOMO SAPIENS (HUMAN)//P42773  
 15 F-HEMBA1005426//TOXIN C10S2C2//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAM-  
 BA)//P25684  
 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.9e-16:78:60//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:57:31//DASYPUS NOVEMCINCTUS  
 20 (NINE-BANDED ARMADILLO)//O21329  
 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS)//0.68:41:  
 31//ARTEMIA SALINA (BRINE SHRIMP)//P19040  
 F-HEMBA1005469  
 F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-39:142:70//HOMO SAPIENS (HU-  
 25 MAN)//P08547  
 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.8e-10:44:68//HOMO SAPIENS (HU-  
 MAN)//P39194  
 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRNP70)//9.2e-  
 14:179:33//HOMO SAPIENS (HUMAN)//P08621  
 30 F-HEMBA1005497  
 F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD  
 FLUKE)//044125  
 F-HEMBA1005506  
 F-HEMBA1005508  
 35 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.5e-30:92:73//HOMO SAPIENS (HUMAN)//  
 P39194  
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//2.0e-39:95:61//DROSOPHILA  
 MELANOGASTER (FRUIT FLY)//O02193  
 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.1e-06:56:44//MUS MUSCULUS  
 40 (MOUSE)//P05142  
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//5.8e-05:192:33//BOS TAURUS (BO-  
 VINE)//P02453  
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.0e-18:87:57//HOMO SAPIENS (HUMAN)//  
 P39188  
 45 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//5.1e-22:77:54//HOMO SAPIENS (HU-  
 MAN)//P39191  
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.2e-81:157:98//MUS MUSCULUS (MOUSE)//  
 Q60809  
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A)//0.98:19:47//AMBROSIA PSI-  
 50 LOSTACHYA (WESTERN RAGWEED)//P43174  
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1//1.4e-72:137:97//RATTUS NORVEGICUS (RAT)//  
 P54842  
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.7e-29:47:78//HOMO SAPIENS (HUMAN)//  
 P39193  
 55 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION//1.6e-20:202:  
 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04272  
 F-HEMBA1005568  
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3)//1.0:80:31//

CAENORHABDITIS ELEGANS.//P24885

F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:75//HOMO SAPIENS (HUMAN).//P51805

F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A.//0.98:57:36//OVIS ARIES (SHEEP).//P02438

F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014

F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGICUS (RAT).//P28023

F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83:119:23//KLEBSIELLA PNEUMONIAE.//Q48453

F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-17:108:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:24:54//HOMO SAPIENS (HUMAN).//P22532

F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.7e-39:257:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036

F-HEMBA1005606

F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-20:27:96//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIOPHAGE 186.//P08711

F-HEMBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40958

F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION.//0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1005631

F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS (STRAIN WR).//P04309

F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-14:93:58//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAPIENS (HUMAN).//Q14142

F-HEMBA1005670

F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIENS (HUMAN).//P35326

F-HEMBA1005685

F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768

F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005717

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7).//0.22:55:41//OVIS ARIES (SHEEP).//P50415

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25296

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:60:63//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

F-HEMBA1005813

F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//GALLUS GALLUS (CHICKEN).//P00789

F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q02722 F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.6e-33:96:73//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:46//NYCTICEBUS COU-

CANG (SLOW LORIS).//P08548  
 F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MUS MUSCULUS (MOUSE).//P05143  
 F-HEMBA1005853//HYPOTHETICAL PROTEIN  
 5 MJ0647.//0.39:28:39//METHANOCOCCUS JANNASCHII.//Q58063  
 F-HEMBA1005884  
 F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O26240  
 F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-29:81:71//HOMO SAPIENS (HUMAN).//  
 10 P39195  
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III.//0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958  
 F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-27:86:70//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-38:99:81//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e-17:76:51//HOMO SAPIENS (HUMAN).//P51522  
 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.024:54:40//HOMO SAPIENS (HUMAN).//  
 20 P39189  
 F-HEMBA1005962  
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620  
 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 25 F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAPIENS (HUMAN).//Q15034  
 F-HEMBA1005999  
 F-HEMBA1006002  
 30 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267  
 F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1.//0.00016:84:39//HOMO SAPIENS (HUMAN).//P04281  
 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154  
 35 F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.2e-64:150:74//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1006042  
 F-HEMBA1006067//METALLOTHIONEIN A (MT-A).//0.86:34:41//THERMARCES CERBERUS.//P52721  
 40 F-HEMBA1006081  
 F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:35:54//SUS SCROFA (PIG).//P31636  
 F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329  
 45 F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.1e-09:58:60//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1).//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902  
 50 F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTHERMOPHILUS.//P23375  
 F-HEMBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794  
 F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-13:41:73//HOMO SAPIENS (HUMAN).//P39194  
 55 F-HEMBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-39:101:77//HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT).//P05432

F-HEMBA1006158

F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT)//0.017:20:95//HOMO SAPIENS (HUMAN)//P54829

5 F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.37:31:61//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23)//0.85:61:29//MUS MUSCULUS (MOUSE)//P09026

F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33//1.0:26:38//AQUIFEX AEOLICUS//O67756

10 F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3//1.0:22:40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE)//P01057

15 F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER)//P22826

F-HEMBA1006259

F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-05:32:65//HOMO SAPIENS (HUMAN)//P39192

20 F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2)//4.8e-112:248:78//HOMO SAPIENS (HUMAN)//P10264

F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//2.5e-71:164:75//HOMO SAPIENS (HUMAN)//P51003

F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32//0.81:27:44//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P80339

25 F-HEMBA1006284//CUTICLE COLLAGEN 2//0.36:42:40//CAENORHABDITIS ELEGANS//P17656

F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION//2.4e-37:143:31//ESCHERICHIA COLI//P76518

F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR//0.20:134:29//RATTUS NORVEGICUS (RAT)//Q63345 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821

30 F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA) (NECTADRIN)//0.71:46:39//RATTUS NORVEGICUS (RAT)//Q07490

F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID PHOSPHOPROTEIN)//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73)//P32531

35 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627//0.98:26:46//ARCHAEOGLOBUS FULGIDUS//028646

F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2)//8.8e-08:91:36//MUS MUSCULUS (MOUSE)//P26040

40 F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//9.1e-48:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY)//O2193

F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1//0.015:59:33//CASUARINA GLAUCA (SWAMP OAK)//Q39511

F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//6.8e-96:261:66//HOMO SAPIENS (HUMAN)//P28160

45 F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-)//0.97:60:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10348

F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20)//0.00023:110:35//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329

F-HEMBA1006380

50 F-HEMBA1006381//METALLOTHIONEIN-II//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114

F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.3e-26:123:52//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1006416

55 F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-24:102:50//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:101:57//HOMO SAPIENS (HUMAN)//P39188



F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVIRUS (STRAIN ME-BUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053  
F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-36:78:74//HOMO SAPIENS (HUMAN).//P39195  
5 F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTO-MONAS PHI).//O78421  
F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280  
F-HEMBA1006446  
10 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.1e-18:68:67//HOMO SAPIENS (HUMAN).//P39192  
F-HEMBA1006467  
F-HEMBA1006471  
F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552  
15 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192  
F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465  
F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547  
20 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907  
F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239  
25 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//P42711  
F-HEMBA1006497  
F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.15:26:73//HOMO SAPIENS (HUMAN).//P39188  
30 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608  
F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716  
F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583  
35 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//O08863  
F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696  
40 F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163  
45 F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437  
F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465  
F-HEMBA1006579  
50 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142  
F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.6e-34:93:77//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195  
55 F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.6e-20:73:63//HOMO SAPIENS (HUMAN).//

P39188

F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506

F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331

F-HEMBA1006635

F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341

F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817

F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014

F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS (MOUSE).//P14148

F-HEMBA1006653

F-HEMBA1006659

F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//O00268

F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:51//OWENIA FUSIFORMIS.//P21260

F-HEMBA1006682

F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1006696

F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53196

F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPIENS (HUMAN).//P28702

F-HEMBA1006717

F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485

F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78//HOMO SAPIENS (HUMAN).//P39191

F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN) (CADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (HUMAN).//P33151

F-HEMBA1006767

F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940

F-HEMBA1006780

F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS MUSCULUS (MOUSE).//P05143

F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:38:42//MUS MUSCULUS (MOUSE).//P70315

F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568

F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q01229

F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III.//1.0:46:36//CAENORHABDITIS ELEGANS.//P34327

F-HEMBA1006849

F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II).//1.0:41:31//BOS TAURUS (BOVINE).//P01001

F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS CUNICULUS (RAB-

BIT).//P16258

F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057

F-HEMBA1006900

5 F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473

10 F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258

F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS JANNASCHII.//Q57945

15 F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS (HUMAN).//P02810

F-HEMBA1006938

F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA TABACUM (COMMON TOBACCO).//P29449

F-HEMBA1006949

20 F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//P25508

F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206

25 F-HEMBA1006993

F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GP1X) (CD42A).//0.00096:60:33//HOMO SAPIENS (HUMAN).//P14770

30 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION.//1.0:25:56//ESCHERICHIA COLI.//P39166

F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828

35 F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007051

F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402

40 F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29//RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063

F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.58:49:38//BOMBYX MORI (SILK MOTH).//P25331

F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696

45 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

50 F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681

F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOCCUS JANNASCHII.//Q57626

F-HEMBA1007112

F-HEMBA1007113

55 F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP).//5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441

F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL LEECH).//P80302

F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//0.92:23:34//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182

F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.0078:17:70//ESCHERICHIA COLI.//P05834

F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS (MOUSE).//Q62477

F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!9.8e-06:38:65//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON TOBACCO).//Q43793

F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845

F-HEMBA1007206

F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.//2.4e-05:92:30//CAENORHABDITIS ELEGANS.//Q09275

F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE).//P00493

F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238

F-HEMBA1007256

F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN).//Q13939

F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421

F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!4.6e-24:98:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007281

F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162

F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156

F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:33//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1007319

F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672

F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:33//ESCHERICHIA COLI.//P11866

F-HEMBA1007327

F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!9.1e-12:37:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1.//Q02268

F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400

F-HEMBA1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA).//P29179

F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!2.7e-35:73:84//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AGROBACTERIUM TUMEFACIENS.//P08061

F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576

F-HEMBA1000037//HYPOTHETICAL 59.9 KD PROTEIN-IN SGA1-KTR7 INTERGENIC REGION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492

F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219  
F-HEMBB1000044  
F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS.//P54942  
5 F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-14:34:79//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-31:45:73//HOMO SAPIENS (HUMAN).//P39193  
10 F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494  
F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-21:82:59//HOMO SAPIENS (HUMAN).//P39195  
15 F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT).//P10354  
F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879  
F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/7.7e-08:31:87//HOMO SAPIENS (HUMAN).//P39189  
20 F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169  
25 F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327  
F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34:64//HOMO SAPIENS (HUMAN).//P20931  
F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-26:81:69//HOMO SAPIENS (HUMAN).//P39191  
30 F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:91:71//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQUUS CABALLUS (HORSE).//P80930  
35 F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:52//PORPHYRA PURPUREA.//P51329  
F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:39:76//HOMO SAPIENS (HUMAN).//P39192  
F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624  
40 F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949  
F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217  
45 F-HEMBB1000240  
F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:44:61//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000250  
F-HEMBB1000258  
50 F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEGANS.//P12114  
F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730  
F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).//0.75:30:43//BOS TAURUS (BOVINE).//P00429  
55 F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SCROFA (PIG).//P35323  
F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30//MUS MUSCULUS (MOUSE).//Q09098

F-HEMBB1000307

F-HEMBB1000312

F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO SAPIENS (HUMAN).//P07996

5 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NON-STRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43).//Q04854

F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT).//0.82:33:45//MUS MUSCULUS (MOUSE).//P10754

10 F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:44:40//ORYCTOLAGUS CUNICULUS (RABBIT).//P80456

F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

15 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-14:54:55//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPHAGE L5.//Q05289

F-HEMBB1000343

20 F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:83:56//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.7e-34:56:78//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1000376

25 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:79:35//BOS TAURUS (BOVINE).//P25508

F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50531

30 F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583

F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//CYANOPHORA PARADOXA.//P48129

F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.023:97:35//HOMO SAPIENS (HUMAN).//Q15427

35 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.8e-20:111:54//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.93:24:50//BACTERIOPHAGE T4.//P07076

40 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-23:85:70//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.88:27:51//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000455

F-HEMBB1000472

45 F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P11905

F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II).//0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//P01427

F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.3e-16:50:80//HOMO SAPIENS (HUMAN).//P39195

50 F-HEMBB1000491

F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE) (IBV).//P30237

F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//HOMO SAPIENS (HUMAN).//P08547

55 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.021:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546

F-HEMBB1000523

F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-14:43:83//GALLUS

GALLUS (CHICKEN).//P32018

F-HEM BB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.19:97:30//TRYPA-  
SOMA BRUCEI BRUCEI.//P04540

F-HEM BB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS LAEVIS (AFRICAN  
CLAWED FROG).//P40744

F-HEM BB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
(TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS (HUMAN).//000268

F-HEM BB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:5:2:34//METRIDIDIUM SENILE  
(BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493

F-HEM BB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.3e-10:52:73//HOMO SAPIENS (HU-  
MAN).//P39191

F-HEM BB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.8e-26:76:76//HOMO SAPIENS (HUMAN).//  
P39192

F-HEM BB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)  
(COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HUMAN).//O00483

F-HEM BB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.9e-25:61:75//HOMO SAPIENS (HUMAN).//  
P39193

F-HEM BB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//PETROMYZON MARINUS  
(SEA LAMPREY).//Q35537

F-HEM BB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPIENS (HUMAN).//P35326

F-HEM BB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32//GALLUS GALLUS  
(CHICKEN).//P12105

F-HEM BB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:41//NYCTICEBUS COU-  
CANG (SLOW LORIS).//P08548

F-HEM BB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//0.0022:98:28//  
CAENORHABDITIS ELEGANS.//P34284

F-HEM BB1000630

F-HEM BB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE  
C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825

F-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:173:28//MUS MUSCU-  
LUS (MOUSE).//P27671

F-HEM BB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.6e-41:94:82//HOMO SAPIENS (HUMAN).//  
P39193

F-HEM BB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P07476

F-HEM BB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.3e-30:77:76//HOMO SAPIENS (HUMAN).//  
P39195

F-HEM BB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-37:58:81//HOMO SAPIENS (HUMAN).//  
P39189

F-HEM BB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.2e-37:61:77//HOMO SAPIENS (HUMAN).//  
P39193

F-HEM BB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA BURGDORFERI (LYME DIS-  
EASE SPIROCHETE).//P70845

F-HEM BB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HOMO SAPIENS (HU-  
MAN).//P08547

F-HEM BB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//0.012:  
37:37//ESCHERICHIA COLI.//P07965

F-HEM BB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.1e-21:66:72//HOMO SAPIENS (HUMAN).//  
P39193

F-HEM BB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:49//RATTUS NORVEGICUS  
(RAT).//P54256

F-HEM BB1000705

F-HEM BB1000706

F-HEM BB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS  
(CYMV).//P16485

F-HEM BB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS NORVEGICUS (RAT).//  
P70550

F-HEM BB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.4e-25:85:70//HOMO SAPIENS (HU-  
MAN).//P39194

F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P35871  
 F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-29:42:85//HOMO SAPIENS (HUMAN).//P39194  
 5 F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045  
 F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG).//P22075  
 F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUSCULUS (MOUSE).//P17095  
 10 F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083  
 F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956  
 F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:93:51//HOMO SAPIENS (HUMAN).//P39188  
 15 F-HEMBB1000794  
 F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS GALLUS (CHICKEN).//P49578  
 F-HEMBB1000810  
 F-HEMBB1000821  
 20 F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV).//P15099  
 F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931  
 F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302  
 25 F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547  
 30 F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBB1000852  
 35 F-HEMBB1000870  
 F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725  
 F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78459  
 F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251  
 40 F-HEMBB1000888  
 F-HEMBB1000890  
 F-HEMBB1000893  
 F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188  
 45 F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552  
 F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.29:56:46//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156  
 50 F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614  
 F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326  
 55 F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:66:36//BOS TAURUS (BOVINE).//O18739



F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG).//0.00042:77:41//HOMO SAPIENS (HUMAN).//P04196

F-HEMBB1000981

F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575

F-HEMBB1000991

F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.58:34:35//ESCHERICHIA COLI.//P33669

F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B.//P26550

F-HEMBB1001008

F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN).//P17097

F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN).//1.0:58:39//RATTUS NORVEGICUS (RAT).//P97545

F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.4e-07:36:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1001024

F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203

F-HEMBB1001047

F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION).//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636

F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-33:95:76//HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1.0:38:36//CAENORHABDITIS ELEGANS.//P34591

F-HEMBB1001063

F-HEMBB1001068

F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROIDES NOXIUS (MEXICAN SCORPION).//P08815

F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067

F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126:287:85//RATTUS NORVEGICUS (RAT).//P38378

F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//BACTERIOPHAGE L2.//P42537

F-HEMBB1001117

F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//HOMO SAPIENS (HUMAN).//Q99715

F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296

F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-09:53:62//HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-05:46:56//HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:34//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393

F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:71:59//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357

F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:27//HOMO SAPIENS (HUMAN).

MAN).//Q15269

F-HEM BB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54858

F-HEM BB1001199

5 F-HEM BB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCULUS (MOUSE).//P15974

F-HEM BB1001209

F-HEM BB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCULUS (MOUSE).//P15974

10 F-HEM BB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:49:67//HOMO SAPIENS (HUMAN).//P39194

F-HEM BB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (EC 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406

15 F-HEM BB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//MUS MUSCULUS (MOUSE).//P46938

F-HEM BB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876

F-HEM BB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.0:23:43//KLEBSIELLA PNEUMONIAE.//P13155

20 F-HEM BB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0).//0.14:16:43//HOMO SAPIENS (HUMAN).//P80294

F-HEM BB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:40:75//HOMO SAPIENS (HUMAN).//P39195

25 F-HEM BB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:33:78//HOMO SAPIENS (HUMAN).//P39193

F-HEM BB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1.0:58:37//CAENORHABDITIS ELEGANS.//Q10928

F-HEM BB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM VINOSUM.//Q06527

30 F-HEM BB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHERICHIA COLI.//P46719

F-HEM BB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSCULUS (MOUSE).//P11260

F-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (HUMAN).//P17081

35 F-HEM BB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626

F-HEM BB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157

F-HEM BB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730

40 F-HEM BB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-24:53:71//HOMO SAPIENS (HUMAN).//P39195

F-HEM BB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782

45 F-HEM BB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCULUS (MOUSE).//P15974

F-HEM BB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEM BB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//SCIARA COPROPHILA (FUNGUS GNAT).//Q01799

50 F-HEM BB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.2e-20:62:62//HOMO SAPIENS (HUMAN).//P39194

F-HEM BB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:34//MYCOBACTERIUM TUBERCULOSIS.//Q50606

55 F-HEM BB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HOMO SAPIENS (HUMAN).//P08547

F-HEM BB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-14:61:62//HOMO SAPIENS (HUMAN).//P39188

F-HEM BB1001356

F-HEMBB1001364  
 F-HEMBB1001366/HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /  
 SENEGAL).//P14586  
 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//8.6e-40:146:61//HOMO SAPIENS (HU-  
 5 MAN).//P39192  
 F-HEMBB1001369  
 F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.9e-25:49:83//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29//MUS MUSCULUS  
 10 (MOUSE).//P70444  
 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P40091  
 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 15 A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE).//P17426  
 F-HEMBB1001410  
 F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.99:37:21//  
 ORYZA SATIVA (RICE).//P12162  
 F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.0035:40:60//HOMO SAPIENS (HUMAN).//  
 20 P39195  
 F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEU-  
 CYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE).//1.1e-  
 99:21:86//BOS TAURUS (BOVINE).//P00727  
 F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.4e-30:57:78//HOMO SAPIENS (HUMAN).//  
 25 P39195  
 F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURSOR (PDP) (EC  
 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT (PDPC)).//2.5e-79:155:97//  
 BOS TAURUS (BOVINE).//P35816  
 F-HEMBB1001449  
 30 F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161  
 F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAUDI.//P14592  
 F-HEMBB1001463  
 F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PALO  
 35 ALTO / UGANDA).//P07765  
 F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLG16.1 (FRAGMENT).//4.2e-10:37:43//XENO-  
 PUS LAEVIS (AFRICAN CLAWED FROG).//P18712 F-HEMBB1001500  
 F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-39:59:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 40 F-HEMBB1001527//HOMEODOMAIN PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT).//0.21:131:25//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019  
 F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L5.//Q05241  
 F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//LUMBRICUS TERRESTRIS  
 (COMMON EARTHWORM).//Q34942  
 45 F-HEMBB1001536  
 F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//0.0063:52:50//HOMO SAPIENS (HU-  
 MAN).//P39191  
 F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.9e-23:69:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 50 F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P47709  
 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.9e-12:51:54//HOMO SAPIENS (HU-  
 MAN).//P39194  
 55 F-HEMBB1001585  
 F-HEMBB1001586  
 F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.0031:31:48//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

F-HEMBB1001603  
 F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS (MOUSE)//P11369  
 5 F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:32//HOMO SAPIENS  
 (HUMAN)//P22531  
 F-HEMBB1001630  
 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:44//LYCOPERSICON ESCULEN-  
 TUM (TOMATO)//Q40157  
 10 F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0042:26:73//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-HEMBB1001641  
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS (DOG)//  
 O02771  
 15 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HU-  
 MAN)//Q05925  
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//  
 P52814  
 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823  
 20 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST)//P32583  
 F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIb)  
 (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175  
 25 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//  
 P10569  
 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.0e-08:35:71//HOMO SAPIENS (HUMAN)//  
 P39195  
 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-  
 MOUS CELL MARKER) (SPRP)//0.91:39:41//SUS SCROFA (PIG)//P35323  
 30 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONI-  
 CUM//P27394  
 F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//  
 LEMUR CATTAL (RING-TAILED LEMUR)//Q34878  
 35 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-35:97:74//HOMO SAPIENS (HU-  
 MAN)//P39194  
 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3  
 P116) (EIF3 P110)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884  
 F-HEMBB1001747  
 40 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-43:75:70//HOMO SAPIENS (HUMAN)//  
 P39195  
 F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722  
 F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9)//0.94:35:42//XENO-  
 PUS LAEVIS (AFRICAN CLAWED FROG)//Q91879  
 45 F-HEMBB1001760  
 F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE L5//Q05245  
 F-HEMBB1001785  
 F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:31//PORPHYRA PURPUREA//  
 P51270  
 50 F-HEMBB1001802  
 F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-39:54:77//HOMO SAPIENS (HUMAN)//  
 P39193  
 F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-19:97:57//HOMO SAPIENS (HU-  
 MAN)//P39194  
 55 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:  
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951  
 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT)//0.0014:40:45//SORGHUM VUL-  
 GARE (SORGHUM)//Q99069  
 F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.1e-14:85:61//HOMO SAPIENS (HU-

MAN).//P39191  
 F-HEMBB1001839//PROBABLE E4 PROTEIN.//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969  
 F-HEMBB1001850  
 F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-30:57:68//HOMO SAPIENS (HUMAN).//P39194  
 5 F-HEMBB1001867  
 F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-11:95:45//HOMO SAPIENS (HUMAN).//P39188  
 10 F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION.//1.0:34:38//AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41459  
 F-HEMBB1001874  
 F-HEMBB1001875  
 15 F-HEMBB1001880  
 F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902  
 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234  
 F-HEMBB1001906  
 20 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80//HOMO SAPIENS (HUMAN).//Q92794  
 F-HEMBB1001910  
 F-HEMBB1001911  
 25 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574  
 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBB1001922  
 30 F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801  
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412  
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.1e-34:63:85//HOMO SAPIENS (HUMAN).//P39189  
 35 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT).//P80450  
 F-HEMBB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P10208  
 F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062  
 40 F-HEMBB1001952  
 F-HEMBB1001953  
 F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.7e-11:51:60//HOMO SAPIENS (HUMAN).//P39188  
 45 F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.6e-24:163:42//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.1e-35:55:80//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-37:108:75//HOMO SAPIENS (HUMAN).//P39192  
 50 F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPHAGE ALPHA-3.//P31280  
 F-HEMBB1001988  
 F-HEMBB1001990  
 F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HOMO SAPIENS (HUMAN).//P08547  
 55 F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-19:38:73//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPHYRA PURPUREA.//

P51369

F-HEMBB1002005/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:94:40//HOMO SAPIENS (HUMAN).//  
P39195

F-HEMBB1002009

5 F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67).//1.0:17:47//  
ESCHERICHIA COLI.//P39395

F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.4e-50:139:55//BLABERUS DIS-  
COIDALIS (TROPICAL COCKROACH).//P29981

10 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3).//0.052:40:42//HERPESVI-  
RUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577

F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTER XYLINUM (AC-  
ETOBACTER PASTEURIANUS).//P37697

F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55//HOMO SAPIENS (HUMAN).//  
P03928

15 F-HEMBB1002049

F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC  
PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUMAN).//P02812

F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56:44//GALLUS GALLUS (CHICK-  
EN).//P17277

20 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-  
BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//2.4e-07:75:40//BABOON ENDOGENOUS VI-  
RUS (STRAIN M7).//P10269

25 F-HEMBB1002094/////ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.9e-24:63:82//HOMO SAPIENS (HU-  
MAN).//P39191

F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.94:26:42//ZEA MAYS  
(MAIZE).//P43401

30 F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NORVEGICUS (RAT).//  
P56163

F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPHYRA PURPUREA.//  
P51270

F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAGO TRUNCATULA (BAR-  
REL MEDIC).//P93329

35 F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102).//  
5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811

F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN  
AD169).//P16835

F-HEMBB1002190

40 F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN  
KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).//1.2e-27:59:100//  
HOMO SAPIENS (HUMAN).//Q06418

F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOMO SAPIENS (HUMAN).//  
Q99676

45 F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBB1002232/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.6e-21:56:71//HOMO SAPIENS (HUMAN).//  
P39195

F-HEMBB1002247

50 F-HEMBB1002249/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-29:93:69//HOMO SAPIENS (HU-  
MAN).//P39194

F-HEMBB002254/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:101:67//HOMO SAPIENS (HU-  
MAN).//P39194

F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:73:28//PARA-  
MECIUM TETRAURELIA.//P15579

55 F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:26//PLASMODIUM FALCI-  
PARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816

F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:36//NYCTICEBUS COU-  
CANG (SLOW LORIS).//P08548

F-HEMBB1002300

F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00011:26:84//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.1e-11:41:85//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

F-HEMBB1002340

F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835

F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:63:96//HOMO SAPIENS (HUMAN).//P23919

F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346

F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895

F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703

F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455

F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//066566

F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626

F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095

F-HEMBB1002415

F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194

F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692

F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-07:31:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642

F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.030:182:28//HOMO SAPIENS (HUMAN).//Q15427

F-HEMBB1002492

F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-08:41:75//HOMO SAPIENS (HUMAN).//P39192

F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:31:77//HOMO SAPIENS (HUMAN).//P12895

F-HEMBB1002509

F-HEMBB1002510

F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRUS B (CVB).//P37990

F-HEMBB1002531

F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.1e-36:80:73//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1002545

F-HEMBB1002550//HOMEBOX PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:83:34//MUS MUSCULUS (MOUSE).//P23813

F-HEMBB1002556

F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2

SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:77//SUS SCROFA (PIG).//Q29350  
 F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBER-  
 GINE).//P01078  
 5 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).//1.9e-20:90:54//  
 PSEUDOMONAS AERUGINOSA.//P28812  
 F-HEMBB1002596  
 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//O14817  
 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//  
 P08089  
 10 F-HEMBB1002603  
 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162  
 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HU-  
 MAN).//P08547  
 15 F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN).//P20553  
 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON  
 20 EUROPEAN SCORPION).//P55902  
 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:  
 31:54//BACTERIOPHAGE P4.//P12552  
 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE  
 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779  
 25 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B)  
 (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136  
 F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COU-  
 CANG (SLOW LORIS).//P08548  
 F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:  
 30 35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879  
 F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885  
 F-HEMBB1002686  
 F-HEMBB1002692  
 F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//  
 35 0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13.//P03669  
 F-HEMBB1002699  
 F-HEMBB1002702  
 F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//3.6e-40:180:37//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212  
 40 F-HEMBB1002712  
 F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO SAPIENS (HU-  
 MAN).//P39189  
 F-MAMMA1000019  
 F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC  
 45 FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HO-  
 MO SAPIENS (HUMAN).//P49326  
 F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO RERIO (ZE-  
 BRAFISH) (ZEBRA DANIO).//Q04475  
 F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//BOVINE LEUKEMIA VI-  
 50 RUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412  
 F-MAMMA1000045  
 F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS MUSCULUS  
 (MOUSE).//P47226  
 F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69//HOMO SAPIENS (HU-  
 55 MAN).//P39194  
 F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORGYIA PSEUDOTSUGATA  
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73//HOMO SAPIENS (HU-



MAN).//P39195

F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS).//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09860

F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.4e-30:43:86//HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:17:52//HOMO SAPIENS (HUMAN).//P22531

F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HALOARCUA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116

F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-MAMMA1000133

F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS JANNASCHII.//Q58063

F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//P29798

F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:27//MUS MUSCULUS (MOUSE).//P51125

F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09456

F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463

F-MAMMA1000171

F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643

F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901

F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523

F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1000221

F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379

F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370

F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771

F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2).//0.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470

F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550

F-MAMMA1000266

F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.5e-42:95:84//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28481

F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//HORDEUM VULGARE (BARLEY).//P17991

F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.4e-17:56:76//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324

F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-32:84:58//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM VULGARE (BAR-

LEY).//P17992

F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832

F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658

F-MAMMA1000312

F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337

F-MAMMA1000331

F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMAUTOTROPHICUM.//O26117

F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039

F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000360

F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000385

F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36//HOMO SAPIENS (HUMAN).//P43489

F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MOUSE).//P47708

F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//HOMO SAPIENS (HUMAN).//Q16718

F-MAMMA1000413//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (MOUSE).//P11369

F-MAMMA1000414

F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232

F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANTIC COD).//P51902

F-MAMMA1000423

F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.3e-25:65:76//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584

F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I.//0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296

F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:106:55//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-35:80:68//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.8e-24:74:77//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682  
 F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506  
 5 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000516  
 F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HOMO SAPIENS (HUMAN).//P08547  
 10 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACCINIA VIRUS (STRAIN WR).//P17359  
 F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CALLINECTES SAPIDUS (BLUE CRAB).//P55949  
 F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF.//0.98:37:35//ESCHERICHIA COLI.//P33939  
 15 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO SAPIENS (HUMAN).//P39191  
 F-MAMMA1000583  
 20 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO SAPIENS (HUMAN).//P39195  
 25 F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318  
 30 F-MAMMA1000616  
 F-MAMMA1000621  
 F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K).//0.0045:25:48//HOMO SAPIENS (HUMAN).//P80296  
 F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00078:79:35//MUS MUSCULUS (MOUSE).//P05143  
 35 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN.//1.0:25:28//MAGUARI VIRUS.//P16607  
 F-MAMMA1000664  
 F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-05:186:30//HOMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.6e-06:195:30//MUS MUSCULUS (MOUSE).//P05143  
 40 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//3.8e-28:184:35//AEDES AEGYPTI (YELLOW FEVER MOSQUITO).//P42660  
 F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21).//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P04487  
 45 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-31:97:74//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB).//P55950  
 F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE).//1.6e-05:88:35//LACTOBACILLUS PENTOSUS.//P21939  
 50 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.44:126:30//RATTUS NORVEGICUS (RAT).//P16636  
 F-MAMMA1000718//METALLOTHIONEIN-IIIE (MT-2E).//1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT).//P80292  
 55 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-28:60:71//HOMO SAPIENS (HUMAN).//P39193  
 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.7e-14:63:53//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)//1.8e-43:258:43//HOMO SAPIENS (HUMAN)//O14647  
 F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-12:76:55//HOMO SAPIENS (HUMAN)//P39188  
 5 F-MAMMA1000733  
 F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN)//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14906  
 F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87115  
 10 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.3e-36:144:47//HOMO SAPIENS (HUMAN)//P39190  
 F-MAMMA1000746  
 F-MAMMA1000752  
 15 F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.6e-29:75:72//HOMO SAPIENS (HUMAN)//P39195  
 F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-09:59:64//HOMO SAPIENS (HUMAN)//P39194  
 F-MAMMA1000775  
 20 F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-35:99:74//HOMO SAPIENS (HUMAN)//P39193  
 F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-19:65:70//HOMO SAPIENS (HUMAN)//P39195  
 F-MAMMA1000782  
 25 F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137//0.015:59:37//MUS MUSCULUS (MOUSE)//P11260  
 F-MAMMA1000802//MYOSIN IC HEAVY CHAIN//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569  
 F-MAMMA1000824//ACTIN 1//0.046:60:31//ZEA MAYS (MAIZE)//P02582  
 F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT//1.0:30:46//ESCHERICHIA COLI//P19929  
 30 F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-28:80:58//HOMO SAPIENS (HUMAN)//P39188  
 F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//1.5e-39:130:36//METHANOBACTERIUM THERMOAUTOTROPHICUM//O27540  
 35 F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.064:43:41//HORDEUM VULGARE (BARLEY)//P17992  
 F-MAMMA1000843  
 F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY)//P03895  
 40 F-MAMMA1000851//CUTICLE COLLAGEN 34//0.019:107:29//CAENORHABDITIS ELEGANS//P34687  
 F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00098:149:32//HOMO SAPIENS (HUMAN)//Q15428  
 F-MAMMA1000856//METALLOTHIONEIN (MT)//0.63:39:41//POTAMON POTAMIOS//P55952  
 45 F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28968  
 F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA)//P17494  
 F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.4e-16:41:68//HOMO SAPIENS (HUMAN)//P39188  
 50 F-MAMMA1000865//SALIVARY PROUNE-RICH PROTEIN II-1 (FRAGMENT)//0.030:100:32//HOMO SAPIENS (HUMAN)//P81489  
 F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX)//0.98:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER)//P49272  
 F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B//0.18:21:47//HOMO SAPIENS (HUMAN)//P02814  
 55 F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO SAPIENS (HUMAN)//P39189  
 F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-38:62:74//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BOS TAURUS (BOVINE).//  
 P25508  
 F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.87:15:60//  
 CAENORHABDITIS ELEGANS.//Q11116  
 5 F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN  
 H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN  
 SENSITIVE GLYCOPROTEIN 120) (PK-120).//5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624  
 F-MAMMA1000905  
 F-MAMMA1000906  
 10 F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS TENAX VIRUS 1  
 (STRAIN KRA1) (TTV1).//P19299  
 F-MAMMA1000921  
 15 F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-10:49:65//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:54//RECLINOMONAS  
 AMERICANA.//O21281  
 F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-25:55:69//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-08:36:75//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-MAMMA1000943  
 F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57).//  
 25 0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P04930  
 F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.024:37:37//ESCHERICHIA  
 COLI.//Q47185  
 F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.0e-39:61:78//HOMO SAPIENS (HU-  
 MAN).//P39189  
 30 F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0054:29:72//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABDITIS ELEGANS.//  
 P35799  
 F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HUMAN).//P02814  
 35 F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCULUS (MOUSE).//  
 P15973  
 F-MAMMA1000998  
 F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426  
 F-MAMMA1001008//PROGASTRICIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT).//3.2e-14:  
 40 131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P03955  
 F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.016:61:42//STREPTO-  
 MYCES FRADIAE.//P20186  
 F-MAMMA1001024  
 F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)  
 45 (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//2.4e-20:234:29//GALLUS GALLUS (CHICKEN).//  
 Q90674  
 F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-15:52:78//HOMO SAPIENS (HU-  
 MAN).//P39193  
 F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II).//0.53:25:48//RADIANTHUS  
 50 PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS).//P01534  
 F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS MUSCULUS  
 (MOUSE).//P15508  
 F-MAMMA1001050  
 F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:187:47//SCHIZOSAC-  
 55 CHAROMYCES POMBE (FISSION YEAST).//Q09747  
 F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722  
 F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1).//1.0:70:37//RAT-  
 TUS NORVEGICUS (RAT).//Q63244

F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//HOMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//HOMO SAPIENS (HUMAN).//P29374  
 5 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//HOMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:82:71//HOMO SAPIENS (HUMAN).//P01764  
 F-MAMMA1001082  
 10 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HOMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51521  
 15 F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//MUS MUSCULUS (MOUSE).//P02463  
 F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.3e-07:66:45//HOMO SAPIENS (HUMAN).//P39189  
 20 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174  
 F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201  
 F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00014:36:66//HOMO SAPIENS (HUMAN).//P39188  
 25 F-MAMMA1001145  
 F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953  
 F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.2e-23:53:64//HOMO SAPIENS (HUMAN).//P39188  
 30 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272  
 F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.//0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486  
 F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-32:44:86//HOMO SAPIENS (HUMAN).//P39194  
 35 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466  
 F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN).//P42566  
 40 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB).//P55950  
 F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.3e-11:82:58//HOMO SAPIENS (HUMAN).//P39192  
 F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:67:71//HOMO SAPIENS (HUMAN).//P39188  
 45 F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994  
 F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-37:55:87//HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS.//Q10690  
 50 F-MAMMA1001243  
 F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055  
 F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774  
 55 F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486

F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219:27//HOMO SAPIENS (HUMAN).//P13535

F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HOMO SAPIENS (HUMAN).//P08547

5 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259

F-MAMMA1001274//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN).//P39194

10 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54//ESCHERICHIA COLI.//P05834

F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:69//HOMO SAPIENS (HUMAN).//Q14681

F-MAMMA1001296//!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN).//P39193

15 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29:37//HAEMOPHILUS INFLUENZAE.//P44668

F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9.9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960

F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46:60//HOMO SAPIENS (HUMAN).//P20931

20 F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808

F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044

25 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS (HUMAN).//P26651

F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927

F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33:45//SOLANUM TUBEROSUM (POTATO).//P01082

30 F-MAMMA1001383//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-30:86:77//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195:92//HOMO SAPIENS (HUMAN).//P02750

35 F-MAMMA1001397//!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-19:55:69//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841

40 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-MAMMA1001419//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-16:99:51//HOMO SAPIENS (HUMAN).//P39194

45 F-MAMMA1001420//!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.0018:23:65//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1001435//!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.7e-22:60:58//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1001442

F-MAMMA1001446//!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-23:48:75//HOMO SAPIENS (HUMAN).//P39194

50 F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIOPHAGE L5.//Q05245

F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS TYPE 2.//P03290

F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623

55 F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-

TRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384  
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE.//  
 P26800  
 F-MAMMA1001510  
 5 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:31//STREPTO-  
 MYCES FRADIAE.//P20186  
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42//HAEMOPHILUS  
 INFLUENZAE.//P45183  
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS JANNASCHII.//  
 10 P81308  
 F-MAMMA1001575  
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED  
 FROG).//P23330  
 F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:38:55//HOMO SAPIENS (HUMAN).//  
 15 P39195  
 F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS  
 (HUMAN).//P29279  
 F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.//0.14:82:29//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902  
 20 F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//  
 P52926  
 F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-05:24:66//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS.//P34804  
 25 F-MAMMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.6e-26:57:78//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910  
 F-MAMMA1001635  
 F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-  
 30 TRALIAN ECHIDNA).//P35311  
 F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 TEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160  
 F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056  
 F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124  
 35 F-MAMMA1001671  
 F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HU-  
 MAN).//P08572  
 F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00026:147:34//STREP-  
 TOMYCES FRADIAE.//P20186  
 40 F-MAMMA1001686  
 F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRA-  
 TORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616  
 F-MAMMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-28:56:69//HOMO SAPIENS (HU-  
 MAN).//P39194  
 45 F-MAMMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:39:71//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS  
 (PURPLE SEA URCHIN).//Q27287  
 F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//  
 50 P09653  
 F-MAMMA1001740  
 F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA  
 55 DANIO).//Q90270  
 F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//P34410



F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645  
 F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.94:30:43//PSEUDOMONAS PUTIDA.//P25753  
 5 F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.6e-34:103:59//HOMO SAPIENS (HUMAN).//P39191  
 F-MAMMA1001764  
 F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818  
 10 F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:97:69//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HOMO SAPIENS (HUMAN).//P51805  
 F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-09:55:61//HOMO SAPIENS (HUMAN).//P39188  
 15 F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143  
 F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HOMO SAPIENS (HUMAN).//P08547  
 20 F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-24:69:69//HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042  
 F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.8e-12:53:69//HOMO SAPIENS (HUMAN).//P39195  
 25 F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO SAPIENS (HUMAN).//P08547  
 F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:86:55//HOMO SAPIENS (HUMAN).//P39188  
 30 F-MAMMA1001818  
 F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238  
 F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271  
 35 F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-35:77:88//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (HUMAN).//O14754  
 F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0e-19:92:58//HOMO SAPIENS (HUMAN).//P39188  
 40 F-MAMMA1001851  
 F-MAMMA1001854  
 F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210  
 F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:161:27//MYCOPLASMA GENITALIUM.//P47435  
 45 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911  
 F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:31//MUS MUSCULUS (MOUSE).//P07978  
 50 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157  
 F-MAMMA1001880  
 F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN).//P39192  
 55 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:44:68//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION.//0.00013:77:

37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03525  
 F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//0.41:106:29//  
 CAENORHABDITIS ELEGANS.//Q09564  
 F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSCULUS (MOUSE).//  
 5 Q06666  
 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT).//1.0:46:28//KLEB-  
 SIELLA AEROGENES.//Q08600  
 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:68//HOMO SAPIENS (HU-  
 MAN).//P08547  
 10 F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:37//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//Q02722  
 F-MAMMA1002009//PROBABLE E5 PROTEIN.//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385  
 F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE  
 15 C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN).//1.0:100:31//HOMO SAPIENS  
 (HUMAN).//P29966  
 F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:86:65//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.5e-20:67:58//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01644  
 F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:46//HOMO SAPIENS (HUMAN).//  
 P39192  
 25 F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMI-  
 NOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NORVEGICUS (RAT).//P04694  
 F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:70:77//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:26:76//HOMO SAPIENS (HUMAN).//  
 30 P39188  
 F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:46//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:26:46//COTURNIX COTURNIX  
 JAPONICA (JAPANESE QUAIL).//P50682  
 35 F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P32583  
 F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN).//P20520  
 F-MAMMA1002093  
 40 F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00079:143:33//STREP-  
 TOMYCES FRADIAE.//P20186  
 F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:43:34//METRIDIDIUM SENILE  
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493  
 F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:68//HOMO SAPIENS (HU-  
 45 MAN).//P39192  
 F-MAMMA1002132  
 F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:69:65//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMAN).//Q00587  
 50 F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCOPERSICON ESCULENTUM (TO-  
 MATO).//Q00451  
 F-MAMMA1002153  
 F-MAMMA1002155  
 F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34//STREPTOMYCES NI-  
 55 GRESCENS.//P01077  
 F-MAMMA1002158  
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.0e-66:157:70//HOMO SAPI-  
 ENS (HUMAN).//P15880

F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:56:64//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//9.0e-09:28:100//HOMO SAPIENS (HUMAN).//P32119

F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.0023:132:33//HOMO SAPIENS (HUMAN).//O00268

F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.00032:68:35//HOMO SAPIENS (HUMAN).//P02452

F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0079:224:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//1.4e-118:151:94//RATTUS NORVEGICUS (RAT).//P70541

F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.028:112:33//MUS MUSCULUS (MOUSE).//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.0012:80:32//ORYZOLAGUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.17:139:28//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:14:57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65//HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40414

F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.00011:138:38//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020

F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:144:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:50//MUS MUSCULUS (MOUSE).//P05143

F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.84:65:32//STRUTHIO CAMELUS (OSTRICH).//O21405

F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00016:70:38//MUS MUSCULUS (MOUSE).//P15265

F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION (URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084

F-MAMMA1002317

F-MAMMA1002319//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS (MOUSE).//P11369

F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931

F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:214:31//BOS TAURUS (BOVINE).//P02453

F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMATIA (ROMAN SNAIL)

(EDIBLE SNAIL).//P55947

F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOCCUS JANNASCHII.//Q57752

F-MAMMA1002352

F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).//P11953

F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78487

F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626

F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-MAMMA1002384

F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241

F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//O21003

F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311

F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926

F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786

F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217

F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002446

F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551

F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532

F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741

F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823

F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848

F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517

F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571

F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//

P47712

F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97:71//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251

F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207

F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084

F-MAMMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962

F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542

F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124

F-MAMMA1002603

F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMUS AQUATICUS.//O07348

F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164

F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINE-REA.//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931

F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.4e-05:53:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021

F-MAMMA1002625

F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-19:49:73//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//HOMO SAPIENS (HUMAN).//P12110

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVEGICUS (RAT).//P37285

F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246

F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:25:44//HOMO SAPIENS (HUMAN).//P22532

F-MAMMA1002662

F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-07:54:57//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P27550

F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS (BOVINE).//Q28062

F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.094:77:27//BACTERIOPHAGE T4.//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//RATTUS NORVEGICUS (RAT).//P02454

F-MAMMA1002698

F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//1.2e-28:127:

47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:14:92//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.9e-27:52:65//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-24:54:75//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002721

F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MOUSE).//Q04891

F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305

F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULFOLOBUS VIRUS-LIKE PARTICLE SSV1.//P20198

F-MAMMA1002748

F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-21:56:64//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.7e-32:79:60//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814

F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//5.4e-54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-MAMMA1002780

F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS (SCORPION).//P40755

F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS FLUORESCENS.//P09815

F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.3e-23:100:59//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002820//NEUROTOXIN IV (LQQ IV).//1.0:18:50//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489

F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.7e-24:55:74//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-31:95:73//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1.0:54:37//CAENORHABDITIS ELEGANS.//Q19417

F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.5e-27:99:70//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-13:65:63//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (MOUSE).//P02798

F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//4.9e-08:119:36//AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37//PAN TROGLODYTES (CHIMPANZEE).//Q35647

F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.8e-10:51:62//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059

F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//O12000

F-MAMMA1002880

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-22:180:35//HOMO SAPIENS (HUMAN).//P48060  
 F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706  
 5 F-MAMMA1002887  
 F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-MAMMA1002892  
 10 F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818  
 F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333  
 F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00011:28:75//HOMO SAPIENS (HUMAN).//P39188  
 15 F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730  
 F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//6.5e-24:147:34//HOMO SAPIENS (HUMAN).//P28698  
 F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.7e-11:44:68//MUS MUSCULUS (MOUSE).//Q61147  
 20 F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q02722  
 F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e-08:152:38//STREPTOMYCES FRADIAE.//P20186  
 F-MAMMA1002964  
 25 F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0057:55:43//HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1002972//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (OCT-T1) (HOMEOBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS (HUMAN).//Q01851  
 F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.6e-11:54:68//HOMO SAPIENS (HUMAN).//P39192  
 30 F-MAMMA1002982  
 F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906  
 F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//8.6e-09:30:73//HOMO SAPIENS (HUMAN).//P39195  
 35 F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0071:41:58//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311  
 40 F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS (RAT).//Q02874  
 F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGUUS (YEAST).//P38479  
 F-MAMMA1003015  
 F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q13496  
 45 F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4).//0.14:49:32//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06459  
 F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4).//5.1e-12:112:34//ZY-MOMONAS MOBILIS.//O66114  
 50 F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-07:68:54//HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//2.8e-39:90:57//HOMO SAPIENS (HUMAN).//P39190  
 55 F-MAMMA1003044  
 F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//BOS TAURUS (BOVINE).//P19782  
 F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969

F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA).//P01415  
 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS PNEUMONIAE.//  
 P35597  
 F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60584  
 5 F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q03381  
 F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//5.1e-15:44:77//HOMO SAPIENS (HU-  
 MAN).//P39190  
 F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN  
 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333  
 10 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:40//SYNECHOCOCCUS  
 ELONGATUS NAEGELI.//P25900  
 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.67:35:45//GALLUS  
 GALLUS (CHICKEN).//P02467  
 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULUS (MOUSE).//P46735  
 15 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//3.6e-05:91:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-MAMMA1003140  
 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P08175  
 20 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//4.4e-10:254:30//  
 CAENORHABDITIS ELEGANS.//Q09625  
 F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN).//O43236  
 F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.15:  
 38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
 25 F-NT2RM1000018  
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41//CYPRINUS CARPIO (COM-  
 MON CARP).//P24948  
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-COA  
 REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH).//P54960  
 30 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA (MUD CRAB).//P02806  
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84:33//DROSOPHILA  
 MELANOGASTER (FRUIT FLY).//Q06521  
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:55//PLASMODIUM LOPHU-  
 RAE.//P04929  
 35 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-  
 TEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN).//Q02080  
 F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUMAN).//P02814  
 F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:40//SYNECHOCYSTIS SP.  
 (STRAIN PCC 6803).//P72655  
 40 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C /  
 STRAIN 488).//P22576  
 F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//5.7e-07:109:28//NEUROSPORA CRASSA.//P87072  
 45 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:135:32//HERPES SIM-  
 PLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276  
 F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:68:32//SORGHUM  
 VULGARE (SORGHUM).//P24152  
 50 F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.82:33:39//BOS  
 TAURUS (BOVINE).//P37359  
 F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3)  
 (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124:91//HOMO SAPIENS (HUMAN).//O75380  
 F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:148:29//HOMO SAPIENS  
 55 (HUMAN).//P49902  
 F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.9e-07:109:27//NEUROSPORA CRASSA.//P87072  
 F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE



SPAC10F6.02C.//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643  
 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:33//CAENORHABDITIS ELEGANS.//  
 P20630  
 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.85:38:36//  
 5 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13931  
 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.0055:98:36//  
 CAENORHABDITIS ELEGANS.//Q11102  
 F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P22793  
 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING]  
 10 (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANS-  
 FERASE) (GFAT).//2.9e-54:153:67//MUS MUSCULUS (MOUSE).//P47856  
 F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
 P49028  
 F-NT2RM1000260  
 15 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS SUBTILIS.//P39574  
 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III.//8.8e-25:131:45//  
 CAENORHABDITIS ELEGANS.//Q09357  
 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-  
 PASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAURUS (BOVINE).//P39942  
 20 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//0.51:145:26//HOMO  
 SAPIENS (HUMAN).//Q13428  
 F-NT2RM1000314  
 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX AEOLICUS.//O66433  
 F-NT2RM1000341  
 25 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.95:43:37//RHODO-  
 BACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159  
 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL).//  
 Q04621  
 F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPIENS (HUMAN).//  
 30 Q14153  
 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-  
 ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4).//4.9e-18:113:  
 38//HOMO SAPIENS (HUMAN).//Q99956  
 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00023:67:  
 35 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915  
 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCU-  
 LUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS  
 (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY),  
 AND DROSOPHILA HYDEI (FRUIT FLY).//P06351  
 40 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//CANIS FAMILIARIS  
 (DOG).//P12064  
 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS CONTORTUS.//  
 P16252  
 F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).//0.13:86:31//NICO-  
 45 TIANA TABACUM (COMMON TOBACCO).//Q03211  
 F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49//HOMO SAPIENS  
 (HUMAN).//Q15057  
 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//2.9e-16:82:  
 51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089  
 50 F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS SCROFA (PIG).//  
 P17403  
 F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//P18395  
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.15:20:50//HO-  
 MO SAPIENS (HUMAN).//P30808  
 55 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCBP) (CLARA CELLS  
 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIENS (HUMAN).//P11684  
 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//SACCHAROMYCES CER-  
 EVISIAE (BAKER'S YEAST).//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713  
 F-NT2RM1000666//COLD SHOCK PROTEIN SCOF.//9.1e-07:67:41//STREPTOMYCES COELICOLOR.//P48859  
 5 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//PORPHYRA PURPUREA.//P51290  
 F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST).//O13475  
 10 F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:42//HOMO SAPIENS (HUMAN).//P29375  
 F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P15565  
 F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.//0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26308  
 15 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:15:60//HOMO SAPIENS (HUMAN).//P02811  
 F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT).//1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q09005  
 F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2).//1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77).//P25049  
 20 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I.//0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09858  
 F-NT2RM1000770//DXS6673E PROTEIN.//2.0e-38:190:48//HOMO SAPIENS (HUMAN).//Q14202  
 F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.3e-12:141:30//PODOSPORA ANSERINA.//Q00808  
 25 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-NT2RM1000781  
 F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28707  
 30 F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921  
 F-NT2RM1000811  
 35 F-NT2RM1000826//UNR PROTEIN.//1.1e-110:144:83//RATTUS NORVEGICUS (RAT).//P18395  
 F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY).//P50270  
 F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:145:841//CANIS FAMILIARIS (DOG).//P38377  
 40 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:136:33//RATTUS NORVEGICUS (RAT).//Q63572  
 F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818  
 F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273  
 45 F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-).//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965  
 F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312  
 50 F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808  
 F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485  
 55 F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//O54888  
 F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:28//OXYTRICHA FAL-

LAX.//P02583

F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY).//P42860

F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.3e-11:169:28//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEGANS.//P08124

F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7.1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14180

F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION.//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045

F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN).//1.6e-21:211:31//GALLUS GALLUS (CHICKEN).//P30997

F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469

F-NT2RM1001044

F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490

F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO).//Q43513

F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174

F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2.//P03291

F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.5e-19:75:54//HOMO SAPIENS (HUMAN).//P39195

F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e-42:200:38//HOMO SAPIENS (HUMAN).//P51522

F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331

F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-05:157:35//STREPTOMYCES FRADIAE.//P20186

F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOS TAURUS (BOVINE).//P02313

F-NT2RM1001115

F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//P10496

F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.76:45:35//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940

F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167

F-NT2RM2000030//TOXINS 1 AND 2.//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER) (TROPIDOLAEMUS WAGLERI).//P24335

F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00059:53:49//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:68:26//HOMO SAPIENS (HUMAN).//P22532

F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION.//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38748

F-NT2RM2000093//OVARY MATURATING PARSIN (OMP).//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80045

F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//3.3e-09:56:35//CAENORHABDITIS ELEGANS.//Q11096

F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-ALPHA).//3.1e-35:77:96//MUS MUSCULUS (MOUSE).//P05132

F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA).//3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q23917  
F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS).//0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV).//P51894  
F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00032:111:32//MUS MUSCULUS (MOUSE).//P05143  
F-nnnnnnnnnnnn//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q43512  
F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.054:46:34//RATTUS NORVEGICUS (RAT).//P08699  
F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA).//P29128  
F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-22:191:35//MUS MUSCULUS (MOUSE).//P05143  
F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I.//5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13868  
F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE).//0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56129  
F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11.//0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P22698  
F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.3e-16:203:30//HOMO SAPIENS (HUMAN).//P11274  
F-NT2RM2000368//DEK PROTEIN.//0.00027:100:32//HOMO SAPIENS (HUMAN).//P35659  
F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE).//6.8e-36:170:47//ESCHERICHTIA COLI.//P05055  
F-NT2RM2000374//NODAL PRECURSOR.//1.1e-32:64:95//MUS MUSCULUS (MOUSE).//P43021  
F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180.//0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32802  
F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.032:105:30//HOMO SAPIENS (HUMAN).//P51805  
F-NT2RM2000420//METALLOTHIONEIN (MT).//0.88:42:38//PLEURONECTES PLATESSA (PLAICE).//P07216  
F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//2.0e-117:237:87//RATTUS NORVEGICUS (RAT).//Q08469  
F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36113  
F-NT2RM2000469//70 KD ANTIGEN.//0.050:207:23//SHIGELLA FLEXNERI.//P18010  
F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.022:25:44//HOMO SAPIENS (HUMAN).//P02811  
F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645  
F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908  
F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT).//3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141  
F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//8.4e-33:214:38//CAENORHABDITIS ELEGANS.//Q18262  
F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-09:133:36//HOMO SAPIENS (HUMAN).//P56524  
F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F).//2.2e-60:244:51//HOMO SAPIENS (HUMAN).//P23229  
F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.3e-09:192:34//MUS MUSCULUS (MOUSE).//P05143  
F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.0e-08:43:72//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//  
 9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505  
 F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:111:34//HOMO SA-  
 PIENS (HUMAN).//Q15427  
 5 F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO SAPIENS (HU-  
 MAN).//P56524  
 F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO SAPIENS (HUMAN).//  
 P02811  
 F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANS-  
 10 FERASE) (DNA METASE) (MCMT) (M.MMU).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864  
 F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP).//P81014  
 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P35197  
 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMY-  
 15 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA  
 (FRUIT FLY).//P13730  
 F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129  
 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONOR-  
 20 RHOEAE.//P11910  
 F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.//  
 Q57694  
 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS  
 (RAT), AND GALLUS GALLUS (CHICKEN).//P36610  
 25 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS.//P05647  
 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND  
 BOS TAURUS (BOVINE).//P32391  
 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I).//3.8e-21:174:35//HO-  
 MO SAPIENS (HUMAN).//Q15404  
 30 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022:  
 174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13695  
 F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:246:74//HOMO SAPIENS  
 (HUMAN).//P28160  
 F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION.//8.5e-51:212:  
 35 49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38144  
 F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.0e-41:125:53//HOMO SAPIENS (HU-  
 MAN).//P39189  
 F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1.1e-128:291:89//  
 RATTUS NORVEGICUS (RAT).//P23514  
 40 F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR  
 P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//P49918  
 F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III.//2.5e-49:273:39//  
 CAENORHABDITIS ELEGANS.//P30646  
 F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)  
 45 (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P16884  
 F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//6.3e-44:216:43//  
 CAENORHABDITIS ELEGANS.//P41879  
 F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RAT).//P09951  
 F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MUSCULUS (MOUSE).//  
 50 Q60809  
 F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:122:31//TRYPANOSOMA BRU-  
 CEI BRUCEI.//P24499  
 F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//3.4e-13:171:30//  
 CAENORHABDITIS ELEGANS.//P46577  
 55 F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME  
 MOLD).//P14328  
 F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18:249:31//SCHIZOSAC-  
 CHAROMYCES POMBE (FISSION YEAST).//Q10475

F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//  
CAENORHABDITIS ELEGANS.//P34681

F-NT2RM2001152

5 F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:42:40//GALLUS GAL-  
LUS (CHICKEN).//P32018

F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P53814

F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//MUS MUSCULUS  
(MOUSE).//P05143

10 F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC  
ELECTRIC RAY).//P56101

F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//1.3e-13:183:32//  
RATTUS NORVEGICUS (RAT).//P97924

F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
DOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT).//P13264

15 F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION.//0.00019:177:  
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945

F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN PEA).//P14594

F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109:207:98//MUS MUS-  
CULUS (MOUSE).//P53995

20 F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.016:22:40//HOMO SAPIENS  
(HUMAN).//P22531

F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P14199

F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN).//  
P39195

25 F-NT2RM2001319

F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584

F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:159:27//PODOSPORA AN-  
SERINA.//Q00808

30 F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//1.0:27:48//  
DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623

F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUBSP. THIOSPHAERA  
PANTOTROPHA).//Q56348

F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN  
LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY).//Q91062

35 F-NT2RM2001420

F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4e-41:140:59//  
HOMO SAPIENS (HUMAN).//Q00839

F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+  
BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR)  
40 (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825

F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS.//P17656

F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//6.7e-47:190:42//  
CAENORHABDITIS ELEGANS.//Q09316

F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//EUPLOTES  
45 CRASSUS.//Q06184

F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.5e-18:91:50//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//3.9e-  
35:212:41//HOMO SAPIENS (HUMAN).//P19474

50 F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160

F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06:115:32//ZEA MAYS  
(MAIZE).//P14918

F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.033:156:23//HO-  
MO SAPIENS (HUMAN).//P26371

55 F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249:82//HOMO SAPIENS  
(HUMAN).//P29375

F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.2e-97:192:100//RATTUS  
NORVEGICUS (RAT).//P38378

F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00068:145:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT).//P52591

5 F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:29:68//HOMO SAPIENS (HUMAN).//P00387

10 F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:132:100//CANIS FAMILIARIS (DOG).//P38377

F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399

15 F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706

F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS).//O34261

F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (HUMAN).//Q15697

20 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.//1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857

F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//1.0:184:21//METHANOCOCCUS JANNASCHII.//Q57695

25 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399

F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966

F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.9e-41:60:81//HOMO SAPIENS (HUMAN).//P39194

30 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//9.8e-16:126:38//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41479

F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059

F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAFII-30) (TAFII30).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962

35 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P50544

F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.5e-33:95:75//HOMO SAPIENS (HUMAN).//P39195

40 F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77:37//BACILLUS SUBTILIS.//P39217

F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BOVINE).//P01154

45 F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//P50781

F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931

F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//P47969

50 F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//Q92609

F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:119:99//CANIS FAMILIARIS (DOG).//P38377

55 F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16761

F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN).//P52742

F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-

PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940  
 F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818  
 5 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871  
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742  
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093  
 10 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706  
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//O33793  
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963  
 15 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//O14647  
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293  
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194  
 20 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723  
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800  
 25 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798  
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582  
 30 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//O06917  
 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350  
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184  
 35 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320  
 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492  
 40 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154  
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814  
 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838  
 45 F-NT2RM2001997  
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034  
 50 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353  
 F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856  
 55 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326  
 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878  
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//



1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990

F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEGICUS (RAT).//Q03351

F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805

F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488

F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39//BOS TAURUS (BOVINE).//P25508

F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210

F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167

F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.99:72:31//MUS MUSCULUS (MOUSE).//P15091

F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36146

F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS NORVEGICUS (RAT).//P13941

F-NT2RM4000061

F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE).//O70133

F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221

F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741

F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874

F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639

F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174

F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469

F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783

F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587

F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162

F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.52:42:40//BACILLUS LICHENIFORMIS.//P22754

F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282

F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT).//P06599

F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10962

F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO SAPIENS (HUMAN).//P51805

F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27//BALAENOPTERA

PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947

F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.1e-38:70:70//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209:94//HOMO SAPIENS (HUMAN).//Q04726

F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q04503

F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION.//0.91:73:28//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41703

F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAENORHABDITIS ELE-GANS.//P54813

F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101

F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371

F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV).//P17574

F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01042

F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.54:46:36//BACTERIOPHAGE RB69.//O64300

F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI.//P16918

F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:29//SACCHAROMYCES CEREVI-SIAE (BAKER'S YEAST).//Q99189

F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-25:46:80//HOMO SAPIENS (HUMAN).//P39193

F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS CONTORTUS.//P16253

F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297

F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALBICANS (YEAST).//P87185

F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GALLUS GALLUS (CHICKEN).//P15988

F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMER-ASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P36594

F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:31//DROSOPHILA SIMU-LANS (FRUIT FLY).//P13729

F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68:32//ARTEMIA SANFRAN-CISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q37708

F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPINACIA OLERACEA (SPIN-ACH).//P08974

F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO SAPIENS (HUMAN).//Q14929

F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01049

F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614

F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26].//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS Y) (HIV-2).//P12450

F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//5.0e-23:224:29//DROSOPHILA MELA-NOGASTER (FRUIT FLY).//Q04652

F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//  
 CAENORHABDITIS ELEGANS.//P34284  
 F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO  
 SAPIENS (HUMAN).//Q14247  
 5 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHRO-  
 MOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963  
 F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550  
 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN  
 10 PCC 6803).//P74168  
 F-NT2RM4000689  
 F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:  
 33//BOMBYX MORI (SILK MOTH).//P05687  
 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURG-  
 15 DORFERI (LYME DISEASE SPIROCHETE).//P53364  
 F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//2.2e-82:152:63//CAENORHABDITIS ELEGANS.//P34547  
 F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROSOPHILA SIMULANS  
 20 (FRUIT FLY).//P13729  
 F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSCULUS (MOUSE).//  
 Q06666  
 F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLGGF26.1 (FRAGMENT).//7.2e-20:205:28//XENO-  
 PUS LAEVIS (AFRICAN CLAWED FROG).//P18715  
 25 F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHORT-NOSED BANDI-  
 COOT).//P42136  
 F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT).//5.2e-77:246:52//  
 MUS MUSCULUS (MOUSE).//P10076  
 F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES (SHEEP).//  
 30 Q02958  
 F-NT2RM4000778  
 F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:45//VOLVOX CARTERI.//  
 P21997  
 F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:73:  
 35 39//MUS MUSCULUS (MOUSE).//P98063  
 F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME  
 MOLD).//P14328  
 F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)  
 (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCHOLINESTERASE).//7.4e-41:271:36//  
 40 HOMO SAPIENS (HUMAN).//P06276  
 F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ES-  
 CHERICHIA COLI.//P15005  
 F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P11075  
 45 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577  
 F-NT2RM4000820  
 F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS JANNASCHII.//  
 Q58536  
 F-NT2RM4000848//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:  
 50 159:33//MUS MUSCULUS (MOUSE).//P17208  
 F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HU-  
 MAN).//P35325  
 F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//  
 P39194  
 55 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P38903  
 F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION.//3.3e-09:80:  
 46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572.//0.090:68:29//METHANOCOCCUS JANNASCHII.//  
 Q57992  
 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC).//0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID).//P46825  
 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC).//1.2e-07:25:  
 5 96//HOMO SAPIENS (HUMAN).//P19105  
 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PRO-  
 TEIN).//1.4e-56:253:46//MUS MUSCULUS (MOUSE).//P17141  
 F-NT2RM4001002  
 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;  
 10 CORE SHELL PROTEIN P30].//0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS.//P29175  
 F-NT2RM4001032//CUTICLE COLLAGEN 2.//2.6e-07:130:39//CAENORHABDITIS ELEGANS.//P17656  
 F-NT2RM4001047//MO25 PROTEIN.//5.6e-107:252:80//MUS MUSCULUS (MOUSE).//Q06138  
 F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.0e-109:209:94//CANIS FA-  
 MILIARIS (DOG).//P38377  
 15 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTERGENIC RE-  
 GION.//0.57:95:30//ESCHERICHIA COLI.//P39376  
 F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//2.5e-47:231:47//  
 CAENORHABDITIS ELEGANS.//Q09531  
 F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//1.3e-08:243:23//  
 20 CAENORHABDITIS ELEGANS.//Q09417  
 F-NT2RM4001140//HOMEODOMAIN PROTEIN MSH-D.//7.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH)  
 (ZEBRA DANIO).//Q01704  
 F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).//0.26:96:34//HOMO SAPIENS (HUMAN).//  
 P17600  
 25 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//3.6e-103:201:91//BOS TAURUS (BOVINE).//  
 Q27969  
 F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRAGMENTS).//1.0:33:36//  
 BRASSICA OLERACEA (CAULIFLOWER).//P48438 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA  
 SUBUNIT.//0.44:158:27//MYCOPLASMA GENITALIUM.//P47318  
 30 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C).//0.99:44:43//ASTROTIA STOKESI (STOKES'S SEA  
 SNAKE) (DSTEIRA STOKESI).//P01381  
 F-NT2RM4001200//ZINC FINGER PROTEIN 135.//2.2e-82:245:59//HOMO SAPIENS (HUMAN).//P52742  
 F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.028:94:  
 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 35 F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.0096:182:34//HOMO  
 SAPIENS (HUMAN).//Q15428  
 F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-21:221:29//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR.//0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S  
 40 YEAST).//P21560  
 F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00031:132:39//STREP-  
 TOMYCES FRADIAE.//P20186  
 F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC  
 PEPTIDE P-F] (FRAGMENT).//0.048:132:28//HOMO SAPIENS (HUMAN).//P02812  
 45 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K).//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54676  
 F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3)  
 (MCAD).//1.7e-10:185:30//RATTUS NORVEGICUS (RAT).//P08503  
 F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.5e-08:197:26//MUS MUSCULUS (MOUSE).//P52734  
 50 F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//7.7e-14:82:36//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32626  
 F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//3.3e-  
 16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53742  
 55 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION.//0.067:111:33//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04511  
 F-NT2RM4001371  
 F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.0e-08:82:39//PLASMODIUM LOPHU-

RAE.//P04929

F-NT2RM4001384

F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

5 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P50904

F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN).//Q13360

10 F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//P39192

F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425

15 F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461

F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN).//P52737

F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//P23246

20 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929

F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

F-NT2RM4001557

25 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919

F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

30 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775

F-NT2RM4001582

F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14737

35 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221

40 F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT).//P37199

F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024

F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368

45 F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS GALLUS (CHICKEN).//P17277

F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:32//HOMO SAPIENS (HUMAN).//P17252

50 F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339

F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORHABDITIS ELEGANS.//P52819

F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//HOMO SAPIENS (HUMAN).//Q15054

55 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//Q14141

F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342

F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//1.1e-05:90:33//  
 CAENORHABDITIS ELEGANS.//P34284  
 F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039  
 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8)  
 5 (HUMAN HERPESVIRUS 4).//P03211  
 F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).//  
 P29400  
 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79//  
 HOMO SAPIENS (HUMAN).//P27448  
 10 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735  
 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS  
 (MOUSE).//P55200  
 F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01643  
 15 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MA-  
 LAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397  
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549  
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-  
 20 18:114:40//MUS MUSCULUS (MOUSE).//P46684  
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SA-  
 PIENS (HUMAN).//P51523  
 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:30//NEPHILA CLA-  
 VIPES (ORB SPIDER).//P46804  
 25 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814  
 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//0.98:35:42//  
 CAENORHABDITIS ELEGANS.//Q11104  
 F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:  
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722  
 30 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-  
 23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377  
 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS.//  
 P36609  
 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-  
 35 SOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179  
 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//  
 P93746  
 F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RAT-  
 TUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793  
 40 F-NT2RM4001922  
 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53//  
 CAENORHABDITIS ELEGANS.//Q09226  
 F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME  
 MOLD).//P54681  
 45 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO  
 SAPIENS (HUMAN).//P78415  
 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.2e-43:56:85//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-  
 50 RILLA).//P20758  
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-  
 TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280  
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SA-  
 PIENS (HUMAN).//P51523  
 55 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSCULUS (MOUSE).//  
 P15974  
 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//6.9e-  
 17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256

F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

5 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132:25//HOMO SAPIENS (HUMAN).//P98171

F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498

10 F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI BRUCEI.//P14044

F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P08105

F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419

F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342

15 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:71//HOMO SAPIENS (HUMAN).//Q93074

F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM4002073//ELASTIN PRECURSOR (TROPOELASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502

20 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599

25 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174

F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.91:49:32//PARACOCCLUS DENITRIFICANS.//P29969

F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371

30 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014

F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028

35 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491

F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590

F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817

40 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805

F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803

F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565

45 F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809

F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (MOUSE).//P97805

F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251

50 F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656

F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288

F-NT2RM4002281

55 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556

F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT)//0.56:43:39//BACILLUS CALDOLYTICUS.//P42832  
 F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BOS TAURUS (BOVINE).//P02313  
 5 F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III).//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL).//P80248  
 F-NT2RM4002344//METALLOTHIONEIN-I (MT-I).//0.84:41:31//MUS MUSCULUS (MOUSE).//P02802  
 F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR.//0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387  
 10 F-NT2RM4002374//5E5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q63003  
 F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.13:17:88//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RM4002390  
 F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074  
 15 F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTRIX SOEHNGENII.//P27095  
 F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.7e-15:41:95//HOMO SAPIENS (HUMAN).//P39194  
 20 F-NT2RM4002446//CRYPTDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C).//0.0058:24:50//MUS MUSCULUS (MOUSE).//P17534  
 F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II).//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL).//P80247  
 F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.9e-07:52:63//HOMO SAPIENS (HUMAN).//P39192  
 25 F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.92:43:30//HORDEUM VULGARE (BARLEY).//P17992  
 F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942  
 30 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W.//8.8e-26:123:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12514 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR.//0.17:126:27//DROSOPHILA MIRANDA (FRUIT FLY).//P91627  
 F-NT2RM4002499//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO SAPIENS (HUMAN).//P39194  
 35 F-NT2RM4002504//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO SAPIENS (HUMAN).//P39189  
 F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2.//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O22468  
 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN.//0.97:19:47//AEROMONAS SOBRIA.//P09165  
 40 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25348  
 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55:204:50//MUS MUSCULUS (MOUSE).//Q60714  
 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:16:62//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852  
 45 F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032  
 F-NT2RM4002571//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124:47//HOMO SAPIENS (HUMAN).//Q10472  
 50 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION.//0.95:36:38//BACILLUS SUBTILIS.//P37509  
 F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS ELEGANS.//P54815  
 F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73851  
 55 F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROSOPHILA MELANOGASTER.//P39194



NOGASTER (FRUIT FLY).//Q04652

F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P17727

F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359

F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847

F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254

F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981

F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:24//MYXOCOCCUS XANTHUS.//P36774

F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//MUS MUSCULUS (MOUSE).//P51859

F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216

F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045

F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485

F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536

F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//O83338

F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE).//P23152

F-NT2RP1000324

F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599

F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447

F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343

F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327

F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION.//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744

F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157

F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESULFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137

F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-131:230:97//RATTUS NORVEGICUS (RAT).//P55161

F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779

F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257

F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (AS-

PERGILLUS NIDULANS).//P17624

F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580

F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207

F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194

F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068

F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

F-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367

F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275

F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO SAPIENS (HUMAN).//Q07092

F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0024:19:94//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:128:93//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIENS (HUMAN).//O00268

F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542

F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5.//0.024:24:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41902

F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP1000767//PSEUDOMONAPEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790

F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732

F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SUS SCROFA (PIG).//P35323

F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HU-

MAN).//Q07960

F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.32:29:48//HOMO SAPIENS (HUMAN).//P22531

F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202:68//RATTUS NORVEGICUS (RAT).//P70473

F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691

F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIENS (HUMAN).//P35326

F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY).//Q04536

F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUSCULUS (MOUSE).//O35566

F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02336

F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531

F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010

F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HOMO SAPIENS (HUMAN).//Q02817

F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMPV).//O10341

F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669

F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010

F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321

F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (HUMAN).//P19338

F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS.//P04123

F-NT2RP1000988

F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638

F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012

F-NT2RP1001014

F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295

F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089

F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826).//P40873

F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218

F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS (HUMAN).//P35326

F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMAN).//P25800

F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT).//Q02874

F-NT2RP1001185

F-NT2RP1001199//NEUROTOXIN I.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01491

F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS (HUMAN).//O00292

F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926

5 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110

F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

10 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

15 F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131

20 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286

25 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993

F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372

30 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382

F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457

35 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

40 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803

F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397

F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758

45 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506

F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381

F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326

50 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730

55 F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665

F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HU-

MAN).//Q07815

F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAPIENS (HUMAN).//P04281  
F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//  
Q56237

5 F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GN-  
RH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALM-  
ON).//P30973

F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-  
SILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446

10 F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:40//SALMO SALAR (AT-  
LANTIC SALMON).//P09637

F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE).//P01328

F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:40//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY).//P51022

15 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:40//HOMO SAPIENS  
(HUMAN).//P09234

F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).//P30034

F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.//1.0:36:44//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245

20 F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:47//HAEMOPHILUS INFLUEN-  
ZAE.//P43953

F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SWINE FEVER VIRUS  
(STRAIN BA71V) (ASFV).//P32510

F-NT2RP2000098

25 F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.4e-09:50:70//HOMO SAPIENS (HUMAN).//  
P39195

F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//HOMO SAPIENS (HU-  
MAN).//P42768

30 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:32//DESULFOVIBRIO VULGARIS  
(STRAIN HILDENBOROUGH).//P33391

F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.5e-23:94:47//HOMO  
SAPIENS (HUMAN).//O14646

F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.6e-10:82:39//HOMO SA-  
PIENS (HUMAN).//Q15427

35 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN  
AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISO-  
MERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA MALAYI.//Q27450

40 F-NT2RP2000157//MLO2 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//  
Q09329

F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS ELEGANS.//Q17632

F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC REGION.//0.99:62:25//  
BACILLUS SUBTILIS.//P54499

45 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY).//Q01643

F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN  
NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//O02675

F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33//MICROTUS PENNSYLVANI-  
CUS (MEADOW VOLE).//P24949

50 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERI-  
PLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.098:88:25//SH-  
EWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463

F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:57//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY).//Q01645

55 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:32//CAENORHABDITIS ELE-  
GANS.//Q09455

F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:38//OVIS ARIES

(SHEEP).//O02761

F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR).//0.34:53:43//CANIS FAMILIARIS (DOG).//P30552

F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.019:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-NT2RP2000248//OVOMUCOID (FRAGMENT).//0.88:18:55//POLYPLECTRON EMPHANUM (PALAWAN PEACOCK-PHEASANT).//P52250

F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556

F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.081:217:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P08799

F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:80:57//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//0.082:22:45//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485

F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//0.39:38:34//CAENORHABDITIS ELEGANS.//P34535

F-NT2RP2000288

F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.40:38:42//ESCHERICHIA COLI.//P22847

F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//2.3e-62:206:47//HOMO SAPIENS (HUMAN).//Q03923

F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//0.55:81:40//CAENORHABDITIS ELEGANS.//P20630

F-NT2RP2000310//RUBREDOXIN (RD).//0.13:43:41//TREPONEMA PALLIDUM.//O83956

F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//GADUS MORHUA (ATLANTIC COD).//P15996

F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-91:155:92//BOS TAURUS (BOVINE).//P08760

F-NT2RP2000337//PROTEIN A54.//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P21072

F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//9.7e-13:114:42//MUS MUSCULUS (MOUSE).//P17564

F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//0.98:47:34//MUS MUSCULUS (MOUSE).//Q09098

F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//0.66:57:36//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//P19960

F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//1.0e-27:96:67//HOMO SAPIENS (HUMAN).//P52597

F-NT2RP2000420//ZINC FINGER PROTEIN 191.//0.16:47:38//HOMO SAPIENS (HUMAN).//O14754

F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

F-NT2RP2000438//TUBULIN GAMMA CHAIN.//0.86:190:27//RETICULOMYXA FILOSA.//P54405

F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN.//3.7e-13:140:42//HOMO SAPIENS (HUMAN).//P22059

F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//1.0:45:35//HOMO SAPIENS (HUMAN).//Q16612

F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.062:25:68//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2000503

F-NT2RP2000510//TOXIN IV-5.//1.0:51:33//TITYUS BAHIIENSIS (BRAZILIAN SCORPION).//P56608

F-NT2RP2000516//SLYX PROTEIN.//1.0:52:32//ESCHERICHIA COLI.//P30857

F-NT2RP2000523//PHORBOLIN I (FRAGMENTS).//1.4e-06:36:47//HOMO-SAPIENS (HUMAN).//P31941

F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III).//0.93:119:26//TRITICUM AESTIVUM (WHEAT).//P04723

F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.056:16:62//OVIS ARIES

(SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934

F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257

F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//P08154

F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607

F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7).//P50498

F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00085:38:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-17:55:74//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//O83950

F-NT2RP2000715

F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPORA CRASSA.//P10713

F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00027:31:74//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120).//P12623

F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLASMA PNEUMONIAE.//P75219

F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e-07:133:31//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083

F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565

F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCULUS (MOUSE).//P21107

F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133:26//MUS MUSCULUS (MOUSE).//P27671

F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//HOMO SAPIENS (HUMAN).//Q92633

F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P24793

F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:199:94//HOMO SAPIENS (HUMAN).//O60841

F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481

F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43244

F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MUSCULUS (MOUSE).//Q05921

F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956

F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992

F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS GALLUS (CHICKEN).//P53352

F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746

F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159

F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//ANDROCTONUS AUSTRALIS HEC-

TOR (SAHARA SCORPION).//P21150  
 F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.2e-33:65:81//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH).//P80302  
 5 F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.0e-24:85:65//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI).//0.41:50:  
 32//VIGNA UNGUICULATA (COWPEA).//P17734  
 10 F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE)  
 (FPRA PROTEIN).//6.2e-18:64:48//MYXOCOCCUS XANTHUS.//P21159  
 F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICUS (RAT).//P50232  
 F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVEGICUS (RAT).//P02803  
 F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.5e-11:61:63//HOMO SAPIENS (HUMAN).//  
 P39195  
 15 F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-47:155:58//MUS MUSCULUS  
 (MOUSE).//P41230  
 F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:39//BOS TAURUS (BOVINE).//  
 P25508  
 F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/1.1e-13:81:59//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.0071:77:33//RATTUS  
 NORVEGICUS (RAT).//P20468  
 F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAP1 (TUBULIN FOLDING COFACTOR B).//  
 1.0:36:41//HOMO SAPIENS (HUMAN).//Q99426  
 25 F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPIENS (HUMAN).//P52743  
 F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//1.0:95:26//CAPRA HIR-  
 CUS (GOAT).//Q36346  
 F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.00024:80:  
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40486  
 30 F-NT2RP2001226//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSCULUS (MOUSE).//P47708  
 F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//HOMO SAPIENS (HU-  
 MAN).//P16415  
 F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05:230:21//HOMO SA-  
 PIENS (HUMAN).//Q15431  
 35 F-NT2RP2001268//HOMEODOMAIN PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS ELEGANS.//Q23175  
 F-NT2RP2001277  
 F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG)  
 (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCULUS (MOUSE).//P28663  
 F-NT2RP2001295  
 40 F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-  
 COSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P50426  
 F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829  
 F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426  
 45 F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.5e-19:66:62//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL).//  
 Q04621  
 F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) (FRAGMENT).//  
 50 0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003  
 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1).//1.0:167:26//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470  
 F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3.//0.0080:82:32//OVIS ARIES (SHEEP).//  
 P02441  
 55 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//P39769  
 F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRICETUS AURATUS (GOLD-  
 EN HAMSTER).//P37883



F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//0.00018:113:38//HOMO SAPIENS (HUMAN).//P04280

F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF A)//0.90:23:43//BACTERIOPHAGE T4.//P17307

5 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-11:38:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2)//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698

10 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1)//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35214

F-NT2RP2001445

F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS (BOVINE).//Q10568

15 F-NT2RP2001450

F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1).//1.0:25:40//BUNGARUS FASCIATUS (BANDED KRAIT).//P10808

F-NT2RP2001506

F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//0.49:124:29//CAENORHABDITIS ELEGANS.//P34681

20 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL (CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//P29377

F-NT2RP2001526

F-NT2RP2001536//METALLOTHIONEIN-I (MT-1).//1.0:19:42//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:35//CAENORHABDITIS ELEGANS.//P20630

25 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-31:102:67//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04174

30 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//HOMO SAPIENS (HUMAN).//P51805

F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924

F-NT2RP2001601

F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:59:32//GALLUS GALLUS (CHICKEN).//P19601

35 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35220

40 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40358

F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//1.2e-26:126:56//HOMO SAPIENS (HUMAN).//P06733

45 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5'REGION (ORF1).//0.25:148:25//CAMPYLOBACTER JEJUNI.//Q46089

F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164

50 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-18:83:61//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2001699//PROTEIN C14.//0:98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21045

F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//Q99317

55 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50534

F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURUS (BOVINE).//P20072

F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-

MENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP2001762

F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//O47040

F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE).//Q61466

F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS SCROFA (PIG).//O19084

F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008

F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHEEP).//Q10991

F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS (HUMAN).//P32019

F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53946

F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:27//CANDIDA ALBICANS (YEAST).//P46593

F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273

F-NT2RP2001936

F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305

F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485

F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880

F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353

F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331

F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSE RADISH TREE) (MORINGA PTERYGOSPERMA).//P24303

F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2002041

F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-NT2RP2002047

F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220

F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157

F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958

F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916

F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVIS ARIES (SHEEP).//Q02958

F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990

F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839

F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206

F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//HOMO SAPIENS (HUMAN).//P18146  
 F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM).//P01526

5 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110  
 F-NT2RP2002172  
 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510

10 F-NT2RP2002192  
 F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGANS.//P34804  
 F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011:45:40//HOMO SAPIENS (HUMAN).//060683

15 F-NT2RP2002219  
 F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43436  
 F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37318

20 F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84//MUS MUSCULUS (MOUSE).//O55127  
 F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAPIENS (HUMAN).//P12524

25 F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930  
 F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P24827

30 F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903  
 F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40269

35 F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A).//2.2e-06:145:26//CANDIDA BOIDINII (YEAST).//Q00316  
 F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524  
 F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE).//P17599

40 F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388  
 F-NT2RP2002394  
 F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:107:37//BOS TAURUS (BOVINE).//P02453

45 F-NT2RP2002426  
 F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA).//P23093  
 F-NT2RP2002442//HESA PROTEIN.//6.0e-16:163:30//PLECTONEMA BORYANUM.//P46037

50 F-NT2RP2002457  
 F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264  
 F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO SAPIENS (HUMAN).//P50238

55 F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//O75027  
 F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:45//PSEUDOMONAS AERUGINOSA.//P04139

F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//1.3e-31:124:59//HOMO SAPIENS (HUMAN).//Q02386

F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT).//P37199

5 F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.94:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680

F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-10:194:23//CAENORHABDITIS ELEGANS.//Q11073

F-NT2RP2002546

10 F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT).//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010

F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e-19:60:61//HOMO SAPIENS (HUMAN).//P51523

F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q92125

15 F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264

20 F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//6.2e-37:180:44//RATTUS NORVEGICUS (RAT).//Q63009

F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.98:37:35//LEMUR CATTI (RING-TAILED LEMUR).//Q34879

F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319

25 F-NT2RP2002672//PROTEIN Q300.//0.0018:41:43//MUS MUSCULUS (MOUSE).//Q02722

F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180.//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

30 F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//6.9e-09:96:40//MUS MUSCULUS (MOUSE).//P55194

F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//3.6e-20:160:36//RATTUS NORVEGICUS (RAT).//P49816

F-NT2RP2002736

35 F-NT2RP2002740

F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2.//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51862

F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN).//P39191

40 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T.//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS.//Q00932

F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE).//0.71:78:33//TRICHODERMA LONGIBRACHIATUM.//Q12714

F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR.//0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P11994

45 F-NT2RP2002778

F-NT2RP2002800//CRAMBIN.//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE).//P01542

F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.010:87:31//HOMO SAPIENS (HUMAN).//P02812

50 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00018:57:45//RATTUS NORVEGICUS (RAT).//P04474

F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP2002880//DNA REPAIR PROTEIN RAD32.//0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09683

55 F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT).//0.99:70:24//RATTUS NORVEGICUS (RAT).//Q64204

F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (ALPHA-1A

ADRENERGIC RECEPTOR).//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100  
 F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40968  
 F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q18964  
 5 F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0022:98:39//CANIS FAMILIARIS (DOG).//P30803  
 F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43333  
 10 F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669  
 F-NT2RP2002979  
 15 F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM.//P10129  
 F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN).//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192  
 20 F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//O54888  
 F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:62:64//HOMO SAPIENS (HUMAN).//P39194  
 25 F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44204  
 F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0051:16:87//HOMO SAPIENS (HUMAN).//P39189  
 F-NT2RP2003099  
 F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIENS (HUMAN).//P04281  
 30 F-NT2RP2003117  
 F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572  
 F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303  
 35 F-NT2RP2003129  
 F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117  
 F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217  
 F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//O43242  
 40 F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS MUSCULUS (MOUSE).//P05142  
 F-NT2RP2003164//ZYXIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523  
 F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-24:77:64//HOMO SAPIENS (HUMAN).//P39194  
 45 F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III.//2.3e-14:87:37//CAENORHABDITIS ELEGANS.//P30629  
 50 F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P41306  
 F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991  
 F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PI/PC TP).//1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P53989  
 55 F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-44:66:84//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOCOCCUS PYO-  
 GENES.//P02977  
 F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P41505  
 F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//5.5e-  
 06:78:35//BRASSICA NAPUS (RAPE).//P40603  
 F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT  
 SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30771  
 F-NT2RP2003280  
 F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE)  
 (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q08096  
 F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:175:33//HOMO SA-  
 PIENS (HUMAN).//P51522  
 F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO SAPIENS (HUMAN).//  
 P23246  
 F-NT2RP2003297  
 F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT).//P37285  
 F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P17886  
 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//  
 CAENORHABDITIS ELEGANS.//P34284  
 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS  
 POLYLEPIS (BLACK MAMBA).//P01416  
 F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//O61570  
 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS AN-  
 GUSTICEPS (EASTERN GREEN MAMBA).//P01408  
 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//Q99189  
 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTO-  
 CHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//0.94:29:34//ARAUCARIA HETERO-  
 PHYLLA.//P37843  
 F-NT2RP2003394  
 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS  
 AQUATICUS (SUBSP. THERMOPHILUS).//P45746  
 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS  
 NORVEGICUS (RAT).//P38378  
 F-NT2RP2003445  
 F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2.//  
 P03290  
 F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MARCHANTIA POLY-  
 MORPHA (LIVERWORT).//P12168  
 F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//6.7e-06:108:  
 32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871  
 F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//7.2e-15:38:  
 50//GALLUS GALLUS (CHICKEN).//Q98937  
 F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q63003  
 F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0e-11:91:43//SUS  
 SCROFA (PIG).//P04175  
 F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//P35416  
 F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HOMO SAPIENS (HU-  
 MAN).//P23246  
 F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYCOBACTERIUM TUBER-  
 CULOSIS.//Q10696  
 F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS TENAX VIRUS 1  
 (STRAIN KRA1) (TTV1).//P19283  
 F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (RAT).//P09951

F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E).//0.98:37:37//HOMO SAPIENS (HUMAN).//Q14657  
 F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//6.4e-35:175:44//HOMO SAPIENS (HUMAN).//P19474  
 5 F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X.//0.72:82:34//CAENORHABDITIS ELEGANS.//Q22544  
 F-NT2RP2003581//HOMEBOX PROTEIN OTX1.//0.90:61:37//MUS MUSCULUS (MOUSE).//P80205  
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P).//0.83:61:32//MYCOPLASMA GENITALIUM.//P47272  
 F-NT2RP2003604//ALPHA-CATENIN.//1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35220  
 10 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE).//P00623  
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYL-NEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE).//3.9e-12:84:40//NEISSERIA MENINGITIDIS.//Q57385  
 15 F-NT2RP2003668//!!!! ALU-SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:74:81//HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-05:40:67//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.5e-37:56:67//HOMO SAPIENS (HUMAN).//P39194  
 20 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.-) (ORFA).//1.3e-07:98:37//LISTERIA MONOCYTOGENES.//P25145  
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE 5) (GGT-REL).//0.66:23:52//HOMO SAPIENS (HUMAN).//P36269  
 25 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160).//1.2e-22:187:35//HOMO SAPIENS (HUMAN).//Q07075  
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2).//2.7e-06:119:34//HOMO SAPIENS (HUMAN).//P35125  
 30 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//6.7e-27:68:75//HOMO SAPIENS (HUMAN).//Q05481  
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG.//0.64:110:30//MYCOPLASMA PNEUMONIAE.//P75105  
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669  
 35 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR.//0.67:68:30//PSEUDOTERRANOVA DECIPIENS (COD WORM).//P26914  
 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.0e-98:235:82//BOS TAURUS (BOVINE).//P53620  
 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 40 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:33:36//EQUUS CABALLUS (HORSE).//P48663  
 45 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.029:35:42//PSEUDOMONAS AERUGINOSA.//P23621  
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION.//0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA).//P14728  
 50 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//4.7e-54:204:47//CAENORHABDITIS ELEGANS.//Q09201  
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN).//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE).//P80359  
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//1.0:35:37//CANIS FAMILIARIS (DOG).//P13206  
 55 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//2.5e-05:80:38//CAENORHABDITIS ELEGANS.//Q11076  
 F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.54:28:50//ESCHERICHIA CO-

LI.//P05834

F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P36193

F-NT2RP2003871

F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736

F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//4.8e-110:268:80//MUS MUSCULUS (MOUSE).//P51954

F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:92:31//RATTUS NORVEGICUS (RAT).//O09175

F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-21:62:62//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702

F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P37806

F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.3e-19:47:70//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.2e-18:80:58//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290

F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746

F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).//P17599

F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//Q26181

F-NT2RP2004066//CALDESMON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN).//P12957

F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:31//GALLUS GALLUS (CHICKEN).//P02314

F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262

F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09010

F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS MUSCULUS (MOUSE).//P05143

F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051

F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (HUMAN).//Q15697

F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730

F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL).//P80247

F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737

F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME MOLD).//P90587

F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-48:211:51//HOMO SAPIENS (HUMAN).//Q15139

F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489



F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE).//1.0:39:28//  
 CAENORHABDITIS ELEGANS.//P17512  
 F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1).//0.0036:  
 64:28//ORYZA SATIVA (RICE).//P25766  
 5 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:21:42//PONGO PYGMAEUS PYG-  
 MAEUS (BORNEAN ORANGUTAN).//P92896  
 F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.00023:118:33//NEPHILA CLA-  
 VIPES (ORB SPIDER).//P46804  
 F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8.//P06425  
 10 F-NT2RP2004316  
 F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//SYNECHOCYSTIS SP. (STRAIN  
 PCC 6803).//Q01904  
 F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:84:77//HOMO SAPIENS (HUMAN).//  
 P39195  
 15 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II.//0.78:96:30//  
 CAENORHABDITIS ELEGANS.//Q09556  
 F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN VP9).//0.059:143:  
 30//BOVINE ROTAVIRUS (STRAIN UK).//P04515  
 F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT).//0.27:38:39//EIMERIA ACERVULINA.//P21959  
 20 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR.//0.64:71:28//MAREK'S DISEASE HERPESVIRUS  
 (STRAIN GA) (MDHV).//P52510  
 F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCO-  
 PROTEIN) (HPRG) (FRAGMENT).//0.59:50:40//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28640  
 F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III.//4.0e-16:89:43//  
 25 CAENORHABDITIS ELEGANS.//P34388  
 F-NT2RP2004392  
 F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN.//0.42:89:29//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P10080  
 F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE).//1.0:72:34//MESOCRICETUS AU-  
 30 RATUS (GOLDEN HAMSTER).//P37886  
 F-NT2RP2004400  
 F-NT2RP2004412//SPERM PROTAMINE P1.//0.24:38:31//NOTORYCTES TYPHLOPS (MARSUPIAL MOLE).//  
 P42143  
 F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40.//0.0087:197:22//SACCHAROMYCES CEREVISIAE (BAK-  
 35 ER'S YEAST).//P32583  
 F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).//  
 1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338  
 F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (RBE-II).//0.20:68:  
 36//RATTUS NORVEGICUS (RAT).//Q07652  
 40 F-NT2RP2004490//FOS-RELATED ANTIGEN 1.//0.94:59:33//HOMO SAPIENS (HUMAN).//P15407  
 F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENTS).//1.0:37:  
 32//PISASTER OCHRACEUS (SEA STAR).//P24998  
 F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-15:57:71//HOMO SAPIENS (HUMAN).//  
 P39194  
 45 F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES).//  
 1.2e-48:121:60//HOMO SAPIENS (HUMAN).//Q12756  
 F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65).//1.0:20:50//EUGLENA GRACILIS.//P32095  
 F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//5.2e-07:150:30//SCHIZOSAC-  
 CHAROMYCES POMBE (FISSION YEAST).//Q09903  
 50 F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.7e-37:100:78//HOMO SAPIENS (HU-  
 MAN).//P39192  
 F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//8.2e-06:  
 150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II.//0.84:105:24//  
 55 CAENORHABDITIS ELEGANS.//Q09458  
 F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS).//0.17:127:29//RAT-  
 TUS NORVEGICUS (RAT).//P30009  
 F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:50:58//HOMO SAPIENS (HUMAN).//

P39188

F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20561

F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250

F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I.//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10328

F-NT2RP2004675

F-NT2RP2004681

F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243

F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS JANNASCHII.//Q58063

F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-15:97:49//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451

F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38692

F-NT2RP2004775

F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996

F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587

F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-NT2RP2004816//H<BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40336

F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P70742

F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS ARIES (SHEEP).//P02443

F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA (SWAMP OAK).//Q39511

F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355

F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.87:36:33//EC-TOTHIORHODOSPIRA VACUOLATA.//P38524

F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220

F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q06730

F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.17:28:57//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301

F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002

F-NT2RP2004982

F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAPIENS (HUMAN).//Q14157

F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378

F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965

F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:54:31//HOMO SAPIENS (HUMAN).//P22531  
 F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e-30:78:56//MUS MUSCULUS (MOUSE).//P15533  
 5 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906  
 F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P06937  
 10 F-NT2RP2005020  
 F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:106:35//PODOSPORA ANSERINA.//Q00808  
 F-NT2RP2005031  
 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447  
 15 F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//O57486  
 F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS ELEGANS.//P17656  
 20 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P34466  
 F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:46:39//PLEUROCHRYSID HAPTONEMOFERA.//P41552  
 F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//BOS TAURUS (BOVINE).//P25508  
 25 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78517  
 F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P50586  
 F-NT2RP2005147  
 30 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (SPINACH).//P12164  
 F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821  
 F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.8e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839  
 35 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624  
 F-NT2RP2005227  
 F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALBICANS (YEAST).//P87185  
 40 F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970  
 F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS GALLUS (CHICKEN).//P17277  
 F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS (RAT).//O35547  
 45 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031  
 F-NT2RP2005288//PROBABLE RUBREDOXIN HUPL.//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).//P28151  
 50 F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972  
 F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDITIS ELEGANS.//P18832  
 55 F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAPIENS (HUMAN).//P10645  
 F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION.//0.00011:124:

28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42846

F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38).//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12675

F-NT2RP2005354

5 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN.//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10).//0.0022:73:36//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038

10 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.00085:135:28//CAENORHABDITIS ELEGANS.//Q09202

F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE).//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32476

F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0011:54:42//ZEA MAYS (MAIZE).//P14918

15 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.039:182:29//MUS MUSCULUS (MOUSE).//P05142

F-NT2RP2005453

F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//4.0e-10:124:37//BOS TAURUS (BOVINE).//Q02827

20 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN.//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20553

F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//4.6e-09:92:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38127

25 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129.//0.76:80:32//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51155

F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-31:39:89//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2005490//METALLOTHIONEIN-II (MT-II).//0.14:27:33//SCYLLA SERRATA (MUD CRAB).//P02806

30 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6).//0.95:45:31//METHANOCOCCUS JANNASCHII.//Q58785

F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION.//0.99:68:30//BACTERIOPHAGE T4.//Q02407

F-NT2RP2005496//ZINC FINGER PROTEIN 135.//1.4e-54:120:59//HOMO SAPIENS (HUMAN).//P52742

35 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//9.5e-76:146:86//RATTUS NORVEGICUS (RAT).//P36876

F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP).//0.025:70:40//HOMO SAPIENS (HUMAN).//P17931

40 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:166:27//GALLUS GALLUS (CHICKEN).//P02457

F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//7.9e-45:118:79//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533

45 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11.//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51354

F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG).//9.8e-13:84:45//HOMO SAPIENS (HUMAN).//P29074

50 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN).//4.9e-10:90:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ.//0.36:119:21//BACILLUS SUBTILIS.//P39115

F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III.//6.0e-39:179:46//CAENORHABDITIS ELEGANS.//Q09253

F-NT2RP2005555

55 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I.//4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09790

F-NT2RP2005581

F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.014:37:40//HOMO SAPIENS (HUMAN).//

P02811

F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247

5 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950

10 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN).//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54.//0.63:41:31//BRASSICA NAPUS (RAPE).//P43402

15 F-NT2RP2005645

F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).//0.0023:50:42//HOMO SAPIENS (HUMAN).//Q01860

F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

20 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II).//0.76:16:50//SCYLLA SERRATA (MUD CRAB).//P02806

F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1).//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P49119

F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275.//0.17:50:40//HAEMOPHILUS INFLUENZAE.//P43975

25 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708

F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAPIENS (HUMAN).//Q15034

F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161

30 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II).//0.19:14:50//STENELLA COERULEOALBA (STRIPED DOLPHIN).//P14425

F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

35 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//HOMO SAPIENS (HUMAN).//P16415

F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALLIDUM.//O83390

40 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296

F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432

F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034

45 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//HOMO SAPIENS (HUMAN).//P02461

F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808

50 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181

F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322

55 F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675

F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-

3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810  
 F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P08393  
 5 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:43:55//OWENIA FUSIFORMIS.//P21260  
 F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004  
 10 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//O07401  
 F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34223  
 15 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:28:53//HOMO SAPIENS (HUMAN).//P22532  
 F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.99:33:48//BACTERIOPHAGE T4.//P22917  
 F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532  
 20 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II).//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853  
 25 F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:28//TETRAHYMENA THERMOPHILA.//P40631  
 F-NT2RP2005890  
 F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933  
 30 F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347  
 F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500  
 35 F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC REGION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185  
 F-NT2RP2006023//DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N) (FRAGMENT).//1.0:40:45//VIBRIO CHOLERA.//P52118  
 40 F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III.//4.0e-11:90:34//CAENORHABDITIS ELEGANS.//P34281  
 F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636  
 F-NT2RP2006052//METALLOTHIONEIN-I (MT-I).//0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797  
 45 F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTUS NORVEGICUS (RAT).//P02466  
 F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//O42184  
 F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651  
 50 F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P80156  
 F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73014  
 55 F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS ELEGANS.//P08124  
 F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 F-NT2RP2006166

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION PRECUR-  
 SOR.//0.95:87:26//ESCHERICHIA COLI.//P75917  
 F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUSCULUS (MOUSE).//  
 P20357  
 5 F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-05:49:61//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//HOMO SAPIENS (HU-  
 MAN).//P05997  
 F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT  
 10 FLY).//P22468  
 F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//0.79:103:28//  
 STREPTOCOCCUS PYOGENES.//P30141  
 F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS  
 (MOUSE).//P05143  
 15 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//  
 P24834  
 F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID  
 SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058  
 F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.2e-28:59:57//  
 20 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401  
 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:  
 53:35//TETRAHYMENA PYRIFORMIS.//P40625  
 F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//  
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612  
 25 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0051:25:76//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HU-  
 MAN).//P42768  
 F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TER-  
 30 RIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333  
 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4)  
 (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401  
 F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3).//0.18:75:29//HOR-  
 DEUM VULGARE (BARLEY).//Q42842  
 35 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS  
 (MAGUS CONE).//P37300  
 F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//1.4e-  
 08:50:50//MUS MUSCULUS (MOUSE).//Q61658  
 F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED  
 40 MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238  
 F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-  
 TRALIAN ECHIDNA).//P35311  
 F-NT2RP2006456  
 F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD  
 45 POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRU-  
 PLICATUM).//P31087  
 F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//  
 Q21184  
 F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA  
 50 (LIVERWORT).//P12202  
 F-NT2RP2006534  
 F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:  
 34//BACILLUS SPHAERICUS.//O32723  
 F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:  
 96//RATTUS NORVEGICUS (RAT).//P56603  
 55 F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP1B10) (TESTOSTERONE 16-ALPHA HY-  
 DROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791  
 F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BO-

VINE).//P02318

F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296

F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755

F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755

F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695

F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-17:64:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787

F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986

F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA GENITALIUM.//P47529

F-NT2RP3000134

F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694

F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-15:36:83//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.91:21:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808

F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//P15858

F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//Q93075

F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103

F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253

F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160

F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214



F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//O67825  
 F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097  
 F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482  
 F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//  
 5 P39189  
 F-NT2RP3000348  
 F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUS-  
 TER 5'REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103  
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:  
 10 84//BOS TAURUS (BOVINE).//P08760  
 F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P19735  
 F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293  
 F-NT2RP3000393//HOMEBOX PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:36:52//HOMO SAPIENS (HU-  
 15 MAN).//P09017  
 F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//  
 5.5e-27:116:44//MUS MUSCULUS (MOUSE).//O35286  
 F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CERE-  
 VISIAE (BAKER'S YEAST).//P33203  
 F-NT2RP3000418//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 20 (EC 2.7.7.49); ENDONUCLEASE].//2.2e-16:228:34//MUS MUSCULUS (MOUSE).//P11369  
 F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//9.8e-10:201:  
 25 26//ESCHERICHIA COLI.//P37908  
 F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.91:48:35//MYCOBACTE-  
 RIUM LEPRAE.//P38388  
 F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:33//GALLUS GALLUS  
 (CHICKEN).//P23681  
 30 F-NT2RP3000451  
 F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN  
 (FRAGMENTS).//0.00018:178:36//RATTUS NORVEGICUS (RAT).//P02454  
 F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.098:40:27//BOS  
 TAURUS (BOVINE).//P37359  
 35 F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16:81//VOLVOX CART-  
 ERI.//P21997  
 F-NT2RP3000512  
 F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACTERIOPHAGE LAMB-  
 DA.//P03769  
 40 F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e-16:234:30//HOMO SA-  
 PIENS (HUMAN).//P51522  
 F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SA-  
 PIENS (HUMAN).//P15151  
 F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//AS-  
 45 TERINA PECTINIFERA (STARFISH).//P11958  
 F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JAN-  
 NASCHII.//Q57866  
 F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//0.99:26:34//  
 DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULANS (FRUIT FLY).//O18666  
 50 F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.5e-26:127:  
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755  
 F-NT2RP3000582  
 F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798  
 F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288  
 55 F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//O00268  
 F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
 P25992

F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00095:90:37//HOMO  
 SAPIENS (HUMAN).//Q15428  
 F-NT2RP3000603//5E5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003  
 F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULA-  
 5 TORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//  
 P36956  
 F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02\_ORF427).//0.15:52:36//MYCOPLAS-  
 MA PNEUMONIAE.//P75277  
 F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//  
 10 Q93073  
 F-NT2RP3000628  
 F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS  
 MUSCULUS (MOUSE).//Q61967  
 F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.7e-40:102:79//HOMO SAPIENS (HU-  
 15 MAN).//P39194  
 F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II.//6.0e-08:83:36//  
 CAENORHABDITIS ELEGANS.//Q09441  
 F-NT2RP3000665//HOMEODOMAIN PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODO-  
 MAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//O75360  
 20 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY).//0.26:202:23//CLOSTRID-  
 IUM KLUYVERI.//P38943  
 F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDRO-  
 LASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P00817  
 F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION.//3.5e-27:211:  
 25 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516  
 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//6.0e-23:114:42//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149  
 F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//6.7e-12:85:36//RATTUS NORVEGICUS  
 30 (RAT).//P10688  
 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER  
 PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q06852  
 F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS (CHICKEN).//P26990  
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:37//PSEUDOMONAS DENI-  
 35 TRIFICANS.//P00103  
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22)).//0.82:51:39//  
 MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458  
 F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.025:79:37//BOS TAURUS (BOVINE).//  
 P25508  
 40 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//0.85:36:47//MYC-  
 OPLASMA CAPRICOLUM.//P43040  
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 (UDPGT) (UGT1\*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT).//1.0:70:34//MUS MUSCULUS  
 (MOUSE).//Q62452  
 45 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.2e-72:247:61//HO-  
 MO SAPIENS (HUMAN).//P27448  
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIENS (HUMAN).//P50876  
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-31:90:75//HOMO SAPIENS (HUMAN).//  
 P39194  
 50 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCINE MAX (SOYBEAN).//P24337  
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SAIMIRI (STRAIN 11).//  
 Q01042  
 F-NT2RP3000865  
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//1.4e-09:232:28//  
 55 GALLUS GALLUS (CHICKEN).//P29616  
 F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGANS.//P17656  
 F-NT2RP3000875//HOMEODOMAIN PROTEIN CDX-2 (CAUDAL-TYPE HOMEODOMAIN PROTEIN 2).//0.90:62:37//  
 MUS MUSCULUS (MOUSE).//P43241

F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.99:124:33//BOS TAURUS (BOVINE)//  
 P02453  
 F-NT2RP3000904  
 F-NT2RP3000917//DHP1 PROTEIN//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION  
 5 YEAST)//P40848  
 F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.4e-19:159:34//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149  
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RAT-  
 TUS NORVEGICUS (RAT)//P39027  
 10 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN)//0.24:19:47//ESCHERICHIA COLI//P13946  
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN//1.4e-10:78:48//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//P25159  
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X//0.70:50:32//  
 CAENORHABDITIS ELEGANS//Q11084  
 15 F-NT2RP3001007  
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG//1.3e-05:  
 138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P36416  
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744)//4.0e-28:141:51//HOMO SAPIENS (HUMAN)//  
 Q02386  
 20 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//3.8e-08:144:29//  
 CAENORHABDITIS ELEGANS//P34568  
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//3.4e-06:217:32//NEPHILA CLA-  
 VIPES (ORB SPIDER)//P46804  
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65//1.1e-30:244:33//RATTUS NORVEGICUS  
 25 (RAT)//Q64375  
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT)//0.041:47:44//HOMO SAPIENS (HU-  
 MAN)//P54793  
 F-NT2RP3001109  
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC//0.17:28:39//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//Q01644  
 30 F-NT2RP3001113//INVOLUCRIN//0.00036:192:23//MUS MUSCULUS (MOUSE)//P48997  
 F-NT2RP3001115  
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT)//0.99:29:51//STREPTOMYCES LIVI-  
 DANS//Q54340  
 35 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT)//0.0015:73:39//BOS TAURUS (BOVINE)//  
 Q29442  
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.3e-57:229:52//HOMO SAPIENS (HU-  
 MAN)//P16415  
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//2.8e-07:83:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888  
 40 F-NT2RP3001133//CALCIUM BINDING PROTEIN//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME  
 MOLD)//P35085  
 F-NT2RP3001140//F-SPONDIN PRECURSOR//2.0e-147:244:97//RATTUS NORVEGICUS (RAT)//P35446  
 F-NT2RP3001147//TROPOMYOSIN 2 (TMII)//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE)//  
 45 P42638  
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2//6.2e-09:163:25//MUS MUSCULUS (MOUSE)//  
 Q06666  
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME  
 REPLICATION PROTEIN CHL15)//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//  
 50 Q01454  
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN)  
 (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3)//0.21:136:26//MUS MUSCULUS (MOUSE)//  
 P15702  
 F-NT2RP3001214//SAP1 PROTEIN//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//  
 55 P39955  
 F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)//2.1e-08:137:33//HOMO SA-  
 PIENS (HUMAN)//P35663  
 F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-

BUTYROBETAINE HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS SP. (STRAIN AK-1).//P80193  
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION (FRAGMENT).//0.75:57:31//  
 ESCHERICHIA COLI.//P33792  
 F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN MUSCULOAPONEUROTIC FIB-  
 5 ROSARCOMA VIRUS AS42.//P23091  
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.2e-55:221:49//  
 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400  
 F-NT2RP3001245  
 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I).//0.0042:142:24//  
 10 DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491  
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89:43//HOMO SAPIENS (HU-  
 MAN).//P53420  
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194:44//HOMO SAPIENS (HUMAN).//  
 Q02386  
 15 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I.//8.2e-17:183:26//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199  
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOS-  
 PHATASE T) (PPT) (FRAGMENT).//1.7e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676  
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.7e-08:38:71//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159:70//HOMO SAPIENS (HU-  
 MAN).//Q92556  
 F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46:39//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-  
 YPUS).//P35307  
 25 F-NT2RP3001318  
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73:24//BRACHYDANIO RERIO (ZE-  
 BRAFISH) (ZEBRA DANIO).//Q98874  
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT).//0.0021:56:  
 35 35//HOMO SAPIENS (HUMAN).//P17037  
 30 F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90:33//MUS MUSCULUS (MOUSE).//P49025  
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202:34//HUMAN CYTOMEGALOVIRUS  
 (STRAIN AD169).//P16818  
 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129:33//HOMO SAPIENS (HUMAN).//P53007  
 35 F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66:28//DICTYOSTELIUM DISCOI-  
 DEUM (SLIME MOLD).//P34141  
 F-NT2RP3001374  
 F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//HOMO SAPIENS (HU-  
 MAN).//P23246  
 40 F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424  
 F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22:45//CAPRINE ARTHRITIS EN-  
 CEPHALITIS VIRUS (CAEV).//P31834  
 F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//STRAWBERRY MILD YELLOW  
 EDGE-ASSOCIATED VIRUS (SMYEA).//Q00848  
 45 F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-  
 08:45:37//HOMO SAPIENS (HUMAN).//P10073  
 F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53538  
 F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 50 P53009  
 F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN).//P20542  
 F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P43735  
 F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS (HUMAN).//Q14191  
 55 F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN).//P12270  
 F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:  
 21//TARSIIUS SYRICHTA (TARSIER).//Q36151  
 F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//

ESCHERICHIA COLI.//P14505

F-NT2RP3001449//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.0043:53:43//GALLUS GALLUS (CHICKEN).//P19601

F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767

F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632

F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA NAPUS (RAPE).//P43402

F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940

F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.13:44:38//BOS TAURUS (BOVINE).//P25508

F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641

F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772

F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820

F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362

F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:177:25//ZEA MAYS (MAIZE).//P14918

F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG).//P80236

F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN).//P39189

F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//Q92609

F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3001672

F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS.//P26843

F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//1.5e-07:63:44//CAENORHABDITIS ELEGANS.//P34679

F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI).//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065

F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:24//HOMO SA-

PIENS (HUMAN).//P12883

F-NT2RP3001698

F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:43//DROSOPHILA MEL-  
ANOGASTER (FRUIT FLY).//P54356

5 F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618

F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS  
(FRUIT FLY).//P13729

F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HO-  
MO SAPIENS (HUMAN).//O14646

10 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//  
CAENORHABDITIS ELEGANS.//P34669

F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//  
Q14141

15 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE  
COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545

F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-21:60:85//HOMO SAPIENS (HUMAN).//  
P39193

F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//  
Q14140

20 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
CIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828

F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-).//0.0096:204:25//  
CANDIDA ALBICANS (YEAST).//Q92212

25 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44//PONGO PYGMAEUS ABELII  
(SUMATRAN ORANGUTAN).//P92694

F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8e-33:159:53//  
HOMO SAPIENS (HUMAN).//P52272

F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTEN-  
NA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS.//P80103

30 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//HOMO SAPIENS (HU-  
MAN).//P08123

F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.99:  
43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466

35 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//9.3e-10:213:  
24//STREPTOCOCCUS PYOGENES.//P30141

F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//2.6e-61:220:60//HO-  
MO SAPIENS (HUMAN).//P55347

F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:213:24//PODOSPORA AN-  
SERINA.//Q00808

40 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.074:124:34//HOMO SA-  
PIENS (HUMAN).//Q15428

F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV).//  
Q89420

45 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021:237:23//SACCHARO-  
MYCES CEREVISIAE (BAKER'S YEAST).//Q12114

F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION.//1.0:63:34//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880

F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-14:35:60//HOMO SAPIENS (HUMAN).//  
P39195

50 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION.//0.86:162:24//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040

F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV).//  
P07645

55 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//1.0:113:27//ES-  
CHERICHIA COLI.//P23839

F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//4.1e-56:208:47//  
CAENORHABDITIS ELEGANS.//Q09251

F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIARA COPROPHILA (FUNGUS

GNAT).//P22312

F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0:41:31//MUS MUSCULUS (MOUSE).//P02319

F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.2e-44:69:79//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.00024:45:40//MUS MUSCULUS (MOUSE).//Q61345

F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPIENS (HUMAN).//P24821

F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232

F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HAKIRI (NEURONAL DEATH PROTEIN DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//O00198

F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (MOUSE).//P17427

F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.046:176:31//STREPTOMYCES FRADIAE.//P20186

F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NORVEGICUS (RAT).//P41777

F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577

F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094

F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INFLUENZAE.//P43709

F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986

F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-17:37:75//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//0.011:166:28//HOMO SAPIENS (HUMAN).//P10163

F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170

F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TARII130).//0.028:191:29//HOMO SAPIENS (HUMAN).//O00268

F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE).//Q02614

F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLUS CASEI.//P55153

F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-26:114:62//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080

F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//MUS MUSCULUS (MOUSE).//P05143

F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45978

F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06922  
 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//1.7e-42:191:43//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14171  
 F-NT2RP3002304  
 5 F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P56183  
 F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q63003  
 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15)  
 / METHENYLtetrahydrofolate cyclohydrolase (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR.//  
 1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995  
 10 F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROEN-  
 DOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//Q92796  
 F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P53327  
 F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//SACCHAROMYCES  
 15 CEREVISIAE (BAKER'S YEAST).//P53091  
 F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:36//EPSTEIN-BARR VIRUS  
 (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204  
 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS.//  
 P50018  
 20 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I.//0.00032:52:48//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438  
 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION.//9.4e-42:209:  
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007  
 F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION.//7.7e-32:162:  
 25 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059  
 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C.//2.1e-45:  
 241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805  
 F-NT2RP3002545  
 F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//2.8e-41:161:52//  
 30 CAENORHABDITIS ELEGANS.//Q10010  
 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIES VIRUS (STRAIN KA-  
 PLAN) (PRV).//P33479  
 F-NT2RP3002587  
 F-NT2RP3002590  
 35 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN- RE-  
 LATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17967  
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION.//1.0:65:40//STREPTOMYCES CA-  
 CAO1.//P33654  
 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC  
 40 6803).//P50027  
 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (HUMAN).//P07438  
 F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830  
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:33//HOMO SAPIENS (HU-  
 MAN).//P08123  
 45 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS ELEGANS.//P37165  
 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS (HUMAN).//P22059  
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION.//6.0e-38:  
 203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893  
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.25:63:31//ARTEMIA  
 50 SALINA (BRINE SHRIMP).//P19049  
 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION.//0.029:60:36//  
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41469  
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULUS (MOUSE).//Q60575  
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:109:33//MUS  
 55 MUSCULUS (MOUSE).//P15265  
 F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).//0.77:  
 70:32//HOMO SAPIENS (HUMAN).//Q13206  
 F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-11:66:40//



SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14056  
 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS MUSCULUS (MOUSE).//Q05722  
 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371  
 5 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY!!!!//0.0034:35:65//HOMO SAPIENS (HUMAN).//P39193  
 10 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790  
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II).//0.97:23:39//BRYONIA DIOICA (RED BRYONY).//P11968  
 15 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00017:140:31//RAT-TUS NORVEGICUS (RAT).//P04474  
 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP).//4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625  
 20 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217  
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 25 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450  
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445  
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//O60488  
 30 F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566  
 F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
 F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE).//P07216  
 35 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705  
 F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879  
 40 F-NT2RP3003032  
 F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254  
 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157  
 45 F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//O33780  
 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552  
 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353  
 50 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981  
 F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 55 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICK-EN).//P46936  
 F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULUS (MOUSE).//P33174  
 F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZOSACCHAROMYCES

POMBE (FISSION YEAST).//Q92337

F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG) (BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (HUMAN).//Q08431

F-NT2RP3003150

F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e-79:260:54//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (HUMAN).//P52742

F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966

F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P32252

F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38190

F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (BOVINE).//Q92176

F-NT2RP3003242//STANNIOCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (HUMAN).//P52823

F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920

F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054

F-NT2RP3003290//BIOH PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001

F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O64948

F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547

F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//ACANTHAMOEBA CASTELLANII (AMOEBIA).//P05659

F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191

F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681

F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991

F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39191

F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III.//3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641

F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP3003384

F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q60649

F-NT2RP3003403

F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//O15370

F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2.//P11300

F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:41//HOLOTRICIA DIOMPHALIA.//Q25055

F-NT2RP3003433

F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3003490

F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PRO-  
 TEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472  
 F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53009  
 5 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HOMO SAPIENS (HU-  
 MAN).//P29400  
 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURUS (BOVINE).//P20072  
 F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//7.3e-27:159:  
 43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529  
 10 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TURNIP YELLOW MOSAIC VI-  
 RUS.//P10358  
 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:32//CAENORHABDITIS ELEGANS.//  
 P34391  
 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN).//  
 15 P39195  
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS (DOG).//P24409  
 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).//  
 2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748  
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA MELA-  
 20 NOGASTER (FRUIT FLY).//Q01645  
 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIO RERIO (ZE-  
 BRAFISH) (ZEBRA DANIO).//Q90267  
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:  
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755  
 25 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENOEID  
 SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060  
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209  
 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//4.3e-25:159:  
 30 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601  
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS  
 (CHICKEN).//P02314  
 F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVEGICUS (RAT).//P35446  
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT  
 35 FLY).//P24014  
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN).//0.47:109:28//AGRO-  
 BACTERIUM TUMEFACIENS.//P05680  
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1).//0.57:34:38//AZORHIZO-  
 BIUM CAULINODANS.//P26486  
 40 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR.//0.75:60:36//SCHIZOPHYLLUM  
 COMMUNE (BRACKET FUNGUS).//P78744  
 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).//4.2e-  
 45 51:72:95//GALLUS GALLUS (CHICKEN).//P00523  
 F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION.//0.00069:160:  
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36121  
 F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.028:135:35//GALLUS GALLUS (CHICK-  
 EN).//P12105  
 50 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT).//0.0026:90:33//HORDEUM VULGARE (BARLEY).//  
 P06472  
 F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//5.6e-20:174:31//BOS TAURUS  
 (BOVINE).//P02720  
 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-  
 55 INHIBITABLE ADENYLYL CYCLASE).//0.0017:111:38//CANIS FAMILIARIS (DOG).//P30803  
 F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).//1.1e-37:187:42//MUS MUSCU-  
 LUS (MOUSE).//O08600  
 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION.//1.0:38:39//ES-

CHERICHIA COLI.//P75979

F-NT2RP3003842

F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB).//0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125

5 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

10 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943

F-NT2RP3003932

15 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:32//THERMOTOGA MARITIMA.//P35874

F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67).//0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476

F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS NORVEGICUS (RAT).//P51400

20 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.00021:64:40//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

25 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE).//0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153

F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-11:51:72//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS (MOUSE).//P48379

30 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REGION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757

F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:72:65//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-10:51:72//HOMO SAPIENS (HUMAN).//P39195

35 F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (HUMAN).//P51815

F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS SOBRIA.//P09165

F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

40 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:178:89//RATTUS NORVEGICUS (RAT).//Q63619

F-NT2RP3004189//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:215:24//PODOSPORA ANSERINA.//Q00808

F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886

45 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:33//CAENORHABDITIS ELEGANS.//P20630

F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:207:29//HOMO SAPIENS (HUMAN).//Q13107

50 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179

F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//1.1e-64:191:63//CAENORHABDITIS ELEGANS.//P34657

F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (HUMAN).//P25440

55 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//1.1e-07:184:35//BOS TAURUS (BOVINE).//P02453

F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40.//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685  
 F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT).//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073  
 5 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 F-NT2RP3004334  
 F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX).//0.91:110:26//MUS MUSCULUS (MOUSE).//P46660  
 F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.60:198:24//CAENORHABDITIS ELEGANS.//P46012  
 10 F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854  
 15 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS (HUMAN).//Q92674  
 F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q13155 F-NT2RP3004428//METALLOTHIONEIN-A (MTA).//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P04734  
 20 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN.//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569  
 F-NT2RP3004454//VERPROLIN.//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370  
 F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215.//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2.//P03291  
 25 F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III.//1.0:33:51//CAENORHABDITIS ELEGANS.//Q09254  
 F-NT2RP3004472//GERM CELL-LESS PROTEIN.//7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820  
 30 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//8.4e-54:214:46//HOMO SAPIENS (HUMAN).//P98171  
 F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110  
 F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 35 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.066:87:35//BACILLUS SUBTILIS.//P50840  
 F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69//HOMO SAPIENS (HUMAN).//P39194  
 40 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40.//0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484  
 F-NT2RP3004527  
 45 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6.//0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32943  
 F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1).//0.38:89:38//RATTUS NORVEGICUS (RAT).//P21743  
 F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2).//0.0024:200:24//MYCOPLASMA PNEUMONIAE.//P75471  
 50 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT).//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18713  
 F-NT2RP3004569//ANKYRIN.//8.3e-07:150:28//MUS MUSCULUS (MOUSE).//Q02357  
 F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325  
 55 F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q02224  
 F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTO-

COCCUS FAECIUM).//P13692

F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//4.5e-08:149:30//CAENORHABDITIS ELEGANS.//P34681

F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.0e-24:75:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54352

F-NT2RP3004670//CUTICLE COLLAGEN 21/0.00090:159:29//CAENORHABDITIS ELEGANS.//P17656

F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79:243:62//BOS TAURUS (BOVINE).//P35526

F-NT2RP4000023

F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALLUS GALLUS (CHICKEN).//P12957

F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-24:182:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP4000102//XPAR7 PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q99166

F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014

F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q10568

F-NT2RP4000129//5E5 ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//Q63003

F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197

F-NT2RP4000150

F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//4.2e-31:180:47//CAENORHABDITIS ELEGANS.//P32740

F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//2.4e-08:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).//5.4e-05:143:32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28284

F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22579

F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20:104:40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287

F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203

F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:207:76//MUS MUSCULUS (MOUSE).//Q03173

F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:43//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//O23968

F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS (BOVINE).//P20072

F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5e-71:209:66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115

F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404

F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370

F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531

F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC REGION.//0.75:125:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596

F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.27:92:

33//RATTUS NORVEGICUS (RAT).//P10164

F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN AD-  
ENOVIRUS TYPE 41.//P23691

F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:  
163:52//HOMO SAPIENS (HUMAN).//O75570

F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:80//RATTUS NOR-  
VEGICUS (RAT).//P54319

F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246

F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//  
Q99676

F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//  
0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098

F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-15:72:61//HOMO SAPIENS (HUMAN).//  
P39195

F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-23:63:82//HOMO SAPIENS (HUMAN).//  
P39192

F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//  
KLUYVEROMYCES LACTIS (YEAST).//P33294

F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS  
(CHICKEN).//P19601

F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
RASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVI-  
RUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009

F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN  
ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276

F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:23//  
CAENORHABDITIS ELEGANS.//Q09475

F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P40484

F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-23:165:35//  
CAENORHABDITIS ELEGANS.//P34535

F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOS-  
PHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P15396

F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//  
Q41657

F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVI-  
SIAE (BAKER'S YEAST).//P45818

F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BOS TAURUS (BOVINE).//  
P25508

F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:187:24//STREP-  
TOCOCCUS AGALACTIAE.//P27951

F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
P33755

F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS GALLUS (CHICK-  
EN).//P13544

F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III.//4.3e-14:174:34//  
CAENORHABDITIS ELEGANS.//Q03574

F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//2.1e-19:155:36//  
CAENORHABDITIS ELEGANS.//P34679

F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290

F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)  
(SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188:44//GALLUS GALLUS (CHICKEN).//P30352

F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:40:40//GLYCINE MAX  
(SOYBEAN).//Q05544

F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2,4e-06:31:74//HOMO SAPIENS (HUMAN).//

P39188

F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOCCUS JANNAS-CHII.//Q58465

F-NT2RP4000704

5 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-07:134:40//STREPTOMYCES FRADIAE.//P20186

F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.1e-62:109:88//HOMO SAPIENS (HUMAN).//P10266

10 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//HOMO SAPIENS (HUMAN).//P23246

F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655

15 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915

F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P29675

20 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-NT2RP4000833

F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST54DB.//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

25 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38129

F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:229:53//RATTUS NORVEGICUS (RAT).//O09175

30 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//HOMO SAPIENS (HUMAN).//P16415

F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCULUS (MOUSE).//O35682

F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:268:43//HOMO SAPIENS (HUMAN).//P22314

35 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B).//5.4e-10:220:25//HOMO SAPIENS (HUMAN).//Q16620

F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

40 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:32//BACILLUS SUBTILIS.//P39217

F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828

F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).//P29128

45 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903

50 F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288

F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6.//2.0e-05:102:37//CAENORHABDITIS ELE-GANS.//P34391

F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

55 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20517



F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.//0.90:94:25//CAENORHABDITIS ELEGANS.//P34343

F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531

5 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722

F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//O54888

10 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377

F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840

F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

15 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996

20 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664

F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830

F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268

25 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586

F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099

30 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911

F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563

F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032

35 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378

F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736

F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793

40 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896

F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750

45 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997

F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331

50 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643

F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178

F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643

55 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307

F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DER-

MORPHIN].//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422  
 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360  
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//Q12404  
 5 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//  
 P36787  
 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124  
 10 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA  
 COLI.//P05834  
 F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273  
 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241  
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 15 0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:190:27//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787  
 F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108:31//PODOSPORA AN-  
 SERINA.//Q00808  
 20 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOCCUS JANNASCHII.//  
 Q58220  
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III.//1.4e-18:244:27//  
 CAENORHABDITIS ELEGANS.//Q10123  
 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)  
 25 (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)  
 (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN).//P53760  
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.7e-11:229:26//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386  
 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//0.00088:84:28//HO-  
 30 MO SAPIENS (HUMAN).//Q15404  
 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.0e-  
 22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180  
 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN).//0.51:92:  
 26//ONCHOCERCA VOLVULUS.//P36991  
 35 F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 TEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160  
 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION.//1.2e-14:207:  
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767  
 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-  
 40 MENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//HOMO SAPIENS (HU-  
 MAN).//Q02224  
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIENS (HUMAN).//Q14141  
 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216:56//HOMO SAPIENS (HU-  
 45 MAN).//P28160  
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//  
 0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P18616  
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//ARTEMIA SALINA (BRINE  
 SHRIMP).//P02399  
 50 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P21560  
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-  
 PHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPIENS (HUMAN).//Q02218  
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2.3e-24:137:37//  
 55 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//6.0e-22:  
 148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206  
 F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561

5 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25656

10 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS.//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT).//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170

15 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:42//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS TAURUS (BOVINE).//P06836

20 F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620

F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS PYOGENES.//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

25 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//SUS SCROFA (PIG).//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO SAPIENS (HUMAN).//P02811

30 F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT).//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462

F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34MS19.//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323

35 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II.//3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS.//Q10690

40 F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-36:103:72//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:37:37//CHLORELLA VULGARIS.//P56338

F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282

45 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//1.0:67:34//HOMO SAPIENS (HUMAN).//P31260

50 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT).//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506

F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28//HOMO SAPIENS (HUMAN).//P11274

F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q07231

55 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENORHABDITIS ELEGANS.//P20630

F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAPIENS (HUMAN).//O14817

F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:42//CAENORHABDITIS ELE-

GANS.//P34391

F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727

F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO SAPIENS (HUMAN).//Q13330

5 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:22//RATTUS NOR-VEGICUS (RAT).//P98089

F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE).//P55194

F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185

10 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS (MOUSE).//Q05921

15 F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42935

F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038

F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

20 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399

F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209

25 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260

F-NT2RP4001953

F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//Q07833

30 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIFTIA PACHYPTILA (TUBE WORM).//P30754

F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

35 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943

F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875

40 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TUBERCULOSIS.//Q10888

F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

45 F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481

F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670

F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29:55//OWENIA FUSIFORMIS.//P21260

50 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P38938

F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56027

F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//O83371

55 F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012

F-NT2RP5003459//HOMEODOMAIN PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40//MUS MUSCULUS (MOUSE).//P02831

F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779  
 F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:215:28//PODOSPORA ANSERINA.//Q00808  
 5 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640  
 F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MUS MUSCULUS (MOUSE).//P05142  
 10 F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.92:49:32//PARACOCCLUS DENITRIFICANS.//P29969  
 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116  
 15 F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//RATTUS NORVEGICUS (RAT).//P02454  
 F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331  
 20 F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501  
 F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658  
 F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262  
 F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060  
 25 F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457  
 F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS ELEGANS.//P17657  
 F-OVARC1000035  
 30 F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143  
 F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022  
 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01452  
 35 F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P13662  
 F-OVARC1000085  
 F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS (RAT).//Q02874  
 40 F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCULUS (MOUSE).//Q06666  
 F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P46756  
 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935  
 45 F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600  
 F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217  
 50 F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-28:57:63//HOMO SAPIENS (HUMAN).//P39194  
 F-OVARC1000133  
 F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:200:29//HOMO SAPIENS (HUMAN).//Q13107  
 55 F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q01702  
 F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12:175:29//CANDIDA AL-

BICANS (YEAST).//P46593

F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAPIENS (HUMAN).//P50876

F-OVARC1000168/////ALU SUBFAMILY J WARNING ENTRY !!!!!0.0030:77:38//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:35//ESCHERICHIA COLI.//P32056

F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268

F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03677

F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS MUSCULUS (MOUSE).//P05142

F-OVARC1000240/////ALU SUBFAMILY SP WARNING ENTRY !!!!!1.8e-10:41:78//HOMO SAPIENS (HUMAN).//P39193

F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSCULUS (MOUSE).//P97481

F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770

F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//P23249

F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBYA GOSSYP II (EREMOTH-ECIUM GOSSYP II).//Q00063

F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5.2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14179

F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPIENS (HUMAN).//P04281

F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004

F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CYANOPHORA PARADOXA.//P48273

F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:115:33//XENOPUS LAE-VIS (AFRICAN CLAWED FROG).//Q05049

F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGICUS (RAT).//P28023

F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:46:34//BACILLUS SUBTILIS.//P54431

F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067

F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION.//0.70:21:47//BACILLUS SUBTILIS.//P39150

F-OVARC1000431

F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q04205

F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059

F-OVARC1000442

F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCHUS CONTORTUS.//P16252

F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLI).//P42710

F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:26//SACCHAROMYCES CEREVI-SIAE (BAKER'S YEAST).//P11075

F-OVARC1000466/////ALU SUBFAMILY SC WARNING ENTRY !!!!!2.3e-08:29:93//HOMO SAPIENS (HUMAN).//P39192

F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-CIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8e-06:96:36//RATTUS NORVEGICUS (RAT).//Q63340

F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:48:37//CYANIDIUM  
 CALDARIUM (GALDIERIA SULPHURARIA).//P31567 F-OVARC1000486  
 F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS JANNASCHII.//  
 Q58610  
 5 F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:40//EIMERIA ACER-  
 VULINA.//P09125  
 F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02722  
 F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO SAPIENS (HUMAN).//  
 Q16612  
 10 F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-  
 AMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:35//HOMO SAPIENS (HUMAN).//Q10472  
 F-OVARC1000556  
 F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:80:47//HOMO SAPIENS (HUMAN).//  
 15 P39188  
 F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//0.45:32:50//HUMAN  
 IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P17760  
 F-OVARC1000573  
 F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVINE).//P46159  
 20 F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).//0.023:96:36//BOS TAURUS (BOVINE).//  
 P02459  
 F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO SAPIENS (HU-  
 MAN).//P09001  
 F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE).//0.91:134:28//  
 25 CHLAMYDOMONAS REINHARDTII.//P31178  
 F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.6e-36:100:80//HOMO SAPIENS (HU-  
 MAN).//P39189  
 F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//ODONTELLA SINENSIS.//  
 P49535  
 30 F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.0036:64:37//HELIAN-  
 THUS ANNUUS (COMMON SUNFLOWER).//P22357  
 F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS NORVEGICUS  
 (RAT).//P02466  
 F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//ESCHERICHIA COLI.//  
 35 P05834  
 F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE  
 OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERICHIA COLI.//P08374  
 F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722  
 F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
 40 7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098  
 F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA (ROMAN SNAIL)  
 (EDIBLE SNAIL).//P33187  
 F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS NORVEGICUS (RAT).//  
 P02684  
 45 F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO SAPIENS (HUMAN).//  
 P02811  
 F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLLGLUCOSAMINE (BETA  
 1->4) GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GA-  
 LACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037  
 50 F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//5.2e-29:224:36//  
 CAENORHABDITIS ELEGANS.//Q18262  
 F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//P25159  
 F-OVARC1000769  
 55 F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS (HUMAN), AND CANIS  
 FAMILIARIS (DOG).//P08886  
 F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX  
 PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS SCROFA (PIG).//Q29303  
 F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-31:47:82//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.16:55:40//  
 5 CAENORHABDITIS ELEGANS.//Q10926  
 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTI-  
 VATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//  
 P35465  
 F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN  
 10 HAMSTER).//P08199  
 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION.//6.9e-09:180:  
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991  
 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 15 LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S  
 YEAST).//P52490  
 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P40484  
 F-OVARC1000883//METALLOTHIONEIN-I.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLA-  
 BRATA).//P15113  
 20 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440  
 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.00033:60:45//BOS TAURUS (BOVINE).//  
 P02465  
 F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774  
 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//  
 25 P15606  
 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEU-  
 DOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10337  
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELE-  
 GANS.//Q09455  
 30 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HU-  
 MAN).//P56524  
 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//  
 P92848  
 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ES-  
 35 CHERICHIA COLI.//P45505  
 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HU-  
 MAN).//P02452  
 F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1).//  
 P12533  
 40 F-OVARC1000948  
 F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS JANNASCHII.//  
 Q58343  
 F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-32:56:75//HOMO SAPIENS (HUMAN).//  
 P39193  
 45 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR)  
 (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//  
 P28375  
 F-OVARC1000971  
 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECUR-  
 50 SOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832  
 F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138  
 F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:  
 40//HOMO SAPIENS (HUMAN).//P20264  
 F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:43:90//HOMO SAPIENS (HUMAN).//  
 55 P39195  
 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01642  
 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS JANNASCHII.//



Q58336

F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949

F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).//Q05561

5 F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640

F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338

F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194

10 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637

F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490

15 F-OVARC1001062

F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44951

F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//O69162

20 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291

25 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197

F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079

F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963

30 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608

F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339

F-OVARC1001118

F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS.//O66439

35 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MUSCULUS (MOUSE).//P28798

F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177

F-OVARC1001162

40 F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070

F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS MUSCULUS (MOUSE).//P97323

F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUMAN).//P02814

45 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00023:28:75//HOMO SAPIENS (HUMAN).//P39188

F-OVARC1001173

F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

50 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510

F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215

F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

55 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOCCUS JANNASCHII.//Q58633

F-OVARC1001240

F-OVARC1001243

F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN).//P25440  
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//  
 Q06666  
 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:41//PSEU-  
 5 DOMONAS AERUGINOSA.//P24563  
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION.//1.0:44:29//  
 BACTERIOPHAGE T4.//P32281  
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//  
 0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504  
 10 F-OVARC1001282  
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:31//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P38968  
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.023:  
 134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13695  
 15 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.3e-14:  
 150:28//ZEA MAYS (MAIZE).//P49133  
 F-OVARC1001330  
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//Q02926  
 20 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.9e-17:110:  
 43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032  
 F-OVARC1001342  
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//STAPHYLOCOCCUS CAR-  
 NOSUS.//P36253  
 25 F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//  
 Q05890  
 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).//0.86:109:  
 31//HOMO SAPIENS (HUMAN).//P48634  
 F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS TAURUS (BOVINE).//  
 30 P02465  
 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECUR-  
 SOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13).//Q47100  
 F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN).//  
 P39188  
 35 F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSI-  
 LON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039  
 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162  
 F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.062:18:77//HOMO SAPIENS (HUMAN).//  
 40 P39195  
 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//  
 CAENORHABDITIS ELEGANS.//Q03570  
 F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//  
 Q05482  
 45 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO SAPIENS (HUMAN).//  
 Q03692  
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30//TOMATO YELLOW  
 LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283  
 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDELLA TRISERIALIS  
 50 (LEECH).//P17138  
 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.74:19:47//MUS  
 MUSCULUS (MOUSE).//P28184  
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P53290  
 55 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//MUS MUSCULUS  
 (MOUSE).//Q02788  
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS INFLUENZAE.//P44149  
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAPIENS (HUMAN).//

P56545

F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161

F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077

F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOMO SAPIENS (HUMAN).//P35325

F-OVARC1001547

F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53081

F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:81//GALLUS GALLUS (CHICKEN).//P30352

F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15898

F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898

F-OVARC1001611

F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.30:43:34//CAENORHABDITIS ELEGANS.//Q11116

F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0e-19:45:82//HOMO SAPIENS (HUMAN).//P39192

F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//O60248

F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514

F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267

F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVINE).//P07106

F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921

F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173

F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945

F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911

F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//0.99:113:27//ESCHERICHIA COLI.//P23839

F-OVARC1001768

F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945

F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878

F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTREURYS TRISTIS (SPIDER).//P36984

F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796

F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RATTUS NORVEGICUS (RAT).//P02454

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260  
 F-OVARC1001828  
 F-OVARC1001846  
 F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216  
 5 F-OVARC1001873  
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//  
 CAENORHABDITIS ELEGANS.//Q09296  
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC  
 PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812  
 10 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//  
 CAENORHABDITIS ELEGANS.//P34408  
 F-OVARC1001901  
 15 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR  
 CRESS).//P34789  
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 CIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174  
 F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050  
 20 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P12945  
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//  
 CAENORHABDITIS ELEGANS.//P34664  
 25 F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360  
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS  
 (MOUSE).//P02319  
 30 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1002044  
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO  
 SAPIENS (HUMAN).//P46939  
 35 F-OVARC1002066  
 F-OVARC1002082  
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.99:149:24//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386  
 F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874  
 40 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P50887  
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:  
 56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328  
 F-OVARC1002143  
 45 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00010:64:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915  
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//  
 AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VI-  
 50 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204  
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-  
 MOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964  
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.//8.8e-05:148:25//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725  
 55 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722  
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547

F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474  
 F-PLACE1000031  
 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-12:97:41//HOMO SAPIENS (HUMAN).//  
 5 P39194  
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-  
 125).//P38373  
 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258  
 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046  
 10 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53538  
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HU-  
 MAN).//Q92934  
 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS  
 15 (MOUSE).//P06798  
 F-PLACE1000094  
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290  
 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN  
 20 ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HU-  
 MAN).//P30084  
 F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924  
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR.//0.11:48:  
 33//MYCOBACTERIUM TUBERCULOSIS.//Q10637  
 25 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P08640  
 F-PLACE1000214  
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS GALLUS  
 30 (CHICKEN).//P02457  
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE HERPESVIRUS TYPE  
 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2).//Q00039  
 F-PLACE1000292  
 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:42//MEDICAGO SATIVA  
 35 (ALFALFA).//P11728  
 F-PLACE1000332  
 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALLIDUM.//O83435  
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C).//1.0:63:25//ORYC-  
 TOLAGUS CUNICULUS (RABBIT).//P16973  
 40 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE  
 A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027  
 F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496  
 F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN).//0.00023:145:30//MUS MUSCULUS  
 (MOUSE).//P54320  
 45 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:63//HOMO SAPIENS  
 (HUMAN).//Q15233  
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//4.7e-  
 07:134:29//MUS MUSCULUS (MOUSE).//P53368  
 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//0.48:72:27//  
 50 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080  
 F-PLACE1000424  
 F-PLACE1000435  
 F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-31:129:63//HOMO SAPIENS (HU-  
 MAN).//P39195  
 55 F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722  
 F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723

F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS JANNASCHII.//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO SAPIENS (HUMAN).//P15803

F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:192:47//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455

F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN ADENOVIRUS TYPE 12.//P36707

F-PLACE1000610

F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558

F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS (HUMAN).//Q13263

F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934

F-PLACE1000716

F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11).//0.90:53:37//SHIGELLA FLEXNERI.//P55794

F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA GENITALIUM.//P47394

F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-15:98:48//CAENORHABDITIS ELEGANS.//P34529

F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021

F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45//MYCOBACTERIUM TUBERCULOSIS.//O06360

F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657

F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:128:30//HOMO SAPIENS (HUMAN).//P50552

F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1000841

F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY).//P23241

F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS JANNASCHII.//Q60319

F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899

F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRAKII (YEAST) (HANSENULA MRAKII).//P10410

F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO SAPIENS (HUMAN).//P49771

F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34109  
 F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941  
 5 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097  
 F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796  
 F-PLACE1001000  
 10 F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584  
 F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P00987  
 F-PLACE1001015  
 F-PLACE1001024  
 15 F-PLACE1001036  
 F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA DIOMPHALIA.//Q25055  
 F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999  
 F-PLACE1001076  
 20 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50//MEDICAGO SATIVA (ALFALFA).//P11728  
 F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057  
 F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.00063:125:32//CAENORHABDITIS ELEGANS.//Q11102  
 25 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309  
 F-PLACE1001136//ALPHA-N-ACETYLGALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA-GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050  
 30 F-PLACE1001168  
 F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895  
 F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 35 F-PLACE1001238  
 F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087  
 F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 40 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040  
 F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01470  
 F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481  
 45 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636  
 F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620  
 F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:66:66//HOMO SAPIENS (HUMAN).//P39189  
 50 F-PLACE1001323  
 F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971  
 F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-I2).//0.070:18:33//NAJA HAJE ANNU-LIFERA (BANDED EGYPTIAN COBRA).//P01422  
 55 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).//P17495

F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYO-  
 GENES.//P16947  
 F-PLACE1001384  
 F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//1.9e-22:142:  
 5 39//HOMO SAPIENS (HUMAN).//Q12929  
 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//  
 BACTERIOPHAGE T4.//P22917  
 F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-32:47:74//HOMO SAPIENS (HUMAN).//  
 P39194  
 10 F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN)  
 (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36//HOMO SAPIENS (HUMAN).//P04921  
 F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35//ASCARIS SUUM (PIG  
 ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852  
 F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814  
 15 F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER  
 RORQUAL).//P11184  
 F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS JANNASCHII.//  
 Q58019  
 F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BA-  
 20 CILLUS SUBTILIS.//P37480  
 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206  
 F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//  
 CAENORHABDITIS ELEGANS.//P34561  
 F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//  
 25 SORGHUM BICOLOR MILO (SORGHUM).//P21924  
 F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//O48408  
 F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ES-  
 CHERICHIA COLI.//P37795  
 F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMOR-  
 30 PHA (LIVERWORT).//P12196  
 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPI-  
 ENS (HUMAN).//Q15431  
 F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//  
 Q60809  
 35 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:  
 77:33//RATTUS NORVEGICUS (RAT).//P10164  
 F-PLACE1001608  
 F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896  
 F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640  
 40 F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SA-  
 PIENS (HUMAN).//P51523  
 F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM  
 (GALDIERIA SULPHURARIA).//O19926  
 F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMU-  
 45 NODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804  
 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:27:66//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842  
 50 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
 (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635  
 F-PLACE1001705  
 F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME L//6.1e-07:157:29//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13798  
 55 F-PLACE1001720  
 F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS  
 (MOUSE).//P05143  
 F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//



0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839  
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-17:90:56//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS (HUMAN).//Q14138  
 5 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-  
 LEAVED BLUE LUPINE).//P09930  
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38//SCHIZOSACCHARO-  
 MYCES POMBE (FISSION YEAST).//O42908  
 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.2e-43:126:77//HOMO SAPIENS (HU-  
 10 MAN).//P39189  
 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYLORI (CAMPYLO-  
 BACTER PYLORI).//P56057  
 F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA  
 MELANOGASTER (FRUIT FLY).//P48994  
 15 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:  
 46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262  
 F-PLACE1001799  
 F-PLACE1001810  
 F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUC-  
 20 CINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RU-  
 MEN FUNGUS).//P53587  
 F-PLACE1001821  
 F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIENS (HUMAN).//P01600  
 F-PLACE1001845  
 25 F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53583  
 F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE).//P01540  
 F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA  
 SNAKE) (DSTEIRA STOKESI).//P01381  
 30 F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:29//BACTERIOPHAGE  
 NF.//P09877  
 F-PLACE1001928  
 F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KA-  
 PLAN) (PRV).//P33479  
 35 F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELLA CATARRHALIS.//Q49091  
 F-PLACE1002004  
 F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE).//Q61211  
 F-PLACE1002052  
 F-PLACE1002066  
 40 F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16:77:31//ARABIDOP-  
 SIS THALIANA (MOUSE-EAR CRESS).//P40602  
 F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//4.0e-11:174:28//  
 CAENORHABDITIS ELEGANS.//Q09564  
 F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:112:99//HOMO SA-  
 45 PIENS (HUMAN).//O76094  
 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A)  
 (P8MTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908  
 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDI-  
 50 ATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOUSE).//P17950  
 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4).//0.0086:39:46//THIOBA-  
 CILLUS FERROOXIDANS.//P20088  
 F-PLACE1002150  
 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.4e-34:56:82//HOMO SAPIENS (HUMAN).//  
 P39189  
 55 F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//  
 P01492  
 F-PLACE1002170  
 F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT

SWI3) (TRANSCRIPTION FACTOR

TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591

F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738

F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION.//0.41:49:36//RHIZOBIUM LEGUMI-  
NOSARUM.//P14310

F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890

F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508

F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867

F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//  
P32219

F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM  
VIVAX.//P08677

F-PLACE1002399

F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)  
(DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023

F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS  
(MOUSE).//P41233

F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC RE-  
GION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545

F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS  
LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMY-  
CES POMBE (FISSION YEAST).//O13765

F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555

F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//  
P39193

F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS  
MACAQUE).//Q95196

F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//  
CAENORHABDITIS ELEGANS.//Q11096

F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PRO-  
TEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//1.0:15:  
60//ESCHERICHIA COLI.//P46878

F-PLACE1002529

F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396

F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//  
P39195

F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT  
FLY).//P45890

F-PLACE1002578

F-PLACE1002583

F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176

F-PLACE1002598

F-PLACE1002604

F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:  
23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//  
Q60604

F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086

F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//  
P38479

F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//  
Q62839

F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749  
 F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378  
 5 F-PLACE1002772  
 F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007  
 F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512  
 10 F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630  
 F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//MUS MUSCULUS (MOUSE).//Q60772  
 15 F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.46:35:42//HORDEUM VULGARE (BARLEY).//P17991  
 F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:201:74//HOMO SAPIENS (HUMAN).//P56524  
 F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.6e-30:54:96//HOMO SAPIENS (HUMAN).//P51522  
 20 F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS (MOUSE).//P02802  
 F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH).//P01065  
 F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5'REGION (ORF1).//1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).//P36866  
 25 F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!4.1e-27:91:70//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III.//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548  
 30 F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!2.6e-11:40:85//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:38:36//CANIS FAMILIARIS (DOG).//P13206  
 F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496  
 35 F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//METHANOCOCCUS JANNASCHII.//Q58560  
 F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121  
 40 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012  
 F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609  
 45 F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P07791  
 F-PLACE1003045  
 F-PLACE1003092  
 F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS (HUMAN).//Q13268  
 50 F-PLACE1003108  
 F-PLACE1003136  
 F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS (BOVINE).//P18892  
 F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//Q01777  
 55 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743  
 F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.24:74:36//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319

F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750

F-PLACE1003200

F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSUS.//P42131

F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:55//HOMO SAPIENS (HUMAN).//Q15391

F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS (HUMAN).//Q14138

F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522

F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAENORHABDITIS ELE-GANS.//P21541

F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SAPIENS (HUMAN).//P11277

F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:94//HOMO SAPI-ENS (HUMAN).//P51522

F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083

F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA MELA-NOGASTER (FRUIT FLY).//Q01643

F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902

F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378

F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:66:75//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS (HUMAN).//P35326

F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:42//SACCHAROMY-CES CEREVISIAE (BAKER'S YEAST).//P32323

F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722

F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS (MOUSE).//Q60890

F-PLACE1003383

F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//P35287

F-PLACE1003401

F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556

F-PLACE1003454

F-PLACE1003478

F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HU-MAN).//Q13201

F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HU-MAN).//P08547

F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-17:77:50//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438 [MUNICH]).//P14366

F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRI-CAN CLAWED FROG).//P03931

F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436

F-PLACE1003553

F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438 [MUNICH]).//P14366

F-PLACE1003575

F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226

F-PLACE1003584

F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998

F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES (SHEEP).//

O78751

F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-87:238:67//CAENORHABDITIS ELEGANS.//P46975

F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554

F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516

F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CANIS FAMILIARIS (DOG).//P04542

F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEUS MIRABILIS.//P42275

F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q02722

F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P22793

F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170

F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074

F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724

F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270

F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI.//P00164

F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//Q24058

F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1003771

F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634

F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523

F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBIUS FORFICATUS.//Q02030

F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR.//0.0046:116:31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS).//O52727

F-PLACE1003870

F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166:75//HOMO SAPIENS (HUMAN).//P51003

F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96:34//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.8e-54:260:46//BOS TAURUS (BOVINE).//P10895

F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792

F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS).//0.58:49:36//DAUCUS CAROTA (CARROT).//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//3.8e-52:92:85//HOMO SAPIENS (HUMAN).//P17812

F-PLACE1003915//PROBABLE ARGINYLYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05506

F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).//0.94:  
 65:29//STREPTOCOCCUS EQUISIMILIS.//P30053  
 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//0.098:79:31//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074  
 5 F-PLACE1003936  
 F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385  
 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:73//HOMO SAPIENS (HUMAN).//  
 P39192  
 10 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P89102  
 F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-15:69:60//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//  
 15 Q89420  
 F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387  
 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAP-  
 LAN) (PRV).//P33485  
 20 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSI-  
 FORMIS.//P21260  
 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//  
 STREPTOCOCCUS PYOGENES.//P49054  
 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:  
 25 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817  
 F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//  
 Q62556  
 F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062  
 F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GAR-  
 30 DEN PEA).//P13555  
 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567  
 F-PLACE1004257//HYPOTHETICAL PROTEIN H10490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006  
 F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:  
 35 35//HOMO SAPIENS (HUMAN).//P25067  
 F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8)  
 (HUMAN HERPESVIRUS 4).//P03186  
 F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286  
 F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//  
 P25508  
 40 F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB).//P37990  
 F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE).//Q62100  
 F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMY-  
 CES COELICOLOR.//P54741  
 F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAK-  
 45 ER'S YEAST).//Q12380  
 F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HU-  
 MAN).//P53420  
 F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33//GALLUS GALLUS  
 (CHICKEN).//P02457  
 50 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//DROSOPHILA HYDEI  
 (FRUIT FLY).//Q08696  
 F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-28:46:76//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//5.7e-34:202:  
 55 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722  
 F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLAC-  
 TOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR  
 SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HELICOBACTER ACINONYX.//Q47947

F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:42//HOMO SAPIENS (HUMAN).//  
P39195

F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-)/1.9e-31:203:39//RATTUS NORVEGICUS  
(RAT).//Q63448

5 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR  
(EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD<sup>+</sup>-SPECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100//  
MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479

F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00013:40:62//HOMO SAPIENS (HUMAN).//  
P39188

10 F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT  
FLY).//P25823

F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:33:87//HOMO SAPIENS (HUMAN).//  
P39193

F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:58//HOMO SAPI-  
15 ENS (HUMAN).//P51522

F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.019:136:27//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903

F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).//0.58:66:34//HO-  
20 MO SAPIENS (HUMAN).//P78358

F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//  
3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325

F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT).//  
0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14587

25 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).//  
P80248

F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAM-  
MA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518

F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656

30 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100  
KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568

F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438

F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.00036:100:30//PYRO-  
COCCUS FURIOSUS.//Q51731

35 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA  
PNEUMONIAE.//Q48481

F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-AS-  
PARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).//  
Q03391

40 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//0.025:125:  
20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I.//7.6e-52:158:56//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//  
45 MUS MUSCULUS (MOUSE).//P12815

F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//  
Q60809

F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:48:62//HOMO SAPIENS (HUMAN).//  
P39192

50 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946

F-PLACE1004693

F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//PAN PANISCUS (PYGMY  
CHIMPANZEE) (BONOBO).//Q35587

F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.95:53:33//  
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565

F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//RATTUS NORVEGI-  
CUS (RAT).//Q05175

F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-09:37:70//HOMO SAPIENS (HUMAN).//

P39194

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.//P21484

F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-  
FERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST)  
(GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//  
RATTUS NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN[CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:  
106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259

F-PLACE1004804

F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN  
AD169).//P16777

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//  
CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1004815

F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:  
38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LI-  
CHENIFORMIS.//P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072

F-PLACE1004838

F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR  
CRESS).//Q08891

F-PLACE1004885

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//  
1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q42643

F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BA-  
CILLUS SUBTILIS.//P54165

F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//  
Q57982

F-PLACE1004934

F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN  
CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//  
CAENORHABDITIS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS  
COMOSUS (PINEAPPLE).//P27478

F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.3e-30:55:72//HOMO SAPIENS (HUMAN).//  
P39192

F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTO-  
COCCUS PYOGENES.//P19401

F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS  
(COMMON EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//  
Q06183

F-PLACE1005027

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY).//Q01645

F-PLACE1005055



F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN)//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652  
 F-PLACE1005077  
 F-PLACE1005085//INSECT TOXIN 1 (BOT IT1)//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION)//P55902  
 5 F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.5e-38:93:76//HOMO SAPIENS (HUMAN)//P39194  
 F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT)//1.6e-11:35:100//HOMO SAPIENS (HUMAN)//P49753  
 10 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13)//3.0e-14:110:38//MUS MUSCULUS (MOUSE)//Q60821  
 F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.41:35:34//BOS TAURUS (BOVINE)//P37359  
 F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II)//1.0:29:41//RATTUS NORVEGICUS (RAT)//P11608  
 15 F-PLACE1005128//RABPHILIN-3A (FRAGMENT)//5.9e-05:95:36//MUS MUSCULUS (MOUSE)//P47708  
 F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15)//0.17:48:35//MUS MUSCULUS (MOUSE)//Q61075  
 F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-31:60:76//HOMO SAPIENS (HUMAN)//P39189  
 20 F-PLACE1005176  
 F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBCUTE SCLEROSE PANENCEPHALITIS VIRUS)//P06831  
 F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE)//0.0025:58:34//NEUROSPORA CRASSA//P38678  
 25 F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20511  
 F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR//0.70:60:35//HOMO SAPIENS (HUMAN)//Q99218  
 30 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS//Q01577  
 F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II//1.2e-38:206:41//CAENORHABDITIS ELEGANS//Q10003  
 F-PLACE1005266  
 35 F-PLACE1005277//PROTEIN GURKEN PRECURSOR//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//P42287  
 F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP)//2.0e-12:211:29//GALLUS GALLUS (CHICKEN)//P53352  
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//1.8e-78:205:78//BOS TAURUS (BOVINE)//P08760  
 40 F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)//Q09020  
 F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67)//0.15:36:41//ESCHERICHIA COLI//P39355  
 45 F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//1.0:19:52//HOMO SAPIENS (HUMAN)//P30808  
 F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN//0.00021:98:35//HOMO SAPIENS (HUMAN)//P11274  
 F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3//0.37:98:33//MUS MUSCULUS (MOUSE)//P81067  
 50 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLASE)//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48567  
 F-PLACE1005374  
 55 F-PLACE1005409  
 F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO)//P07979  
 F-PLACE1005467//KERATIN, FEATHER (F-KER)//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

GULL).//P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA (HONEYBEE).//P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT).//P16359

F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).//P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29//BOS TAURUS (BOVINE).//P03929

F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625

F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM.//P30725

F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164

F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222

F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894

F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60561

F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36:41//PORPHYRA PURPUREA.//P51224

F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405

F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603

F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53//MUS MUSCULUS (MOUSE).//Q60710

F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951

F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635

F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.028:96:32//HOMO

SAPIENS (HUMAN).//P26371

F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P29617

F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.0:95:25//MUS MUSCULUS (MOUSE).//P17564

F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098

F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-23:56:76//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIOPHAGE 186.//P08711

F-PLACE1005845

F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.5e-28:96:73//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1005851

F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568

F-PLACE1005884

F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P54069

F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//O00483

F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURELIA.//P15617

F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01010

F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAGMENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326

F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983

F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP).//0.64:57:33//RHODOFERAX FERMENTANS.//P80882

F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821

F-PLACE1005966//TACHYPLESIN II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P14214

F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259

F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.5e-36:102:75//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473

F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP- RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q11207

F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOG).//Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:76//HOMO SAPIENS (HUMAN).//P56211

F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:40//ARACHIS HYPOGAEA (PEANUT).//P01066

5 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//O00410

F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

10 F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616

F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110

15 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10863

F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049

20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MOUSE).//P17427

25 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864

F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965

30 F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-PLACE1006205

F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:22:50//MUS MUSCULUS (MOUSE).//P15265

F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805

35 F-PLACE1006236

F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407

F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS MUSCULUS (MOUSE).//Q61420

40 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777

F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777

45 F-PLACE1006288

F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231

F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918

50 F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814

F-PLACE1006357

F-PLACE1006360

F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380

55 F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777

F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482

F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160  
 F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547  
 5 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676  
 F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910  
 F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876  
 10 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550  
 F-PLACE1006470  
 F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595  
 15 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004  
 F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261  
 F-PLACE1006506  
 20 F-PLACE1006521  
 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681  
 F-PLACE1006534  
 F-PLACE1006540  
 25 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922  
 F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190  
 F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038  
 30 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861  
 F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529  
 35 F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371  
 F-PLACE1006640  
 F-PLACE1006673  
 F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456  
 40 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295  
 F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263  
 45 F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198  
 F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941  
 50 F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517  
 F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875  
 F-PLACE1006792  
 F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972  
 55 F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569  
 F-PLACE1006805

F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818

F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547

5 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102

F-PLACE1006860

F-PLACE1006867

10 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087

F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281

F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567

15 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015

F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442

20 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000

F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//O00268

25 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722

F-PLACE1006961

F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929

30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160

F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083

35 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542

F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260

40 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531

F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063

45 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663

F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME L//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13730

F-PLACE1007111

50 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853

F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

55 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10826

F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062

F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//5.5e-10:98:44//ACANTHAMOEBA  
 CASTELLANII (AMOEBEBA)//P19706  
 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR  
 A)//3.9e-19:96:57//HOMO SAPIENS (HUMAN)//P23193  
 5 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF)//1.0:  
 132:30//RATTUS NORVEGICUS (RAT)//Q03386  
 F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION//0.041:114:29//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39981  
 10 F-PLACE1007257//DIAPHANOUS PROTEIN//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT  
 FLY)//P48608  
 F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT)//0.054:60:30//HELIX POMATIA (ROMAN SNAIL)  
 (EDIBLE SNAIL)//P33187  
 F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1)//1.0:42:28//SUS SCRO-  
 FA (PIG)//O62697  
 15 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CON-  
 TAINS: OUTER CAPSID PROTEINS VP5 AND VP8]//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 /  
 STRAIN ST. THOMAS 3)//P11200  
 F-PLACE1007286  
 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168//0.042:61:39//HOMO SAPIENS (HUMAN)//P50749  
 20 F-PLACE1007317  
 F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIV-  
 ITY) (TRANSCRIPTION FACTOR NTF-1)//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//  
 P13002  
 F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN)  
 25 (KRIP-1)//0.0026:147:27//MUS MUSCULUS (MOUSE)//Q62318  
 F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.3e-37:110:76//HOMO SAPIENS (HU-  
 MAN)//P39189  
 F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13//4.7e-07:71:39//  
 CAENORHABDITIS ELEGANS//P27715  
 30 F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION//0.74:48:29//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39561  
 F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R)//0.99:63:36//CIT-  
 ROBACTER FREUNDII//O69280  
 F-PLACE1007409//WHITE PROTEIN//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//  
 35 P10090  
 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26)  
 (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP)//0.031:159:23//HOMO SAPIENS  
 (HUMAN)//P27487  
 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT)//0.023:36:50//  
 40 HOMO SAPIENS (HUMAN)//P17038  
 F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION//2.2e-18:85:  
 54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36149  
 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN//0.66:13:53//CHLAMYDOMONAS RE-  
 INHARDTII//Q06480  
 45 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.93:45:33//SUS SCROFA (PIG)//Q35914  
 F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE]//5.3e-08:50:56//MUS MUSCULUS (MOUSE)//P11369  
 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION//0.87:43:37//ES-  
 CHERICHIA COLI//P03849  
 50 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 CIOGENITAL DYSPLASIA PROTEIN)//1.2e-25:202:31//HOMO SAPIENS (HUMAN)//P98174  
 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION//0.12:128:25//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53139  
 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19)//2.1e-45:209:48//  
 55 BOS TAURUS (BOVINE)//P08728  
 F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN)//P20550  
 F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144

F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

5 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT) .//P06600

10 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621

15 F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//P02465

F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//O21401

20 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0:47:46//HOMO SAPIENS (HUMAN).//P39192

25 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457

F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

30 F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001

F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898

F-PLACE1007725

35 F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10271

F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS (HUMAN).//P81489

F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.78:39:56//HOMO SAPIENS (HUMAN).//P39195

40 F-PLACE1007743

F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS (HUMAN).//Q14690

F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIUS FORFICATUS.//Q01872

45 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446

F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530

F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801

50 F-PLACE1007843

F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669

55 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275

F-PLACE1007866

F-PLACE1007877



F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EX-  
TRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR)  
(HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTI-  
GEN).//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60522

5 F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.5e-28:61:65//HOMO SAPIENS (HUMAN).//  
P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:37//PSEU-  
DOMONAS AERUGINOSA.//P04139

10 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//0.00070:96:29//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//0.00027:255:23//  
CAENORHABDITIS ELEGANS.//Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17).//  
1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453

15 F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//2.4e-05:104:37//  
AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-  
YPUS).//P35307

20 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-  
SITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
CLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).//P52590

25 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BO-  
VINE).//P25508

F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VI-  
RUS.//P20126

F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:25//MYCOBACTERIUM  
TUBERCULOSIS.//O53230

30 F-PLACE1008111//HYPOTHETICAL PROTEIN MJEC512.//0.30:38:42//METHANOCOCCUS JANNASCHII.//  
Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P40091

35 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8e-06:154:36//GAL-  
LUS GALLUS (CHICKEN).//P02467

F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.4e-13:227:36//  
CAENORHABDITIS ELEGANS.//Q09531

F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P22793

F-PLACE1008181

40 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.00044:121:34//  
XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERUS SALMOIDES  
(LARGEMOUTH BASS).//P38621

45 F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MON-  
KEY) (GRIVET).//P02797

F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN)  
(PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI.//P08469

F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:148:38//PODOSPORA AN-  
SERINA.//Q00808

50 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.1e-97:222:  
81//BOS TAURUS (BOVINE).//P53620

F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//SACCHAROMYCES CEREVI-  
SIAE (BAKER'S YEAST).//P12689

55 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//HOMO SAPIENS (HU-  
MAN).//P08547

F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//0.47:99:37//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14302

F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//OVIS ARIES (SHEEP).//P08105

F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-37:75:81//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-08:70:50//HOMO SAPIENS (HUMAN).//  
 P39188  
 5 F-PLACE1008356//FRUIT PROTEIN PKIW1501./0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO).//  
 P43393  
 F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 F-PLACE1008369  
 10 F-PLACE1008392  
 F-PLACE1008398//GENE 33 POLYPEPTIDE./1.5e-102:225:84//RATTUS NORVEGICUS (RAT).//P05432  
 F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//MUS MUSCULUS  
 (MOUSE).//P05143  
 F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED  
 15 PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541  
 F-PLACE1008405  
 F-PLACE1008424//PROTEIN UL56./1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM).//P36297  
 F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//4.4e-05:185:28//  
 DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323  
 20 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22./0.00054:172:25//RATTUS NOR-  
 VEGICUS (RAT).//Q05175  
 F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III./1.9e-23:226:34//  
 CAENORHABDITIS ELEGANS.//P34681  
 F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DIS-  
 25 EASE VIRUS (BFDV).//P13893  
 F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-12:89:47//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:  
 43//HOMO SAPIENS (HUMAN).//P17040  
 30 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61./9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS  
 (STRAIN AD169).//P16818  
 F-PLACE1008524//HOMEODOMAIN PROTEIN HLX1 (HOMEODOMAIN PROTEIN HB24).//0.95:74:36//HOMO SAPIENS  
 (HUMAN).//Q14774  
 F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.1e-05:86:45//HOMO SAPIENS (HUMAN).//  
 35 P39192  
 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:  
 45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298  
 F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830  
 40 F-PLACE1008568//NEURONATIN./0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517  
 F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FORFICATUS.//Q02030  
 F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-  
 CLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199  
 F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS  
 45 (HUMAN).//P20931  
 F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNI-  
 THODOROS MOUBATA (SOFT TICK).//P36235  
 F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805  
 F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:  
 50 31//HOMO SAPIENS (HUMAN).//P25713  
 F-PLACE1008629  
 F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLLIORHINUS CANICULA (SPOT-  
 TED DOGFISH) (SPOTTED CATSHARK).//P30258  
 F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN  
 55 H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN  
 SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624  
 F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABI-  
 DOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTEL-  
 LATA (SNAIL MEDIC).//P80321  
 F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC  
 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//  
 5 O00217  
 F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834  
 F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:  
 26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 10 F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:  
 44:34//ESCHERICHIA COLI.//P33669  
 F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA  
 S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//O35345  
 F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS.//P80696  
 15 F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746  
 F-PLACE1008813  
 F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:  
 20 62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309  
 F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBERO-  
 SUM (POTATO).//P15478  
 25 F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COU-  
 CANG (SLOW LORIS).//P08548  
 F-PLACE1008902  
 F-PLACE1008920  
 F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ES-  
 30 CHERICHIA COLI.//P76242  
 F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT).//0.14:77:45//GLU-  
 CONOBACTER SUBOXYDANS.//O05543  
 F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928  
 F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-  
 35 14:136:39//MUS MUSCULUS (MOUSE).//P27790  
 F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072  
 F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOP-  
 TERA MUSCULUS (BLUE WHALE).//P41301  
 F-PLACE1009039  
 40 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:  
 43//ESCHERICHIA COLI.//P46879  
 F-PLACE1009048  
 F-PLACE1009050  
 F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.//4.9e-23:244:31//  
 45 CAENORHABDITIS ELEGANS.//P34552  
 F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITALIUM.//P47439  
 F-PLACE1009091  
 F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS (HUMAN).//Q92832  
 F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//  
 50 MUS MUSCULUS (MOUSE).//P10077  
 F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//  
 P81492  
 F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN).//  
 P39195  
 55 F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS (BOVINE).//P20072  
 F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS (HUMAN).//  
 Q15034  
 F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN).//

P39195

F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J11).//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711

F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).//P49902

F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246

F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009183

F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783

F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250

F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P39194

F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSUM (POTATO).//P48504

F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110

F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371

F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P78352

F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433

F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120

F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281

F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492

F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523

F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489

F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791

F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356

F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874

F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319

F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1009477

F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-18:138:39//CAENORHABDITIS ELEGANS.//Q11069

F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418

5 F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA LAMBLIA (GIARDIA INTESTINALIS).//P38543

F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00016:31:77//HOMO SAPIENS (HUMAN).//P39188

10 F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952

F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P30788

F-PLACE1009595

15 F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963

F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-43:73:69//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1009613

20 F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).//Q13891

F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159

F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P30905

25 F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591

F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660

F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600

30 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835

F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876

35 F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35200

F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120

F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765

40 F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779

45 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688

F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779

50 F-PLACE1009886

F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896

F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190

55 F-PLACE1009921

F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.99:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P30902

F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258//0.063:75:32//METHANOCOCCUS JANNASCHII//Q57706

5 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)//0.33:51:45//BOS TAURUS (BOVINE)//P35722

F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//0.022:84:27//MUS MUSCULUS (MOUSE)//P28575

10 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1)//0.00011:35:51//HOMO SAPIENS (HUMAN)//P13497

F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1//0.052:185:22//CIONA INTESTINALIS//Q07068

F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS)//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//P20232

15 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III//6.6e-06:111:32//CAENORHABDITIS ELEGANS//Q18262

F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//0.0024:72:33//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479

F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593//0.83:24:45//HAEMOPHILUS INFLUENZAE//P44022

20 F-PLACE1010069

F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331

F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT)//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT)//Q01790

25 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//2.7e-48:177:46//HOMO SAPIENS (HUMAN)//P98171

F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055)//7.9e-07:55:43//HOMO SAPIENS (HUMAN)//P40818

30 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)//1.0e-107:232:90//RATTUS NORVEGICUS (RAT)//Q62671

F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)//1.0:33:45//METHANOCOCCUS JANNASCHII//Q57649

F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

35 F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.2e-14:94:41//MUS MUSCULUS (MOUSE)//P11369

F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53115

F-PLACE1010148//GAR2 PROTEIN//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891

40 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574

F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175

45 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//1.4e-07:95:43//GALLUS GALLUS (CHICKEN)//P30352

F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36)//0.094:109:29//RATTUS NORVEGICUS (RAT)//P47973

50 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068

F-PLACE1010261//SEGREGATION DISTORTER PROTEIN//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25722

F-PLACE1010270

55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14177

F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-26:94:64//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1010310//SYNAPSINS IA AND IB.//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951  
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KA-  
 PLAN) (PRV).//P33479  
 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS  
 5 PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567  
 F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S  
 MAMBA).//P01419  
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0049:49:55//HOMO SAPIENS (HUMAN).//  
 P39189  
 10 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE)  
 (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC).//0.0034:89:30//  
 TRYPANOSOMA CRUZI.//015886  
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COM-  
 PLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259  
 15 F-PLACE1010383  
 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22//RATTUS NORVEGI-  
 CUS (RAT).//P41777  
 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III.//1.5e-21:170:35//  
 CAENORHABDITIS ELEGANS.//P46555  
 20 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//1.0:31:41//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490  
 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.77:97:30//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874  
 F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.74:45:37//HOMO SAPIENS  
 25 (HUMAN).//P22531  
 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE  
 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE  
 (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIAL-  
 DEHYDE DEHYDROGENASE)].//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296  
 30 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227  
 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//  
 P51255  
 F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260  
 35 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSAC-  
 CHAROMYCES POMBE (FISSION YEAST).//Q09747  
 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-17:192:31//PICHIA  
 ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723  
 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.44:32:37//PSEUDOMONAS PUT-  
 40 IDA.//P25753  
 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//0.00036:134:321//HOMO SAPIENS (HUMAN).//P10162  
 45 F-PLACE1010628  
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1010630  
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN  
 50 SKINK).//P28118  
 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOBOBSCURA  
 (FRUIT FLY).//Q24617  
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332  
 55 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//O14628  
 F-PLACE1010714  
 F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AF-  
 RICAN CLAWED FROG).//P50532

F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//  
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612  
 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//MUS MUSCULUS  
 (MOUSE).//P05143  
 5 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//1.5e-14:175:25//  
 CAENORHABDITIS ELEGANS.//Q09217  
 F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:89//MUS MUSCULUS  
 (MOUSE).//Q02614  
 10 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER  
 (FRUIT FLY).//P54623  
 F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//  
 0.0060:111:31//ESCHERICHIA COLI.//Q99390  
 F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//  
 Q07415  
 15 F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.//  
 P38587  
 F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).//  
 P41208  
 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP  
 20 CRAYFISH).//P55848  
 F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-  
 RILLA).//P20758  
 F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HO-  
 MO SAPIENS (HUMAN).//Q05481  
 25 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277  
 F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.95:51:27//  
 BACILLUS SUBTILIS.//P54436  
 F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.).//0.98:71:30//SACCHA-  
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P36002  
 30 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897  
 F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3.//0.060:59:35//OVIS ARIES (SHEEP).//  
 P02444  
 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).//  
 0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191  
 35 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1  
 (STRAIN KRA1) (TTV1).//P19285  
 F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45//HOMO SAPIENS (HU-  
 MAN).//Q92558  
 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 40 EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567  
 F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS  
 (BOVINE).//P41987  
 F-PLACE1010947  
 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26//HOMO SAPIENS  
 45 (HUMAN).//P09493  
 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P45890  
 F-PLACE1010965  
 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT  
 50 FLY).//Q03293  
 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37//  
 SALMONELLA TYPHIMURIUM.//P23329  
 F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899  
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC  
 55 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGI-  
 CUS (RAT).//P10687  
 F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN).//  
 P39195



F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283  
 F-PLACE1011057  
 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//1.8e-07:133:  
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892  
 5 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.4e-25:63:88//RAT-  
 TUS NORVEGICUS (RAT).//Q07803  
 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:45//SCHIZOSAC-  
 CHAROMYCES POMBE (FISSION YEAST).//Q09916  
 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPRO-  
 10 TEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743  
 F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE31.//P17385  
 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX  
 (SOYBEAN).//Q02917  
 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /  
 15 SENEGAL).//P14586  
 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-13:98:50//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1011203  
 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS ASINUS (DONKEY).//  
 20 P92479  
 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//1.9e-15:162:31//STREPTOMYCES ANTIBI-  
 OTICUS.//Q03326  
 F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MU-  
 NICH]).//P14369  
 25 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
 TOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107  
 F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485  
 30 F-PLACE1011273  
 F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.011:36:50//RATTUS  
 NORVEGICUS (RAT).//P20468  
 F-PLACE1011296//HOMEBOX PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA  
 DANIO).//Q98877  
 35 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//  
 0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060  
 F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I.//0.00021:171:27//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411  
 F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//  
 40 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211  
 F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-07:40:62//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
 H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703  
 45 F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
 F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868  
 F-PLACE1011419  
 F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICK-  
 EN).//P55879  
 50 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HU-  
 MAN).//Q92838  
 F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN  
 55 LOBSTER).//P29499  
 F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER  
 PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852  
 F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178  
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:  
 32:40//ESCHERICHIA COLI.//P52102  
 F-PLACE1011520  
 5 F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490  
 F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.2e-31:78:76//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HO-  
 MO SAPIENS (HUMAN).//Q05481  
 10 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-  
 TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37//HOMO SAPIENS (HUMAN).//Q00975  
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN  
 INDIANA-FUNKHAUSER /BECKER) (PRV).//P11675  
 F-PLACE1011641  
 15 F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS.//P34804  
 F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:44:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIRUS TYPE 2.//P03291  
 F-PLACE1011650  
 20 F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P17886  
 F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS.//P21305  
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION.//1.0:40:22//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098  
 25 F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPI-  
 DER).//P29425  
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//  
 0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083  
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULAR-  
 IUS.//P40654  
 30 F-PLACE1011749  
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS  
 MUSCULUS (MOUSE).//Q60925  
 F-PLACE1011778  
 35 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:  
 43//MUS MUSCULUS (MOUSE).//P20863  
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206  
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHE-  
 COCHLORIS AESTUARII.//P11741  
 40 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//AC-  
 TERIOPHAGE T4.//P39495  
 F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814  
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 45 F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCU-  
 LUS (MOUSE).//P50715  
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//  
 1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351  
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM  
 50 COMMUNE (BRACKET FUNGUS).//Q02593  
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COU-  
 CANG (SLOW LORIS).//P08548  
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:  
 83:31//PLASMODIUM FRAGILE.//P22622  
 55 F-PLACE1011995  
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543  
 F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.4e-18:63:73//HOMO SAPIENS (HUMAN).//  
 P39193

F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072  
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS  
 (MOUSE).//P05143  
 5 F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//  
 CAENORHABDITIS ELEGANS.//Q09475  
 F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN).//  
 P39193  
 10 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE  
 RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPI-  
 ENS (HUMAN).//P14207  
 F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KI-  
 NASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496  
 15 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01642  
 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTI-  
 CUS.//Q03326  
 F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYC-  
 OPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246  
 20 F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NOR-  
 VEGICUS (RAT).//P38650  
 F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.4e-06:63:49//HOMO SAPIENS (HU-  
 MAN).//P39191  
 25 F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-22:74:64//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-PLACE2000061  
 F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B).//1.9e-  
 06:108:37//BACILLUS SUBTILIS.//P26907  
 30 F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910  
 F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDAT-  
 RA ZIBETHICUS (MUSKRAT).//P00681  
 F-PLACE2000100  
 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS (MAIZE).//P33626  
 35 F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708  
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:  
 52//CLOSTRIDIUM PERFRINGENS.//Q46185  
 F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-37:108:68//HOMO SAPIENS (HU-  
 MAN).//P39194  
 40 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN  
 B95-8) (HUMAN HERPESVIRUS 4).//P03224  
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUI-  
 TARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEP-  
 TOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588  
 45 F-PLACE2000140  
 F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//  
 O15736  
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1).//  
 1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579  
 50 F-PLACE2000172  
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS FULGIDUS.//O29724  
 F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//  
 Q02973  
 F-PLACE2000216  
 55 F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIA-  
 TUS (EGYPTIAN SCORPION).//P01487  
 F-PLACE2000235  
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//Q04652

F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191

F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098

F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709

F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329

F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA+)/GLUCOSE COTRANSPORTER 1 (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170

F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360

F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194

F-PLACE2000366

F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259

F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583

F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978

F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40:42//HOMO SAPIENS (HUMAN).//P02811

F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465

F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209

F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996

F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676

F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211

F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407

F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000435

F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III.//4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678

F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-23:88:62//HOMO SAPIENS (HUMAN).//P39195

F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CENTRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630

F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450

F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-23:73:63//HOMO SAPIENS (HUMAN).//P39188

F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-37:90:78//HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480  
 F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:34//CAENORHABDITIS ELE-  
 GANS.//Q09457  
 F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOS-  
 PHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932  
 F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009  
 F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427  
 F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.29:22:59//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P38898  
 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280  
 F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-41:87:78//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:22//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P22224  
 F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-29:97:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRA-  
 TORIA (MIGRATORY LOCUST).//P80059  
 F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63).//0.82:34:41//MARCHAN-  
 TIA POLYMORPHA (LIVERWORT).//P38468  
 F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q04205  
 F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-30:61:65//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS.//P21414  
 F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014:107:33//ZEA MAYS  
 (MAIZE).//P14918  
 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10272  
 F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//  
 MYCOBACTERIUM TUBERCULOSIS.//Q11053  
 F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.7e-49:56:80//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY).//  
 0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779  
 F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.6e-28:99:59//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//Q12446  
 F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053  
 F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.5e-09:32:78//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE3000208  
 F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-34:96:70//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE  
 GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455  
 F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:178:45//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//O07815  
 F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE  
 TILAPIA) (TILAPIA MOSSAMBICA).//P52726  
 F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SA-  
 PIENS (HUMAN).//P43361  
 F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUS-

CULUS (MOUSE).//P53995

F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681

F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-12:63:53//HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000276//COLLAGEN ALPHA 1 (VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658

F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808

F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258

F-PLACE3000320

F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074

F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS (HUMAN).//P22532

F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516

F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968

F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//3.9e-50:168:60//CAENORHABDITIS ELEGANS.//P46549

F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-29:76:71//HOMO SAPIENS (HUMAN).//P39194

F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HOMO SAPIENS (HUMAN).//Q10472

F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLIDUM.//O83103

F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951

F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040

F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.5e-18:90:47//HOMO SAPIENS (HUMAN).//P10267

F-PLACE3000388

F-PLACE3000399//!!!!ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.3e-45:60:75//HOMO SAPIENS (HUMAN).//P39193

F-PLACE3000400

F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-09:46:73//HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.036:43:44//HOMO SAPIENS (HUMAN).//P39188

F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BOVINE).//P01154

F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-09:49:67//HOMO SAPIENS (HUMAN).//P39195

F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//BOS TAURUS (BOVINE).//P35662

F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814

F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817

F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281

F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P80970

F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749

F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100

F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//P22815

F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-32:79:75//HOMO SAPIENS (HUMAN).//P39194

F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1./2.2e-99:178:97//MUS MUSCULUS (MOUSE).//P41233

F-PLACE4000063//IMMEDIATE-EARLY PROTEIN./0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042

F-PLACE4000089

F-PLACE4000093

F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-14:68:60//HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000106//1A PROTEIN[CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:41//BROAD BEAN MOTTLE VIRUS.//Q00020

F-PLACE4000128//HYPOTHETICAL PROTEIN E-115./0.00020:101:30//HUMAN ADENOVIRUS TYPE 2.//P03290

F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN).//0.15:57:31//HOMO SAPIENS (HUMAN).//P22528

F-PLACE4000131

F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR./1.0:45:24//BACILLUS SUBTILIS.//P45453

F-PLACE4000156//ZINC FINGER PROTEIN 136./2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737

F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654)./0.083:148:26//HOMO SAPIENS (HUMAN).//P52746

F-PLACE4000211//CALPHOTIN./0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910

F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:20:85//HOMO SAPIENS (HUMAN).//P39188

F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45) (DHFR-TS)./1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI.//Q27783

F-PLACE4000233

F-PLACE4000247//METALLOTHIONEIN (MT)./1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE).//P07216

F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN)./0.99:33:42//CAPRINE ARTHRITIS EN-CEPHALITIS VIRUS (CAEV).//P31834

F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB./0.42:24:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)./3.5e-09:189:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639

F-PLACE4000261//PEREGRIN (BR140 PROTEIN)./5.0e-11:103:37//HOMO SAPIENS (HUMAN).//P55201

F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1./0.037:181:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21)./1.0:46:39//MUS MUSCULUS (MOUSE).//P70375

F-PLACE4000300//50S RIBOSOMAL PROTEIN L32./0.81:28:46//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P80339

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN)./1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345

F-PLACE4000323

F-PLACE4000326//PARATHYMOSIN./0.0018:54:48//HOMO SAPIENS (HUMAN).//P20962

F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT)./0.97:28:42//SUS SCROFA (PIG).//Q00968

F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI)./1.0:33:36//STOICHACTIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS).//P19651

F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)./0.071:42:42//SORGHUM VULGARE (SORGHUM).//P24152

F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-16:54:77//HOMO SAPIENS (HUMAN).//P39193

F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR./0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877

F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)

(FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.//Q05338  
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-29:96:67//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-18:41:73//HOMO SAPIENS (HUMAN).//  
 5 P39188  
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:237:33//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32639  
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR.//0.00081:210:26//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442  
 10 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR  
 HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922  
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X).//0.20:18:38//HOMO SAPIENS (HUMAN).//P80297  
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-19:73:52//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-PLACE4000489  
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS  
 (MOUSE).//Q03173  
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400  
 20 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//  
 RATTUS NORVEGICUS (RAT).//Q07008  
 F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA.//  
 P00122  
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUI-  
 25 TIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING EN-  
 ZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824  
 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)  
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:281//HOMO  
 SAPIENS (HUMAN).//P16109  
 30 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414  
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS  
 NORVEGICUS (RAT).//P30969  
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;  
 35 CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//  
 P32594  
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ES-  
 CHERICHIA COLI.//P37910  
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HO-  
 40 MO SAPIENS (HUMAN).//P17020  
 F-PLACE4000654  
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:  
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313  
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:  
 45 31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O60100  
 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:  
 35//GALLUS GALLUS (CHICKEN).//Q98937  
 F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124  
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 50 TRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655  
 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//  
 0.0032:154:35//HOMO SAPIENS (HUMAN).//O14511  
 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXI-  
 DASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939  
 55 F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-13:54:66//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//  
 P03163



F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763

F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244

F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341

F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872

F-THYRO1000085

F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:59:33//HOMO SAPIENS (HUMAN).//P49901

F-THYRO1000107

F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203

F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEbrio MOLITOR (YELLOW MEALWORM).//Q27270

F-THYRO1000129//FBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE).//Q60791

F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.7e-14:104:42//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1000156

F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.7e-20:71:71//HOMO SAPIENS (HUMAN).//P39189

F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585

F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.9e-24:72:77//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000187

F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871

F-THYRO1000197

F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III.//2.0e-06:88:35//CAENORHABDITIS ELEGANS.//34379

F-THYRO1000206

F-THYRO1000221

F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41661

F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523

F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808

F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477

F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842

F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN-SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071

F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755

F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859

F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339

F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563

F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:136:26//DRO-

SOPHILA MELANOGASTER (FRUIT FLY).//Q09101

F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330

F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531

F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AU-REUS.//P48860

F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997

F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61).//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578

F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2,1e-31:94:72//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P39195

F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917

F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533

F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//P31504

F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS (CHICKEN).//Q03352

F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS (RAT).//P02454

F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725

F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247

F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319

F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACERVULINA.//P21959

F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GILTHEAD SEA BREAM).//P52727

F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19925

F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39189

F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155

F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//P46870

F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39193

F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129

F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.97:20:85//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.2e-10:69:59//HOMO SAPIENS (HUMAN).//

P39188

F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.6e-10:204:32//HOMO SAPIENS (HUMAN)//P04280

F-THYRO1000734

F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT)//1.8e-46:130:70//HOMO SAPIENS (HUMAN)//O43295

F-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)//1.1e-06:95:31//RATTUS NORVEGICUS (RAT)//Q64686

F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0031:119:34//HAEMONCHUS CONTORTUS//P16252

F-THYRO1000783//MYOSIN IC HEAVY CHAIN//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT)//0.54:25:52//PHOLCUS PHALANGIOIDES//Q02031

F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P19736

F-THYRO1000796

F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION//0.081:31:38//HUMAN ADENOVIRUS TYPE 41//P23691

F-THYRO1000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30:81:70//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1000829//NEUROTOXIN III (BOM III)//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROCCAN SCORPION)//P13488

F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109)//0.98:25:44//BACTERIOPHAGE P22//P26750

F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//7.3e-09:83:42//VOLVOX CARTERI//P21997

F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR//1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

F-THYRO1000865//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.2e-17:66:57//HOMO SAPIENS (HUMAN)//P39188

F-THYRO1000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12:58:62//HOMO SAPIENS (HUMAN)//P39189

F-THYRO1000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32:101:69//HOMO SAPIENS (HUMAN)//P39189

F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN//5.5e-05:108:27//KLEBSIELLA OXYTOCA//P56267

F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//3.9e-50:147:40//HOMO SAPIENS (HUMAN)//P32322

F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE)//1.8e-31:136:56//CITROBACTER FREUNDII//P45510

F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170

F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32580

F-THYRO1000975

F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//1.3e-20:96:51//CAENORHABDITIS ELEGANS//Q11076

F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25160

F-THYRO1000988

F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION//0.97:60:31//ESCHERICHIA COLI//P36675

F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521//5.0e-13:126:35//HOMO SAPIENS (HUMAN)//P31948

F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-35:97:79//HOMO SAPIENS (HUMAN)//

P39194

F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN).//

P39194

F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168

F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427

F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263

F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161

F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610

F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS (MOUSE).//P08043

F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO SAPIENS (HUMAN).//P02811

F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//P39193

F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62:126:30//STREPTOMYCES FRADIAE.//P20186

F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888

F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413

F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258

F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123

F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404

F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//P43683

F-THYRO1001374//PROTEIN VDLD.//1.6e-3:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//O05729

F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1001403

F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS (HUMAN).//P22531

F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e-81:97:83//MUS MUSCULUS (MOUSE).//O70503

F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN).//P39193

F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN).//

P39193

F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4)//0.68:44:34//BOS TAURUS (BOVINE)//  
P46162

F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
B) (NMMHC-B)//3.8e-64:216:62//HOMO SAPIENS (HUMAN)//P35580

F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.3e-29:88:75//HOMO SAPIENS (HUMAN)//  
P39194

F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6)//0.99:59:37//MUS MUSCULUS (MOUSE)//  
P10284

F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-14:40:82//HOMO SAPIENS (HUMAN)//  
P39194

F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION//2.4e-07:142:  
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38892

F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.98:26:61//HOMO SAPIENS (HUMAN)//  
P39195

F-THYRO1001559//PROTEIN Q300//2.6e-05:20:75//MUS MUSCULUS (MOUSE)//Q02722

F-THYRO1001570

F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.033:71:36//MUS MUS-  
CULUS (MOUSE)//P15265

F-THYRO1001584//SUPPRESSOR PROTEIN SRP40//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST)//P32583

F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//6.1e-21:35:91//HO-  
MO SAPIENS (HUMAN)//Q15404

F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH//1.0:57:42//HAEMOPHILUS INFLU-  
ENZAE//P44843

F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB//1.0:34:38//BUNGARUS FASCIA-  
TUS (BANDED KRAIT)//P25660

F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.0e-18:55:81//HOMO SAPIENS (HUMAN)//  
P39194

F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.00020:25:80//HOMO SAPIENS (HU-  
MAN)//P39195

F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.0091:54:42//MUS MUSCULUS  
(MOUSE)//P05142

F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182)//0.033:  
77:35//ESCHERICHIA COLI//P09160

F-THYRO1001671//((2'-5'))OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5'))OLIGO(A) SYNTHETASE 1)  
(2-5A SYNTHETASE 1) (P46/P41) (E18/E16)//4.3e-34:207:34//HOMO SAPIENS (HUMAN)//P00973

F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.9e-08:49:65//HOMO SAPIENS (HUMAN)//  
P39194

F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION//6.4e-16:134:  
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06053

F-THYRO1001706

F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN)//2.7e-27:191:36//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY)//Q04652

F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE  
A INTERFERENCE PROTEIN)//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36027

F-THYRO1001745

F-THYRO1001746//GENE 10 PROTEIN//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B//P15901

F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-05:41:63//HOMO SAPIENS (HUMAN)//  
P39188

F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III//1.5e-26:161:42//  
CAENORHABDITIS ELEGANS//P41880

F-THYRO1001809//LATENCY-RELATED PROTEIN 2//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 /  
STRAIN F)//P17589

F-THYRO1001828//PROTEINASE INHIBITOR//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBER-  
GINE)//P01078

F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HO-  
MOLOG) (DBI)//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG)//P45883

F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.1e-09:72:47//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327

5 F-VESEN1000122//HOMEBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).//P50219

F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC SALMON).//P52720

F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYS SCRIPTA (SLIDER TURTLE).//P80345

10 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226

F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTOMYCES FRADIAE.//P20186

F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162

15 F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//P50770

F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//MUS MUSCULUS (MOUSE).//P05143

F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:47:53//OWENIA FUSIFORMIS.//P21260

20 F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CHICKEN).//P02272

F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148

25 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O04658

F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142

F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941

30 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260

F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794

F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372

35 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620

F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120

40 F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343

F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS.//P35103

45 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.9e-20:62:79//HOMO SAPIENS (HUMAN).//P39194

F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970

F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III.//2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426

50 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.37:41:48//HOMO SAPIENS (HUMAN).//P39195

55 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170

F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135

F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE).//P17427

5 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-) (FRAGMENT).//0.010:35:60//STREPTOMYCES PEUCETIUS.//P32009

F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320

F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN).//P52741

10 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P31380

F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//0.00037:108:27//CANDIDA BOIDINII (YEAST).//Q00316

F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//1.0e-23:210:34//CAENORHABDITIS ELEGANS.//Q09316

15 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990

F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS.//P17656

20 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//PLASMODIUM LOPHURAE.//P04929

F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.043:13:53//HOMO SAPIENS (HUMAN).//P30808

F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES).//Q01200

25 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53882

F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50998

30 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234

F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER).//P05209

35 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.0078:57:31//HOMO SAPIENS (HUMAN).//P22532

F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:26//GALLUS GALLUS (CHICKEN).//P10587

40 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT).//P70541

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALLUS GALLUS (CHICKEN).//P02457

45 F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN).//P24709

F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38250

50 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1].//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818

F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-25:85:69//HOMO SAPIENS (HUMAN).//P39194

55 F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481

F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).//0.99:36:41//ARANEUS DI-

ADEMATUS (SPIDER).//P80515

F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//1.0e-06:197:23//  
CAENORHABDITIS ELEGANS.//P34492

F-Y79AA1001105//HOMEBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206

F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.024:42:59//HOMO SAPIENS (HUMAN).//  
P39195

F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//  
AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41471

F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN  
B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELE-  
GANS.//Q09456

F-Y79AA1001211

F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205

F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//  
Q02817

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
DROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657

F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238

F-Y79AA1001281

F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS  
(MOUSE).//P05143

F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOP-  
SIS THALIANA (MOUSE-EAR CRESS).//P92959

F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-  
MOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323

F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS  
(MOUSE).//P33622

F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//  
P31271

F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283

F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS  
(MOUSE).//P70459

F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//  
CAENORHABDITIS ELEGANS.//Q11076

F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:  
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:  
155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080

F-Y79AA1001541

F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).//  
P39192

F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873

F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
TIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550

F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUS-  
CULUS (MOUSE).//P15265

F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//O09116

F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
(TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//O00268

F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO  
SAPIENS (HUMAN).//P28698

F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBER-  
CULOSIS.//P71779

F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1).//0.79:90:26//MUS MUSCU-  
LUS (MOUSE).//P40764

F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT).//P14755



F-Y79AA1001692//GERM CELL-LESS PROTEIN.//3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820  
 F-Y79AA1001696//INSULIN.//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//P42633  
 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN.//0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN).//0.032:38:34//RATTUS NORVEGICUS (RAT).//P04550  
 F-Y79AA1001781  
 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0063:128:30//HOMO SAPIENS (HUMAN).//P50552  
 F-Y79AA1001827//SPERM PROTAMINE P1.//0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305  
 F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN).//P39188  
 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT).//1.8e-10:63:44//PSYCHODA CINEREA.//Q02035  
 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//0.00036:108:37//MUS MUSCULUS (MOUSE).//Q61967  
 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN).//3.2e-07:100:35//HOMO SAPIENS (HUMAN).//P43489  
 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.020:25:64//HOMO SAPIENS (HUMAN).//P20931  
 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.016:83:36//HOMO SAPIENS (HUMAN).//P10162  
 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q42643  
 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743  
 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.036:53:45//HOMO SAPIENS (HUMAN).//P30808  
 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III.//0.12:171:22//CAENORHABDITIS ELEGANS.//P34384  
 F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P52161  
 F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//P19958  
 F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS JANNASCHII.//Q58237  
 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206  
 F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24133  
 F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSCULUS (MOUSE).//P70327  
 F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357  
 F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48527  
 F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321  
 F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN).//P39193  
 F-Y79AA1002220  
 F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264  
 F-Y79AA1002234  
 F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-45:164:48//CAENORHABDITIS ELEGANS.//Q02328  
 F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161  
 5 F-Y79AA1002307  
 F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24//CAENORHABDITIS ELEGANS.//P46012  
 F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687  
 10 F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036  
 F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691  
 F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899  
 15 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812  
 F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS (HUMAN).//P22531  
 F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558  
 20 F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620  
 F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928  
 F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN  
 25 CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

## Homology Search Result Data 2.

**[0300]** The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.

**[0301]** Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 35 the Accession No. of the top hit data, as in the order separated by //.

**[0302]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953  
 F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787  
 40 F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344  
 F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-Pase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693  
 F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581  
 45 F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528  
 F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477  
 F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182  
 50 F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey sequence.//2.8e-16:132:79//AQ004134  
 F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104  
 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340  
 55 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331  
 F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324  
 F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033

F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034

F-HEMBA1000185

F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476

F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.0e-73:440:92//U04847

F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559

F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194

F-HEMBA1000227//H.sapiens CpG island DNA genomic MseI fragment, clone 179h6, reverse read cpg179h6.rt1a.//1.9e-14:95:98//Z64921

F-HEMBA1000231//H.sapiens CpG island DNA genomic MseI fragment, clone 90a5, reverse read cpg90a5.rt1a.//5.1e-34:186:97//Z56144

F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481

F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankydn.//0.029:316:59//X69065

F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.35:467:60//AC004454

F-HEMBA1000264

F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825

F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.2e-08:134:77//AC004617

F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459

F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764

F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730

F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131

F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226

F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495

F-HEMBA1000327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492

F-HEMBA1000333

F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078

F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848

F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056

F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178

F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748

F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843

F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587

F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116

F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520

F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984

F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409

F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584

F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112

F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554

F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393

F-HEMBA1000442

F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188

F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808

F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839

F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213

F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160

F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033

F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334

F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740

F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//9.4e-41:591:69//AC005884

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666

F-HEMBA1000505

F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661

F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642

F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616

F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006

F-HEMBA1000523

F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215

F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177\_H\_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973

F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAI project).//0.057:265:63//AL033545

F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340

F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237

F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555

F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611

F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564

F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504

F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628

F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571

F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506

F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573

F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733  
 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822  
 F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING  
 5 DRAFT SEQUENCE.//2.9e-21:158:75//AL021394  
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925  
 F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382  
 F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68//D85773  
 10 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590  
 F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815  
 F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776  
 F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 15 0.019:695:57//AC004907  
 F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090  
 F-HEMBA1000682//Homo sapiens (subclone 5\_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411  
 F-HEMBA1000686  
 20 F-HEMBA1000702  
 F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507  
 F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL031124  
 F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762:57//U87145  
 25 F-HEMBA1000726//H.sapiens HLA-DRB1\*15 gene.//9.8e-49:189:89//X88791  
 F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158  
 F-HEMBA1000747  
 F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S  
 30 Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509  
 F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073  
 F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 35 0.011:179:67//AC005043  
 F-HEMBA1000773//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870  
 F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953  
 F-HEMBA1000791  
 40 F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678  
 F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370  
 F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164  
 45 F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394  
 50 F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273  
 F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295  
 F-HEMBA1000867  
 55 F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424:75//Z72519  
 F-HEMBA1000870//Gnamptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products.//0.0049:211:66//AF034598

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583

F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826

5 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523

F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840

F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158

10 F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147

F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224

F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878

15 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//5.8e-140:661:99//AC005324

F-HEMBA1000946

F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967

20 F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735

F-HEMBA1000971//H.sapiens CpG island DNA genomic MseI fragment, clone 182f4, forward read cpg182f4 ft1a.//1.5e-20:126:96//Z57528

25 F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.34:642:59//AB020858

F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817

F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023

30 F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929

F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064 F-HEMBA1001007

35 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577

F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937

F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//1.6e-16:521:64//AC006213

40 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence.//3.8e-50:367:72//AC005702

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658

45 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064

F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521

F-HEMBA1001051//Human Chromosome X clone bWXD342, complete sequence.//4.8e-79:308:84//AC004072

50 F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341

F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

55 F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21 complete sequence.//0.98:280:62//AC006079

F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742

F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219

F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105

5 F-HEMBA1001099

F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

10 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383

F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247

F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909

15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341

F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077

F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507

20 F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604

F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815

F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410

25 F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917

F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009

F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601\_N\_13, complete sequence.//0.0086:372:58//AC005389

30 F-HEMBA1001247//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, reverse read cpg11b11.rt1a.//2.0e-24:154:93//Z64441

F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020

F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

35 F-HEMBA1001281

F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131

F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960

40 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003

F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260

F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505

45 F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054

F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408

50 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861

F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368

55 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713

F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, com-

plete sequence.//0.0037:254:62//AL010208

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.1e-103:516:97//AF057358

F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.7e-150:706:99//AC006241

F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505

F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297

F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence.//0.00035:317:60//AE001431

F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035

F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//4.2e-47:159:89//AC005073

F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256

F-HEMBA1001398//H.sapiens CpG island DNA genomic MseI fragment, clone 70d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591

F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645

F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050

F-HEMBA1001413

F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732

F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146

F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917

F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//1.2e-74:284:84//AC005670

F-HEMBA1001442//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-66, complete sequence.//0.056:194:63//AL010138

F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047

F-HEMBA1001450

F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115

F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337

F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794

F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193

F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258



F-HEMBA1001533

F-HEMBA1001557//*Chionoecetes opilio* (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

F-HEMBA1001620//*Oryza sativa* RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//*Salmo salar* DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//*M.musculus* COL3A1 gene for collagen alpha-1.//2.4e-30:742:62//X52046

F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126

F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349

F-HEMBA1001681

F-HEMBA1001702//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398

F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

F-HEMBA1001711//*Lysiphlebus melandriicola* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178

F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519

F-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250

F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367

F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793

F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617

F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295

F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102

F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995

F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109

F-HEMBA1001781

F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces.//5.5e-13:296:65//AC002099

F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458

F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222

F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286:74//Z31360

F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969

F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801

F-HEMBA1001815

F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616

F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243

F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275

F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161

F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867

F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517

F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//AC005395

F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735

F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065

F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693

F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954

F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065

F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732

F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766

F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//AB020873

F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145

F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)

pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310  
 F-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629  
 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE,  
 5 66 unordered pieces.//0.097:107:71//AC006057  
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934  
 F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728  
 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390  
 10 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507  
 F-HEMBA1001964  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains  
 15 a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178  
 F-HEMBA1001979//HS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506  
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551  
 F-HEMBA1001991//HS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283  
 20 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449  
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948  
 F-HEMBA1002018  
 F-HEMBA10020227//Human p37NB mRNA, complete cds.//0.014:58:96//U32907  
 25 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284  
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053  
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216  
 30 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422  
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703  
 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943  
 35 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649  
 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840  
 F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378  
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815  
 40 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549  
 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888  
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263  
 45 F-HEMBA1002151  
 F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519120, genomic survey sequence.//8.5e-61:334:94//AQ277613  
 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232  
 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829  
 50 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210  
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712  
 55 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066  
 F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589

F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150

5 F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence.//1.2e-06:178:65//AQ235350

F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149

F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989

10 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035

F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044

15 F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861

F-HEMBA1002241

F-HEMBA1002253

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.//3.5e-151:731:97//AF061936

20 F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183

F-HEMBA1002267

F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210

25 F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence.//0.019:564:58//AC004944

F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836

F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.84:547:57//AB020754

30 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314

F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676

F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:57//U69551

35 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563

F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868

F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546

40 F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617

F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165

F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697

45 F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216

F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347

F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378

F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912

50 F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514

F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034

F-HEMBA1002486

F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410

55 F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404

F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.9e-24:306:68//AC004873

F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972

5 F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329

F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315

10 F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875

F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670

15 F-HEMBA1002558//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366

F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687

20 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587

F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102

F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.9e-35:430:70//AC005940

25 F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403

F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169

F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413

30 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351

F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153

F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446

35 F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118

F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839

F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100

40 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535

F-HEMBA1002666

F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421

45 F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099

F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195

50 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924

F-HEMBA1002712

F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782

55 F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481

F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC003694

F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126

F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829

F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965

F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence.//1.8e-32:180:98//AQ036891

F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592

F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756

F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534:57//AL034558

F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185

F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043

F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870

F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153

F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.4e-170:744:99//AC004707

F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186

F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419

F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

F-HEMBA1002886

F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

F-HEMBA1002921

F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148

F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence.//1.7e-41:215:99//AQ266676

F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538

F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290

F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797

F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286

5 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484

F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557

10 F-HEMBA1003034//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704

F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//2.3e-05:591:57//AC004617

F-HEMBA1003037//RPC11-88F2.TJ RPC11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677

15 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182

20 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505

F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783

F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648

F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257

25 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297

F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673

30 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548

F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550

35 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750

F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308

F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564

40 F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635

F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259

F-HEMBA1003136

45 F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670

F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302

F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882

50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325

F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824

55 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302

F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037

5 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPC11-47P17.TJ RPC11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

10 F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230

F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142

15 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII-fragment, SC6pA19H4.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

20 F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599

F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

25 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

30 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

35 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

40 F-HEMBA1003330//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

45 F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528

50 F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

55 F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066

F-HEMBA1003408



F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321

F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334

F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066

F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090

F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098

F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041

F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687

F-HEMBA1003531//Homo sapiens PAC clone DJ1185107 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058

F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571

F-HEMBA1003548

F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724

F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071

F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810

F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539

F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U60170

F-HEMBA1003579//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744

F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123

F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11\_192K18, complete sequence.//4.4e-70:273:94//AC006075

F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395

F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398

F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:98//AC005153

F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592

F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344

F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080

F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139

F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984

F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077

F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987

F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130

F-HEMBA1003646

F-HEMBA1003656

F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.6e-175:824:98//AC005746

F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces

es.//1.1e-24:190:87//AC004765

F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065

F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322

F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723

F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691

F-HEMBA1003692

F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//AC003101

F-HEMBA1003714

F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575

F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056

F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348

F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345

F-HEMBA1003733//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.7e-104:761:82//AC006213

F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731

F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181

F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070

F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516

F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125

F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810

F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875

F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300

F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430

F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030

F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036

F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079

F-HEMBA1003893//H.sapiens CpG island DNA genomic MseI fragment, clone 11b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012

F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455

F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401

F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING

DRAFT SEQUENCE.//3.6e-27:278:76//AL031658

F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718

F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195

5 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140

F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098

10 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:9611AQ285498

15 F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-10:129:80//AQ141146

F-HEMBA1003978

F-HEMBA1003985//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

20 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446

F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354

F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

25 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859

30 F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

35 F-HEMBA1004045//Homo sapiens (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435

40 F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

45 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

50 F-HEMBA1004111//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393

F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

55 F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811

F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913

5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855

F-HEMBA1004199

F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

10 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807

F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619

25 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707

30 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831

F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

35 F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795

40 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395

F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254

F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897

F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271

45 F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130

F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720

F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094

50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995

F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980

F-HEMBA1004335//Human DNA-sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498

55 F-HEMBA1004341

F-HEMBA1004353//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571

F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:

190:92//U75968

F-HEMBA1004356

F-HEMBA1004366//*P.falciparum* complete gene map of plastid-like DNA (IR-A)//2.2e-07:736:57//X95275

F-HEMBA1004372//*H.sapiens* dystrophin gene intron 44//1.0:129:62//X77644

5 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end//4.7e-42:237:94//M21977

F-HEMBA1004394//*Plasmodium falciparum* chromosome 2, section 39 of 73 of the complete sequence//5.2e-05:519:59//AE001402

F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence//4.0e-32:261:76//AC002463

10 F-HEMBA1004405//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//1.4e-07:693:58//AC005507

F-HEMBA1004408//*Homo sapiens* clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces//1.2e-69:195:100//AC005037

F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence//5.1e-67:386:91//AQ172942

15 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence//3.2e-27:242:82//AC002554

F-HEMBA1004460//*Homo sapiens* clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces//1.7e-75:590:81//AC004846

20 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence//0.045:215:66//AL034407

F-HEMBA1004479//*Mus musculus* hypoxia inducible factor three alpha mRNA, complete cds//5.2e-43:364:79//AF060194

F-HEMBA1004482//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//6.8e-17:791:59//AC005505

25 F-HEMBA1004499//*Homo sapiens* chromosome 17, clone hRPC.1073\_F\_15, complete sequence//4.4e-125:251:94//AC004686

F-HEMBA1004502//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.012:635:57//AC004709

30 F-HEMBA1004506//*Homo sapiens* PAC clone DJ0844F09 from 7p12-p13, complete sequence//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//*Arabidopsis thaliana* DNA chromosome 4, BAC clone T10I14 (ESSAII project)//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280)//1.6e-72:678:74//X53416

35 F-HEMBA1004538//Sequence 1 from patent US 5612190//0.00015:416:59//I36871

F-HEMBA1004542//*Homo sapiens* clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.95:202:64//AC005038

F-HEMBA1004554//*Arabidopsis thaliana* BAC T26D22//0.45:624:56//AF058826

F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds//9.1e-10:173:70//D87457

40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence//6.1e-23:134:73//AC002542

F-HEMBA1004577//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-582J2, complete sequence//1.6e-15:190:77//AC004525

F-HEMBA1004586//*Homo sapiens* clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces//3.1e-31:388:76//AC004895

45 F-HEMBA1004596//RPCI11-81O21.TJ RPCI11 *Homo sapiens* genomic clone R-81O21, genomic survey sequence//2.2e-90:458:90//AQ285136

F-HEMBA1004604//*Mus musculus* COP9 complex subunit 7a (COPS7a) mRNA, complete cds//8.6e-105:699:84//AF071316

50 F-HEMBA1004610//*Homo sapiens* PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence//5.4e-20:267:72//AC004983

F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP *Homo sapiens* genomic clone 2319H15, genomic survey sequence//6.2e-26:147:99//AQ034944

F-HEMBA1004629//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//5.6e-06:766:56//AC005504

55 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs//4.7e-73:412:92//Z83843

F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44//0.92:181:61//X90418

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904  
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431  
 F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
 5 WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865  
 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432  
 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:59//AC000045  
 10 F-HEMBA1004672  
 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308  
 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence.//0.23:238:65//AQ040642  
 15 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357  
 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210  
 F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.1e-133:639:99//AC005562  
 20 F-HEMBA1004725//RPC11-75013.TJ RPC11 Homo sapiens genomic clone R-75O13, genomic survey sequence.//6.2e-32:169:100//AQ266512  
 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029  
 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence.//4.9e-18:209:69//AQ017556  
 25 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-13:451:62//AF028340  
 F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//5.0e-87:646:78//Z94056  
 30 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//0.24:526:57//AC002461  
 F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-25:268:76//AC004913  
 F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//1.1e-07:503:61//X83546  
 35 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence.//4.5e-38:314:81//AC000028  
 F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005854  
 F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//I23472  
 40 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds.//3.6e-47:404:79//U75285  
 F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.//6.7e-107:890:78//AC004941  
 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59//AC004709  
 45 F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:61//X65063  
 F-HEMBA1004776  
 F-HEMBA1004778  
 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:778:64//AF003622  
 50 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.3e-82:580:82//AC004617  
 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083  
 55 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:171:92//L01042  
 F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257  
 F-HEMBA1004820//C.botulinum progenitor toxin complex genes.//0.0014:343:62//X87972

F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744

F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBRI) gene, exon 1.//0.0065:284:61//AF054590

F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250:59//AC000400

5 F-HEMBA1004864

F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120

F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020

10 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155:69//U32943

F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.00055:323:60//L12043

F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence.//9.6e-16:166:80//AC003051

15 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial.//0.81:146:65//M94003

F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338:78//AC003006

F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 2373I16, genomic survey sequence.//2.4e-86:443:96//AQ108676

20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219:73//AC004109

F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216:85//B30726

F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence.//0.53:222:61//AF042091

25 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509:78//AC005482

F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243:99//AQ229758

30 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421:58//X95276

F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333:58//Z97343

F-HEMBA1004972

F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245:77//AQ238471

35 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08.//9.0e-11:84:98//AF086080

F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.0021:152:66//AQ075713

F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence.//1.9e-77:392:97//AQ071873

40 F-HEMBA1004983//Albinaria corrugata isolate cor. Prn1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.0030:276:61//AF031680

F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence.//4.2e-138:640:99//AC005590

45 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160:88//U52077

F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668:99//AF041474

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.4e-146:693:98//AB014548

F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179

50 F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//4.6e-138:591:98//AC004596

55 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence.//3.7e-61:271:88//AQ055486

F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z22819

F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688

F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410

5 F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-07:176:68//X76589

F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720

F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575

10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561

F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854

15 F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808

F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542

F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469

20 F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023

F-HEMBA1005185//H.sapiens CpG island DNA genomic Mse1 fragment, clone 91b2, forward read cpg91b2.ft1a./12.2e-14:93:100//Z63847

25 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//AL009194

F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744

F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320

30 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914

F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542

F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308

35 F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154

F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365

F-HEMBA1005251

40 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.5e-160:392:99//AC005837

F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291

F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:64//AL033521

45 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018

F-HEMBA1005296

F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012

50 F-HEMBA1005311

F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031

F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198

55 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823

F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//3.3e-90:300:90//AC005803



F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581  
 F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145  
 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414  
 5 F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714  
 F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900  
 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813  
 F-HEMBA1005382//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204  
 10 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175  
 F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749  
 F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 15 DRAFT SEQUENCE.//4.5e-131:278:98//AL034379  
 F-HEMBA1005408//HS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366  
 F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496  
 20 F-HEMBA1005411  
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248  
 F-HEMBA1005426  
 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130  
 25 F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234  
 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete  
 30 sequence.//1.5e-118:868:83//AL022576  
 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212  
 F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
 DRAFT SEQUENCE.//3.4e-20:187:74//AL031985  
 35 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041  
 F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941  
 F-HEMBA1005497//HS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810  
 40 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957  
 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147  
 45 F-HEMBA1005508//Homo sapiens clone hRPK.1\_A\_1, complete sequence.//0.00012:455:60//AC006196  
 F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066  
 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219  
 F-HEMBA1005517//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216  
 50 F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X99384  
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913  
 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//AC006241  
 55 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855  
 F-HEMBA1005530  
 F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING

DRAFT SEQUENCE.//9.4e-87:422:99//AL034431

F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743

F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377

F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153

F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971

F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531

F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275

F-HEMBA1005583

F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025

F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:99//AC005746

F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527

F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484

F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089

F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175

F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731

F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110

F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460

F-HEMBA1005632

F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850

F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478

F-HEMBA1005680

F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742

F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001

F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513

F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348

F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697

F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156

F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535

F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181

F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432

F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079

F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523

F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020

F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094

F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577

F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749

F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952

F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351

F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945

F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086

F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026

F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584

F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.3e-41:431:77//AC005666

F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086

F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974

F-HEMBA1005962//RPCI11-17O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821

F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357

F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516

F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408

F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599

F-HEMBA1006002

F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405

F-HEMBA1006031

F-HEMBA1006035

F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009

F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386

F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153

F-HEMBA1006081

F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500

F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880

F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177

F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672

F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966

F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085

F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162

F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500

F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428

F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693

F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400

F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318

F-HEMBA1006198

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557

F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074

F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664

F-HEMBA1006253

F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722

F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673

F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791

F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134

F-HEMBA1006283

F-HEMBA1006284//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289

F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804

F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415

F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070

F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183

F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074

F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563

F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420

F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219

F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671

F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244

F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327  
 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570  
 F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 5 Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813  
 F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806  
 F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179  
 10 F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165  
 15 F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885  
 F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//  
 20 0.027:293:64//AL031781  
 F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930  
 F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465  
 F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088  
 25 F-HEMBA1006446//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749  
 F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560  
 F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//AC006120  
 30 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709  
 F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247  
 35 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752  
 F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031  
 F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577  
 40 F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283  
 45 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//6.0e-122:337:100//AC005828  
 F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence.//3.8e-23:459:68//AF093117  
 F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846  
 50 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62364  
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566  
 F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//4.3e-27:406:71//AC003991  
 F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650  
 55 F-HEMBA1006535//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557  
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:654:98//AF093419

F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986

F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944

F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925

5 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504

F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357

F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107

10 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841

F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156

F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166

15 F-HEMBA1006612//RPC111-88F20.TJ RPC111 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726

F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685

20 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284

F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036

25 F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745

F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896

30 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148

F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479

F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601

35 F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189

F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554

40 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065

F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755

F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346

45 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011

F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738

F-HEMBA1006708

F-HEMBA1006709

50 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537

F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//5.8e-162:497:98//AC005828

F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796

55 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752

F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465

5 F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727

F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208

F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474

10 F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511

F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298

F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644

15 F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//6.0e-116:541:99//AC004797

F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262

F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196

20 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.//0.15:403:60//AB020872

F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.20:472:57//AE001369

25 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757

F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246

F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321

30 F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104

F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027

F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704

F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275

35 F-HEMBA1006936

F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841

F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat.//0.67:217:62//Z82205

40 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828

F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058

F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071

45 F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209

F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328

50 F-HEMBA1007017//Sequence 3 from Patent WO9416067.//0.96:220:62//A39358

F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088

F-HEMBA1007045

F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281

F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056

55 F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572

F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467

F-HEMBA1007073//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library)

complete sequence.//9.3e-54:519:68//AC004242

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076

F-HEMBA1007080

F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447

F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865

F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875

F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035

F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780

F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:97//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987

F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68//J00060

F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899

F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240

F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128

F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//3.1e-31:401:72//AC004638

F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467

F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399

F-HEMBA1007320

F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-18:408:64//AC006120

F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:500:62//AC005377

F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence.//0.75:269:61//AC005738



F-HEM BB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

F-HEM BB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

5 F-HEM BB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEM BB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

10 F-HEM BB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEM BB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEM BB1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

15 F-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEM BB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

20 F-HEM BB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

F-HEM BB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEM BB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene.

25 Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170

F-HEM BB1000054//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

F-HEM BB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880

30 F-HEM BB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEM BB1000083

F-HEM BB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

35 F-HEM BB1000099//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEM BB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

F-HEM BB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

40 F-HEM BB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521

F-HEM BB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697

F-HEM BB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090

45 F-HEM BB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542

F-HEM BB1000173//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996

F-HEM BB1000175

50 F-HEM BB1000198//HS\_3071\_A2\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388

F-HEM BB1000215//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEM BB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808

55 F-HEM BB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792

F-HEM BB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890

F-HEM BB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918

F-HEM BB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522

5 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587

F-HEM BB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818

10 F-HEM BB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968

F-HEM BB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470

F-HEM BB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379:58//AE001369

15 F-HEM BB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAll project).//0.92:272:61//AL022580

F-HEM BB1000284//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics) , PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366

20 F-HEM BB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745

F-HEM BB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007

F-HEM BB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242

25 F-HEM BB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951

F-HEM BB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//0.63:285:61//AC005968

F-HEM BB1000336

30 F-HEM BB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051

F-HEM BB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356

F-HEM BB1000339//Homo sapiens 12q24 PAC RPC11-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351

35 F-HEM BB1000341

F-HEM BB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547

F-HEM BB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989

40 F-HEM BB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090

F-HEM BB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409

F-HEM BB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:88//AL034377

45 F-HEM BB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982

F-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838

F-HEM BB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368

50 F-HEM BB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714

F-HEM BB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228

F-HEM BB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263

55 F-HEM BB1000438//RPC11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110

F-HEM BB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone ll47g11, complete sequence.//2.5e-33:372:72//AC000035

F-HEMBB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821

5 F-HEMBB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899

F-HEMBB1000472

F-HEMBB1000480

F-HEMBB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742

10 F-HEMBB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423

F-HEMBB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388

15 F-HEMBB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577

F-HEMBB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553

20 F-HEMBB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676

F-HEMBB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212

F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710

25 F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.9e-56:683:71//AB020860

F-HEMBB1000554//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929

30 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293

F-HEMBB1000564

F-HEMBB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077

35 F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476

F-HEMBB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883

F-HEMBB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300

40 F-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184

F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19.//0.012:185:64//AF009074

45 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356

F-HEMBB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207

F-HEMBB1000623//cDNA encoding Coliulus manganese peroxidase.//0.89:284:62//E12284

50 F-HEMBB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231

F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80057

F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349

F-HEMBB1000637//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478

55 F-HEMBB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234

F-HEMBB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077

F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//5.2e-64:775:69//AC003009

F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186

5 F-HEM BB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493

F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488

10 F-HEM BB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-50:293:92//AQ155121

F-HEM BB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65 :282:83//Z93241

F-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds.//1.6e-118:575:97//AF040723

15 F-HEM BB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//AC005507

F-HEM BB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118

20 F-HEM BB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554

F-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475

F-HEM BB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321

25 F-HEM BB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889

F-HEM BB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//AC005849

30 F-HEM BB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405

F-HEM BB1000770//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727

F-HEM BB1000774

F-HEM BB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//AR008277

35 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577

F-HEM BB1000790//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC004801

F-HEM BB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-74:378:97//AQ117099

40 F-HEM BB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpg39d7.rt1a.//8.5e-14:95:97//Z58412

F-HEM BB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read.//3.2e-05:138:71//Z79983

45 F-HEM BB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence.//0.85 :208:60//AQ086361

F-HEM BB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361:60//AC003015

F-HEM BB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360:69//AC002431

F-HEM BB1000827

F-HEM BB1000831

50 F-HEM BB1000835//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234:63//AL023581

F-HEM BB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence.//4.5e-61:328:79//U73649

F-HEM BB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//9.7e-144:809:87//AL021068

F-HEM BB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING

DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157

F-HEM BB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157

F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351

F-HEM BB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687

F-HEM BB1000887

F-HEM BB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence.//1.5e-31:172:98//AQ044369

F-HEM BB1000890

F-HEM BB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558

F-HEM BB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968

F-HEM BB1000910//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557

F-HEM BB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507

F-HEM BB1000915//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215

F-HEM BB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077

F-HEM BB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65/D16593

F-HEM BB1000947//CpG0856B CplOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493

F-HEM BB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 346O6, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487

F-HEM BB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973

F-HEM BB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//0.98:196:63//AB005234

F-HEM BB1000981

F-HEM BB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476

F-HEM BB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753

F-HEM BB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802

F-HEM BB1001004

F-HEM BB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551

F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310

F-HEM BB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751

F-HEM BB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291

F-HEM BB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717

F-HEM BB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539

F-HEM BB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671

F-HEM BB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586

F-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014

F-HEM BB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060

F-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973

F-HEM BB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803

F-HEM BB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210

5 F-HEM BB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612

F-HEM BB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987

F-HEM BB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630

10 F-HEM BB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//7.2e-07:459:59//AC005284

F-HEM BB1001117//HS\_2178\_B1\_E12\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244

F-HEM BB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778

15 F-HEM BB1001126

F-HEM BB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673

F-HEM BB1001137

20 F-HEM BB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617

F-HEM BB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264

F-HEM BB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724

25 F-HEM BB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712

F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334

F-HEM BB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473

30 F-HEM BB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188

F-HEM BB1001199

F-HEM BB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237

35 F-HEM BB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357

F-HEM BB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196

40 F-HEM BB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291

F-HEM BB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504

F-HEM BB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39f9, forward read cpg39f9.ft1e//4.0e-30:171:97//Z65435

45 F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754

F-HEM BB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087

F-HEM BB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032

50 F-HEM BB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173

F-HEM BB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//AC005303

55 F-HEM BB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217

F-HEM BB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20; genomic survey sequence.//1.8e-16:109:97//AQ060969

F-HEM BB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366  
 F-HEM BB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387  
 F-HEM BB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035  
 5 F-HEM BB1001302  
 F-HEM BB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey se-  
 quence.//2.2e-07:370:61//B69144  
 F-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:  
 663:85//U92703  
 10 F-HEM BB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3 map 10q26.1-10q26.2, WORKING  
 DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096  
 F-HEM BB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
 plete sequence.//1.4e-122:680:91//AC006210  
 F-HEM BB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//  
 15 AC004129  
 F-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-  
 56:458:79//D63850  
 F-HEM BB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384  
 20 F-HEM BB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.0e-74:319:85//AC003983  
 F-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056  
 F-HEM BB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871  
 F-HEM BB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//  
 AC006041  
 25 F-HEM BB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:  
 386:59//AC005079  
 F-HEM BB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//0.97:349:61//  
 AC004662  
 F-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete se-  
 30 quence.//5.5e-161:766:98//AC005876  
 F-HEM BB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complete sequence.//3.0e-55:510:  
 76//AC004408  
 F-HEM BB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//  
 AC005192  
 35 F-HEM BB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:  
 78//AC006204  
 F-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//  
 AF071314  
 F-HEM BB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354  
 40 F-HEM BB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//  
 AC005023  
 F-HEM BB1001410//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete  
 cds.//4.8e-11:632:59//AF045555  
 F-HEM BB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//  
 45 AC003019  
 F-HEM BB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 3.8e-17:360:64//AC005482  
 F-HEM BB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367  
 F-HEM BB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931  
 50 F-HEM BB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//  
 L18966  
 F-HEM BB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:  
 385:62//AC004768  
 F-HEM BB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//  
 55 AC005790  
 F-HEM BB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered  
 pieces.//8.0e-40:377:78//AC000382  
 F-HEM BB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:

59//AF001549

F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320

F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564

F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873

F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080

F-HEMBB1001527

F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696:79//AC000089

F-HEMBB1001535//O.aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268

F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548

F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262

F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605

F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003

F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677

F-HEMBB1001586

F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261

F-HEMBB1001603

F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289

F-HEMBB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089

F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559

F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155

F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.00097:721:58//AB006702

F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038

F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320

F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

F-HEMBB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429

F-HEMBB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey sequence.//2.3e-34:191:97//B99261

F-HEMBB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding



exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEM BB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STss, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEM BB1001706

F-HEM BB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEM BB1001717//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEM BB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEM BB1001736//*S.pombe* chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEM BB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEM BB1001753//*S.maximus* repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEM BB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEM BB1001760//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEM BB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEM BB1001785//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEM BB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEM BB1001802//*Plasmodium falciparum* MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEM BB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEM BB1001834//CIT-HSP-2291O12.TF CIT-HSP Homo sapiens genomic clone 2291O12, genomic survey sequence.//7.6e-08:73:94//AQ004168

F-HEM BB1001836//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEM BB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

F-HEM BB1001850//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

F-HEM BB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEM BB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEM BB1001868//*Rattus norvegicus* clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

F-HEM BB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974

F-HEM BB1001872

F-HEM BB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000

F-HEM BB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

F-HEM BB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403

F-HEM BB1001899//*Plasmodium falciparum* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//0.0038:425:58//AL010216

F-HEM BB1001905//*S.pombe* chromosome III cosmid c330.//1.1e-23:520:62//AL031603

F-HEM BB1001906

F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

F-HEM BB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505

F-HEM BB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705

5 F-HEM BB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812

F-HEM BB1001921//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//3.4e-07:803:58//AC003950

F-HEM BB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391

10 F-HEM BB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181

F-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867

F-HEM BB1001944//, complete sequence.//4.1e-60:638:73//AC005815

15 F-HEM BB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882

F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390

F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899

20 F-HEM BB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341

F-HEM BB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//0.11:589:58//AC005284

F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941

25 F-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:727:97//AC005736

F-HEM BB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963

30 F-HEM BB1001973//Homo sapiens chromosome 12p13.3-clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844

F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071

F-HEM BB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189

35 F-HEM BB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689

F-HEM BB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507

40 F-HEM BB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069

F-HEM BB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153

F-HEM BB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685

45 F-HEM BB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506

F-HEM BB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056

50 F-HEM BB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

F-HEM BB1002043

F-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740

F-HEM BB1002045

55 F-HEM BB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence.//0.87:177:65//AC006237

F-HEM BB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355

F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

F-HEM BB1002069

F-HEM BB1002092//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064

F-HEM BB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476

F-HEM BB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035

F-HEM BB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843

F-HEM BB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714

F-HEM BB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748

F-HEM BB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421

F-HEM BB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998

F-HEM BB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140

F-HEM BB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846

F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332

F-HEM BB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711

F-HEM BB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648

F-HEM BB1002247

F-HEM BB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918

F-HEM BB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506

F-HEM BB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547

F-HEM BB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504

F-HEM BB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682

F-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642

F-HEM BB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164

F-HEM BB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752

F-HEM BB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402

F-HEM BB1002340

F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841

F-HEM BB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991

F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766

F-HEM BB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946

F-HEM BB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153

F-HEM BB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEM BB1002383

F-HEM BB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052

F-HEM BB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3

precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712  
 F-HEMBB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 36411, WORKING  
 DRAFT SEQUENCE.//8.9e-35:334:75//AL031319  
 F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//  
 5 U62317  
 F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//  
 U92010  
 F-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING  
 DRAFT SEQUENCE.//2.7e-43:419:78//AL034349  
 10 F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.3e-27:542:68//AC005534  
 F-HEMBB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993  
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885  
 15 F-HEMBB1002489  
 F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919  
 F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//1.1e-16:297:  
 68//AC006141  
 F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230  
 20 F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-  
 11:648:60//AC004605  
 F-HEMBB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992  
 F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//  
 25 AC006152  
 F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library)  
 complete sequence.//5.6e-22:516:64//AC004553 F-HEMBB1002531  
 F-HEMBB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING  
 DRAFT SEQUENCE.//6.9e-62:265:87//AL034346  
 30 F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//  
 AC000059  
 F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:  
 68//AC004927  
 F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//  
 35 AC004861  
 F-HEMBB1002579  
 F-HEMBB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//0.00018:431:61//AL033520  
 F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471  
 40 F-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 9E21, WORKING  
 DRAFT SEQUENCE.//3.6e-50:692:69//AL008639  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749  
 F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381  
 F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454  
 45 F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, com-  
 plete cds.//0.0042:460:60//AF009614  
 F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human  
 PAC library) complete sequence.//6.3e-23:559:63//AC003029  
 F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//  
 50 AC000025  
 F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:  
 324:56//AE001417  
 F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:  
 441:60//AF001550  
 55 F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304  
 F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//  
 U34819  
 F-HEMBB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

omic clone Plate=2265 Col=11 Row=O, genomic survey sequence.//0.54:115:67//AQ101557

F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774

F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492

F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748

F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077

F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525

F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955

F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363

F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720

F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151

F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187

F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117

F-MAMMA1000019

F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//2.0e-40:185:97//Z47553

F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence.//1.0:211:65//AC005483

F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275

F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:495:79//AL031073

F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-35:559:66//X78989

F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//5.5e-121:703:89//AC005829

F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region.//0.00013:329:60//AF048727

F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023

F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541

F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//1.2e-70:598:78//AC004744

F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.1e-156:857:92//AC003976

F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160

F-MAMMA1000129//ryanodine receptor.//0.055 :492:59//A20359

F-MAMMA1000133

F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362

F-MAMMA1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete sequence.//3.3e-14:322:65//AC002369

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds.//6.9e-25:148:97//AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds.//1.0e-29:219:87//AF031924

F-MAMMA1000163

F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//AC005393

F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.//2.2e-114:698:87//U58884

F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678  
 F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 DRAFT SEQUENCE.//4.6e-94:904:73//AL023808  
 F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610  
 5 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//  
 AC004583  
 F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING  
 DRAFT SEQUENCE.//0.36:312:62//AL031283  
 F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 10 nomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401  
 F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000  
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140  
 F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST  
 15 and STS.//0.00036:230:65//AL022717  
 F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:  
 499:68//L81612  
 F-MAMMA1000266//Bacillus lynceorum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430  
 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:  
 20 788:96//AF001549  
 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//  
 AL021897  
 F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I80055  
 F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS,  
 25 GSS, complete sequence.//2.4e-49:262:77//AL031643  
 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004  
 F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.7e-54:401:83//AC006213  
 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541  
 30 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SE-  
 QUENCE, 67 unordered pieces.//0.15:449:59//AC006205  
 F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359  
 F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING  
 DRAFT SEQUENCE.//0.27:301:60//AL031274  
 35 F-MAMMA1000313  
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:  
 71//AC002400  
 F-MAMMA1000339  
 F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288  
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//  
 AC004139  
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.8e-52:264:76//AC005052  
 45 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//  
 AC004879  
 F-MAMMA1000361//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950  
 F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
 50 DRAFT SEQUENCE.//2.9e-114:516:89//AL022345  
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey  
 sequence.//6.9e-26:377:71//AQ279944  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:  
 98//AB015132  
 55 F-MAMMA1000395  
 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999  
 F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768

F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456

F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369

5 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640

F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630

F-MAMMA1000422

F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240

10 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973

F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484

F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283

15 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755

F-MAMMA1000446

F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620

F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING

20 DRAFT SEQUENCE.//0.75:303:60//Z93017

F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543

F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081

25 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381

F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686

F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence.//4.8e-29:175:94//AQ044812

30 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545

35 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576

40 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101

F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922

F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238

45 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370

F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104

F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M22, genomic survey sequence.//9.6e-102:487:99//AQ198091

50 F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195

F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338

55 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//1.5e-32:259:82//AC005839

F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

F-MAMMA1000612//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793

F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310

5 F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371

F-MAMMA1000623

F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898

F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674

10 F-MAMMA1000664//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137

F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785

F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650

15 F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367

20 F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302O19, genomic survey sequence.//1.8e-08:131:77//AQ017947

F-MAMMA1000713//Rattus norvegicus clonol polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762

25 F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028

F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289:60//B95401

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781

30 F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917

F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274

F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859

35 F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141

F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408

F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123

40 F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158

F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075

F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048

45 F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166

F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.3e-51:789:68//AC005703

F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116

50 F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118

F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987

F-MAMMA1000798//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656

55 F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//



AC005339

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPC11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502

F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146

F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747

F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553

F-MAMMA1000862

F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906

F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336

F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283

F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117

F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308

F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643

F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001

F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

5 F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458

F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991

10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401

15 F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567

20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444

25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903

F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597

30 F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

35 F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.0e-22:334:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256

F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

50 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825

F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//1.6e-84:406:82//S70011  
 F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence//1.3e-14:182:76//AL022339  
 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187  
 5 F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence.//0.00051:249:61//AQ055735  
 F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518  
 10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123  
 F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629  
 F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//6.8e-57:670:72//AC005696  
 F-MAMMA1001191  
 15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156  
 F-MAMMA1001202  
 F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412  
 F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5:1e-30:535:65//AC004099  
 20 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393  
 F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875  
 25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M34398  
 F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726  
 F-MAMMA1001244  
 F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence.//6.7e-09:502:58//U67616  
 30 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495  
 F-MAMMA1001259  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561  
 35 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453  
 F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206  
 F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840  
 40 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05 :276:66//AC003035  
 F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314  
 45 F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084  
 F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.6e-182:860:98//AC005703  
 50 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244  
 F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290  
 55 F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390  
 F-MAMMA1001330

F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906

F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744

F-MAMMA1001346

F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086

F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826

F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23 :209:75//AL022332

F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872

F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75 :424:93//AQ244585

F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049

F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400

F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684

F-MAMMA1001452//RPC111-48022.TJ RPC111 Homo sapiens genomic clone R-48O22, genomic survey sequence.//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543

F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783

F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486

F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714

F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378

F-MAMMA1001522

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931

F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548

F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764

F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949

F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-66:405:90//AQ163791

F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626

F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685

F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630

F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833

F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796

F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577

5 F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284

F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

10 F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatogenesis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

15 F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

20 F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

25 F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687

F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001

F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//3.2e-16:194:75//AC006017

30 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1; Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

35 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065

F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338

F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865

40 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722

45 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514

F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801

50 F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801

F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991

F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563

F-MAMMA1001785

55 F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129

F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262

F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128

F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031

F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930

10 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148

F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508

F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete sequence.//3.4e-45:312:85//AC006211

15 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042

F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620

F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390

20 F-MAMMA1001854

F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631

F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013

25 F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455

F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63h5, reverse read cpg63h5.rta.//1.0:127:63//Z62129

F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

30 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465

F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

35 F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597

F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157

40 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656

F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986

45 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071

F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646

F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_O\_I, complete sequence.//1.5e-07:244:62//AC005224

50 F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803

55 F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227

F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//

AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPC11-78F11.TJ RPC11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576  
 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:  
 67//AC003108  
 F-MAMMA1002292//B.garinii (strain Tls1) p83/100 gene (partial).//0.73:200:64//X81533  
 5 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
 1.6e-56:408:75//AC006023  
 F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258  
 F-MAMMA1002297  
 10 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:  
 525:61//AC004221  
 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey se-  
 quence.//1.2e-90:446:98//AQ053994  
 F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING  
 DRAFT SEQUENCE.//1.3e-35:329:78//AL031680  
 15 F-MAMMA1002310//Human gastric (H<sup>+</sup> + K<sup>+</sup>)-ATPase gene, complete cds.//0.0060:301:60//J05451  
 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syn-  
 drome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737  
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and  
 STS.//1.3e-09:741:58//Z86064  
 20 F-MAMMA1002317  
 F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//  
 AC005756  
 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:  
 617:70//AC004796  
 25 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//  
 U93871  
 F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING  
 DRAFT SEQUENCE.//1.6e-31:287:74//AL034402  
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//  
 30 AL022022  
 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases  
 1.41604.//2.1e-57:522:77//AJ011932  
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//  
 AC004129  
 35 F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORK-  
 ING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100  
 F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING  
 DRAFT SEQUENCE.//5.8e-17:326:70//Z98742  
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 40 1.1e-14:399:63//AC004825  
 F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING  
 DRAFT SEQUENCE.//3.7e-43:420:75//AL023879  
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153  
 45 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence.//5.3e-18:156:75//AC005831  
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome  
 4p16.3, contains EST.//4.9e-43:353:69//Z68885  
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs  
 and a GSS, complete sequence.//1.8e-22:282:74//AL008719  
 50 F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938  
 F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey se-  
 quence.//4.4e-10:85:92//AQ196889  
 F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey se-  
 55 quence.//2.7e-56:286:98//AQ284134  
 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey se-  
 quence.//5.5e-46:335:84//AQ043985  
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//



AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875

F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74\_E\_22 complete sequence.//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING

DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666

F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029

F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome oxidase, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:97//AC005856

F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D; genomic survey sequence.//0.00018:219:63//AQ175845

F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553

5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462

10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388

20 F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

25 F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814

F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906

30 F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096

F-MAMMA1002895//H.sapiens CpG island DNA genomic Mse1 fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616

F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402

35 F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467

F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623

F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598

F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032

40 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366

F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056

45 F-MAMMA1002972//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2g10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272

F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919

50 F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:63//AL022098

F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998

55 F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601

F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139  
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//  
 AC003694  
 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-  
 13:443:61//AC003661  
 F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271  
 F-MAMMA1003026  
 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//  
 0.0037:134:73//AC005214  
 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey se-  
 quence.//1.1e-07:66:100//B74936  
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//2.1e-19:220:76//AC004671  
 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, poly-  
 morphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257  
 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS,  
 complete sequence.//0.21:289:61//AL031321  
 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-  
 139:663:98//AF077952  
 F-MAMMA1003049  
 F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940  
 F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772  
 F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352  
 F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING  
 DRAFT SEQUENCE.//1.0:142:71//AL034371  
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:  
 373:78//AC004796  
 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166  
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:  
 477:64//U72634  
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:  
 85//AF071316  
 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199  
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:  
 676:58//U67916  
 F-MAMMA1003140  
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062  
 F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE.//7.3e-123:266:88//AL021579  
 F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
 DRAFT SEQUENCE.//1.6e-33:143:82//Z99716  
 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
 complete sequence.//0.50:216:61//Z95400  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-  
 135:565:84//U67060  
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590  
 F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155  
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671  
 F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING  
 DRAFT SEQUENCE.//1.0:257:59//AL031600  
 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520  
 F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155

5 F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335

10 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155

F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

15 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474

20 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206\_C\_20, complete sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:473:64//Z68336

F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:80//D50920

25 F-NT2RM1000271

F-NT2RM1000272

F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

30 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494

35 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302

40 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

F-NT2RM1000399

F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

45 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993

50 F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737

55 F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542

F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134

F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840

F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228

F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125

F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245

5 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391

F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905

10 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263

F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731

F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757

15 F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489

F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964

F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973

F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678

20 F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624

F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755

25 F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291

F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826

F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863

30 F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379

F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418

35 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269

F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905

40 F-NT2RM2000101

F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224

45 F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289

F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

F-nnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

50 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

55 F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C124C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

5 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

10 F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343

F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274

F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973

15 F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430

F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

20 F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290

F-NT2RM2000502

25 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243

F-NT2RM2000522

F-NT2RM2000540

F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466

30 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132

F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252

F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

35 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987

F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466

40 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626

F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988

F-NT2RM2000609

45 F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776

F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

F-NT2RM2000624

2.9e-06:231:64//Z82061

50 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558

F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576

55 F-NT2RM2000669

F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984



F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342  
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244  
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691  
 F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING  
 5 DRAFT SEQUENCE.//1.0e-78:723:76//AL021392  
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228  
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//  
 AC005017  
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046  
 10 F-NT2RM2000952  
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-  
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//  
 7.6e-41:239:76//AF109905  
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-  
 15 quence.//1.1e-11:298:66//AQ035862  
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855  
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//  
 AF071314  
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-  
 20 145:614:99//AC004873  
 F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//2.7e-95:461:99//AL034380  
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-  
 24:726:62//U52064  
 25 F-NT2RM2001141  
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the  
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-  
 ponent A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-  
 plete sequence.//0.98:300:62//AL022401  
 30 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 1.2e-147:741:96//AC005488  
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial  
 cds.//0.026:408:59//U66829  
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-  
 35 135:627:98//AC004987  
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700  
 F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514  
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150  
 F-NT2RM2001243  
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey  
 sequence.//0.0011:274:59//AQ276184  
 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169  
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-  
 quence.//4.6e-09:156:72//B57734  
 45 F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey se-  
 quence.//0.069:234:64//B84850  
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:  
 81//AC005919  
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118  
 50 F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING  
 DRAFT SEQUENCE.//3.7e-44:340:85//Z84465  
 F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514  
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//  
 55 U56429  
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//  
 AC004899  
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete

sequence.//4.0e-54:394:75//AC004033

F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509

F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113

F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624

F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708

F-NT2RM2001544

F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657

F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551

F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902

F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667

F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431

F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630

F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518

F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020

F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913

F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629

F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451

F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195

F-NT2RM2001668

F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147

F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157

F-NT2RM2001675//RPCI11-51J16.TJ RPCI11 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677

F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//AL021890

F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948

F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854

F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668

F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920

F-NT2RM2001699//HS\_3195\_8B2\_DO1\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056

F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556

F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469

F-NT2RM2001716

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123  
 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931  
 5 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598  
 F-NT2RM2001743  
 F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117  
 F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629  
 F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993  
 10 F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116  
 F-NT2RM2001782  
 F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053  
 15 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770  
 F-NT2RM2001797//HS\_3045\_AT\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456  
 F-NT2RM2001800  
 20 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195  
 F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126  
 F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870  
 25 F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274  
 F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759  
 F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347  
 30 F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285  
 F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177  
 35 F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328  
 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610  
 F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720  
 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931  
 F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818  
 F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028  
 45 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080  
 F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700  
 F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825  
 50 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816  
 F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981  
 F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955  
 F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151  
 55 F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407  
 F-NT2RM2002014  
 F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//

1.5e-89:822:74//U00932

F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132

F-NT2RM2002055

F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936

F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840

F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435

F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152

F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121

F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936

F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423

F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826

F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429

F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685

F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059

F-NT2RM4000061

F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829

F-NT2RM4000086

F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865

F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101

F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ000070

F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586:60//X67336

F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646

F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157

F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726

F-NT2RM4000197

F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667

F-NT2RM4000200

F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255

F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852

F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383

F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430

F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757

F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855

F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689

F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

M99438

F-NT2RM4000324

F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085

5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430

F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449

10 F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542

F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217

F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485

15 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//1.5e-37:295:82//AC005921

20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476

F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111

F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952

25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908

F-NT2RM4000511

F-NT2RM4000514

30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113

F-NT2RM4000520

F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297

35 F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706

40 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125

F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390

45 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303

50 F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

F-NT2RM4000717

55 F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

F-NT2RM4000764

F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790

5 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

10 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

15 F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

20 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//3.4e-29:229:83//AC003957

25 F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

30 F-NT2RM4000971//RPC11-53H3.TJ RPC11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245

F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

35 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

40 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

45 F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593

F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

50 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

F-NT2RM4001160

F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378

55 F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828

F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

5 F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163

10 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127

15 F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786

20 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023

25 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183

F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563

30 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

35 F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585

40 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

F-NT2RM4001566

45 F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720

F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317

50 F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942

F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355

F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334

55 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//D90910

F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196

F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320  
 F-NT2RM4001666  
 F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699  
 F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 5 DRAFT SEQUENCE.//1.9e-151:564:97//AL031447  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957  
 F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
 complete sequence.//1.2e-91:488:94//AL034430  
 F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312  
 10 F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123  
 F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING  
 DRAFT SEQUENCE.//2.3e-49:320:89//AL031709  
 F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//6.3e-64:379:76//AC005831  
 15 F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270  
 F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017  
 F-NT2RM4001810  
 F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//  
 20 AC005036  
 F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
 4.4e-34:195:95//M37712  
 F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046  
 F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:  
 25 72//U28687  
 F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete se-  
 quence.//1.0:406:60//AC000076  
 F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2,  
 complete cds.//1.6e-131:831:86//AF033275  
 30 F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513  
 F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855  
 F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711  
 35 F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//  
 Z88651  
 F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey se-  
 quence.//0.0025:61:88//AQ060809  
 F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335  
 40 F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732  
 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence.//  
 4.9e-10:269:63//AB005248  
 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:  
 45 100//AC005207  
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162  
 F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046  
 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 50 non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868  
 F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341  
 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:  
 502:60//Z82253  
 55 F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-  
 quence.//2.6e-33:177:99//AQ051701  
 F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//  
 AC005921



F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344  
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712  
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//  
 5 U01882  
 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283  
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540  
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORK-  
 10 ING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122  
 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267  
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783  
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216  
 15 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569  
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789  
 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646  
 F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RM4002140  
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152  
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940  
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763  
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//  
 30 AE000540  
 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636  
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430  
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//  
 35 1.5e-40:292:84//L14684  
 F-NT2RM4002213  
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160  
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448  
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959  
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779  
 F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653  
 45 F-NT2RM4002281  
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515  
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457  
 50 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881  
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822  
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865  
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549  
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22. TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484

F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7. TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402

F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1 a.//6.0e-27:163:95//Z60555

F-NT2RP1000111//CIT-HSP-2307O14. TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//E08546

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//

1.9e-20:431:64//AC006030

F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535

F-NT2RP1000191

F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496

F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508:69//AC004373

F-NT2RP1000259

F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383

F-NT2RP1000324//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.8e-29:182:92//AQ285136

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551

F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525

F-NT2RP1000348//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rt1c.//1.7e-09:71:100//Z56610

F-NT2RP1000357

F-NT2RP1000358 5.7e-16:403:61//AC005456

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594

F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558

F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159

F-NT2RP1000416

F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//L40178

F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305

F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047

F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//4.9e-80:196:95//AC002985

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634

F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:562:88//Z99297

F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686

F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648

F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895

F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.//1.2e-08:331:63//U26264

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418

F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128

F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989

F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907  
 F-NT2RP1000695  
 F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536  
 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932  
 5 F-NT2RP1000730  
 F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742  
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
 10 cds.//8.0e-122:604:96//AF101434  
 F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344  
 F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442  
 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//  
 15 AF054840  
 F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213  
 F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244  
 20 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837  
 F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020  
 F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the  
 25 HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398  
 F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629  
 30 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812  
 F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840  
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094  
 F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
 35 DRAFT SEQUENCE.//0.0097:55:100//Z82199  
 F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761  
 F-NT2RP1000916  
 F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362  
 F-NT2RP1000944//HS\_2179\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269  
 40 F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483  
 F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950  
 45 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068  
 F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263  
 F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981//M60858  
 F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126  
 50 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435  
 F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925  
 F-NT2RP1001013//HS\_3068\_B1\_809\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667  
 55 F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711  
 F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073\_F\_15, complete sequence.//1.3e-134:241:99//AC004686

F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267

5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938

F-NT2RP1001113

F-NT2RP1001173

F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681//U79139

10 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508

F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128:99//AC002036

15 F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63//L44140

F-NT2RP1001294

20 F-NT2RP1001302

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

F-NT2RP1001311//RPCI11-67O14.TK RPCI11 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291

F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

25 F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

30 F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424

35 F-NT2RP1001432

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

40 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375

F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316

F-NT2RP1001494

F-NT2RP10015431//Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280

45 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840

F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP100T616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081

F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856

55 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390

F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//

AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092

F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610

F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338

F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363

F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961

F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356

F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924

F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632

F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401

F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:

87//AC004066

F-NT2RP2000248

F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388

5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence.//5.7e-82:416:97//AQ059184

F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//4.5e-29:310:73//AC006116

F-NT2RP2000274

10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904

F-NT2RP2000288

F-NT2RP2000289

F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//4.6e-69:744:70//M27877

15 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530

F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082

F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398

20 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430

F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//M25757

25 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333

F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.6e-129:627:97//U83981

30 F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835

F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010

F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093

35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265

F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey sequence.//0.96:61:78//AQ276878

40 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691

F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747

F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844

F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//AC005229

45 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277

F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//0.19:72:81//U21671

50 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318

F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543

F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321

55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514

F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486

F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386

F-NT2RP2000668

F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916

F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913

F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122

F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540

F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965

F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293

F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887

F-NT2RP2000809

F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698

F-NT2RP2000814

F-NT2RP2000816

F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292

F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479

F-NT2RP2000845

F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045

F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284

F-NT2RP2000892

F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266

F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014

F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890

F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298

F-NT2RP2000965

F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393

F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//1.6e-72:498:82//AC005277

F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394

F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167

F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224

F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957

F-NT2RP2001065

F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561

F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423

F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063

F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596

F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072

F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187



F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076

F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949

F-NT2RP2001174//RPCI11-58L2.TK RPCI11 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760

F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430

F-NT2RP2001290//M.musculus mRNA for l47 clone.//8.6e-102:641:86//X61455

F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594

F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967

F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783

F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539

F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147

F-NT2RP2001366//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305

F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721

F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371

F-NT2RP2001392//S.pristinaespiralis snbC gene & amp; snbDE gene.//0.019:267:59//Y11548

F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242

F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219

F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759

F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454

F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350

F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275

F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430

5 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784

10 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354

15 F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699

20 F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

25 F-NT2RP2001721//Homo sapiens DNA sequence from clone 466I8 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697

30 F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378

35 F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D\_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309

40 F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161

45 F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic MseI fragment, clone 97f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125

50 F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033

55 F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442

F-NT2RP2001969//H.sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.rt1a.//1.0e-20:123:99//Z59378

F-NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117  
 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299  
 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:  
 65//AC005895  
 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-  
 12:160:79//AC004825  
 F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029  
 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete  
 sequence.//2.2e-86:722:77//AC004552  
 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon  
 of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375  
 F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301  
 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//  
 U87306  
 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=ad-  
 ducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human,  
 Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183  
 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//  
 0.14:191:64//AQ249805  
 F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509  
 F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpg10h8.ft1a.//  
 2.4e-29:178:94//Z58857  
 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-  
 quence.//2.5e-32:202:92//B64468  
 F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//  
 M25874  
 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923  
 F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169  
 F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey se-  
 quence.//2.8e-18:109:100//AQ201833  
 F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complete cds.//2.7e-36:363:78//U09215  
 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-  
 82:477:89//AF032872  
 F-NT2RP2002208  
 F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//1.0:378:58//AL034557  
 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308  
 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998  
 F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418  
 F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING  
 DRAFT SEQUENCE.//9.7e-67:340:89//AL033527  
 F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey se-  
 quence.//2.9e-18:79:93//AQ268098  
 F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
 DRAFT SEQUENCE.//1.0:290:60//AL031033  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//  
 AF069532  
 F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673  
 F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594  
 F-NT2RP2002333  
 F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//

Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742

F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682

F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169

F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045

F-NT2RP2002475

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//7.2e-18:134:90//AC006213

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334

F-NT2RP2002520

F-NT2RP2002537

F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127

F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317

F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304

F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155

F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181

F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397

F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572

F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107

F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388

F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861

F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016

F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433

F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837

F-NT2RP2002800

F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

TRB-4.//0.85:93:68//M18845

F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344

F-NT2RP2002880

F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

F-NT2RP2002929//F.rubripes GSS sequence, clone 123123aA1, genomic survey sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424

F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//4.2e-23:202:82//AC005703

F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362

F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:

86//AF023657

F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286

F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572

F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722

F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666

F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374

F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288

F-NT2RP2003339

F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559

F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510

F-NT2RP2003391

F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356

F-NT2RP2003394

F-NT2RP2003401

F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630

F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023

F-NT2RP2003446

F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770

F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977

F-NT2RP2003499 2.1e-08:408:61//AB000826

F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236

F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460

F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702

F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977

F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899

F-NT2RP2003543

F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cp90a5.rt1a.//1.1e-20:122:99//Z56144

F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931

F-NT2RP2003581

F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//J1.9e-11:210:65//AL012756

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:98//AF030233

F-NT2RP2003629

5 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215

F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081

F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684

10 F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807

F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803

F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, clone 2a9, reverse read cpg2a9.rt1e.//3.8e-17:170:84//Z60615

15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097

F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895

F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973

20 F-NT2RP2003727//RPC111-77I19.TV RPC111 Homo sapiens genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303

F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951

F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964

25 F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987

F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275

F-NT2RP2003769

30 F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:98//AC004771

F-NT2RP2003777

F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011

F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761

35 F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491

F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167

F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467

40 F-NT2RP2003859

F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375

F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722

45 F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828

F-NT2RP2003952

50 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458

F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)

55 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347

F-NT2RP2003984

F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382

5 F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681

F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580

F-NT2RP2004014

10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780

F-NT2RP2004042

F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555

15 F-NT2RP2004081

F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694

F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993

20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645

F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493

25 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140

F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235

F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816

F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093

30 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998

F-NT2RP2004196

F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676

35 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756

F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718

F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006

40 F-NT2RP2004242

F-NT2RP2004245

F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446

F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781

45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416

F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519

50 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

F-NT2RP2004364

F-NT2RP2004365

55 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864

F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397



F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969

F-NT2RP2004392

5 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164

F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799

F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441

10 F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369

F-NT2RP2004425

F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530

F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388

F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591

15 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556

F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163

F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555

20 F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100

F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908

25 F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020

F-NT2RP2004600

F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176

30 F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929

F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805

35 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525

F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714

40 F-NT2RP2004710//HS\_3185\_82\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947

F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022

45 F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636

F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398

50 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353:84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179

55 F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519

F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence.//0.96:183:64//AL025645

F-NT2RP2004897//Human Chromosome X clone bWDX187, complete sequence.//4.8e-142:710:96//AC004383  
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144  
 F-NT2RP2004936  
 5 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183  
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-  
 59:339:79//U56732  
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-  
 chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-  
 10 19:187:72//U91328  
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551  
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029  
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:  
 273:61//B12642  
 15 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375  
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200  
 20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141  
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//  
 AC004849  
 F-NT2RP2005020  
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 25 3.0e-43:98:93//AC000380  
 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464  
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454  
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//  
 30 AC005696  
 F-NT2RP2005108  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//  
 X98743  
 35 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//  
 0.00024:547:59//AJ223012  
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
 quence.//0.95:191:62//AC004527  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583  
 40 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226  
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read  
 cpg132g6.ft1a.//1.1e-13:93:97//Z59162  
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070  
 45 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509  
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:  
 60//U80808  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//  
 AC005189  
 50 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536  
 F-NT2RP2005254  
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513  
 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666  
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335  
 55 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//  
 AF060219  
 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590  
 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//  
 U11701  
 5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds.//0.39:353:62//AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138  
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//  
 Z92844  
 10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:  
 96//AF072247  
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358  
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184  
 F-NT2RP2005407  
 15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:  
 62//AC005346  
 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey se-  
 quence.//4.0e-107:532:97//AQ055548  
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//  
 20 1.0:239:61//B97865  
 F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647  
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat,  
 STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679  
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-  
 25 18:152:75//AC006116  
 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of  
 a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)  
 gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2,  
 TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat poly-  
 30 morphism, complete sequence.//4.4e-12:89:97//AL031276  
 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//  
 AC004130  
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//  
 3.2e-115:228:99//AC006030  
 35 F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847  
 F-NT2RP2005495  
 F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097  
 40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931  
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//  
 0.86:183:63//AC005880  
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695  
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:  
 45 444:92//AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307  
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449  
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963  
 50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734  
 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723  
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA,  
 complete cds.//2.5e-44:473:71//AF062529  
 55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016  
 F-NT2RP2005600//H.sapiens CpG island DNA genomic Mse1 fragment, clone 172d12, reverse read  
 cpg172d12.r1a.//0.32:134:63//Z57359  
 F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556

F-NT2RP2005637//NATI (NATI\*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829

F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980

F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763

F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626

F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814

F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342

F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367

F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528

F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017

F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270

F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868

F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516

F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853

F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849

F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336

F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853

F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579

F-NT2RP2005812

F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103

F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086

F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873

F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564

F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553

F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//AL027276

F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316  
 F-NT2RP2005901//H.sapiens CpG island DNA genomic MseI fragment, clone 15b5, reverse read cpg15b5.rt1a.//0.0026:66:84//Z54729  
 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-  
 5 brary) complete sequence.//6.4e-49:481:75//AC004241  
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840  
 F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770  
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207  
 10 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553  
 F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey se-  
 quence.//3.9e-06:102:74//B51912  
 F-NT2RP2006043//Human intercrine-alpha (HIRH) mRNA, complete cds.//1.9e-05:418:59//U19495  
 15 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//  
 AF016861  
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047  
 F-NT2RP2006071  
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//  
 20 AF027207  
 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073  
 F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602  
 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//11.2e-62:655:71//AC000378  
 25 F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING  
 DRAFT SEQUENCE.//1.2e-69:316:98//AL034405  
 F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063  
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mR-  
 NA, complete cds.//0.99:111:73//U62587  
 30 F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554  
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232  
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66  
 unordered pieces.//6.5e-83:239:94//AC006057  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484  
 35 F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-  
 quence.//2.0e-18:118:97//AQ012480  
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//  
 U49055  
 F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey se-  
 40 quence.//8.6e-05:181:63//B71615  
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630  
 F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257  
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262  
 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851  
 45 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//  
 AC003973  
 F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING  
 DRAFT SEQUENCE.//8.9e-18:131:90//AL033532  
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:  
 50 98//AC004893  
 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//  
 AC005514  
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:  
 70//AL029590  
 55 F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and  
 pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727  
 F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441

F-NT2RP2006454//Sequence 8 from Patent WO9517522.//2.9e-06:180:66//A45338

F-NT2RP2006456

F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266

5 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201:66//U50149

F-NT2RP2006472

10 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929

F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965

F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966

15 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855

F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315

F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537

F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571

20 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972

F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320

F-NT2RP3000047

25 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626:74//M27877

F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227

F-NT2RP3000068

F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746

30 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391

F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536

F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237

35 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189

F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164

40 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884

F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583

F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063

45 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569

50 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972

F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213

F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174:88//AF065393

F-NT2RP3000255

55 F-NT2RP3000267

F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853

F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932

F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107

F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090

5 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533

F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181

F-NT2RP3000348

10 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393

F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757

F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743

15 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966

F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318

F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185

20 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, complete sequence.//7.9e-53:817:68//AC006083

F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471

25 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488

F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

30 F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420

F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

35 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667

F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

40 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

45 F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

F-NT2RP3000562

F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

50 F-NT2RP3000584

F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868

55 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305

F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320

F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128

5 F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104

F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890

F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313

10 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363

F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089

F-NT2RP3000661

15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237

20 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961

F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872

F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930

F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264

25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655

F-NT2RP3000753

F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281

F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252

30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387

F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009

35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062

F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581

40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938

F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082

F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast. plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940

50 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831

F-NT2RP3000865

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445

55 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367

F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007

F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//



AF021340

F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505:99//M27223

F-NT2RP3000917//Mouse mRNA for Dhml1 protein, complete cds.//3.1e-132:691:93//D38517

F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//

3.2e-97:585:88//AF015264

F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326

F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335

F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529

F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.rt1a./15.9e-27:150:99//Z60925

F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039

F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325

F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969

F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317

F-NT2RP3001111

F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189

F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581

F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367

F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078

F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305

F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266

F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507

F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619

F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396

F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14. TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465

F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966

F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

F-NT2RP3001374

F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198

F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521

F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668

F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836

5 F-NT2RP3001490

F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

10 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:91//U36499

F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176

15 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPC111-91E19.TV RPC111 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

20 F-NT2RP3001589//RPC111-68M15.TK RPC111 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674

25 F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//M90050

F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808

30 F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449

35 F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250

40 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273

45 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.8e-19:123:95//AQ012480

F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962

F-NT2RP3001708//H.sapiens CpG island DNA genomic MseI fragment, clone 4g7, reverse read cpg4g7.rt1d.//1.3e-17:113:97//Z61312

50 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642

F-NT2RP3001716

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177

F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:88//AF008554

55 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918

F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence.//6.5e-07:178:69//AC000097

F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311

F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381

F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888

5 F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928

F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262

10 F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284

F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hydroxystreptomycin prduction and transport polypeptides.//0.084:526:58//X89010

F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433

15 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505

F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknx1) mRNA, complete cds.//2.7e-39:575:67//AF061270

20 F-NT2RP3001857//M.musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434

F-NT2RP3001896

F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733

F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:56//Z73969

25 F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557

F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651

F-NT2RP3001931

30 F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475

F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575

F-NT2RP3001944

F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844

35 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694

F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822

40 F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386

F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137

F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640

45 F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493

F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773

F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841

50 F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249

F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682

F-NT2RP3002062

55 F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272

F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494

F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-

plete sequence.//9.6e-66:562:77//AC006210

F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040

F-NT2RP3002108

F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020

F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370

F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710

F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742

F-NT2RP3002163

F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061

F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//0.090:394:59//AC006121

F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219

F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808

F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321

F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880

F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321

F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004

F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898

F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810

F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862

F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331

F-NT2RP3002399

F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068

F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821

F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418

F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.6e-13:199:76//

AC004617

F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804

F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331

5 F-NT2RP3002603

F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050

F-NT2RP3002631

F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469

F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205

10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946

F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129

F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704

15 F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507

F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656

F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577

20 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530

F-NT2RP3002713

F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594

F-NT2RP3002770

25 F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718

30 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//AC005549

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601

F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430

35 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895

F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314

40 F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815

F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500

F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754

F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024

45 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666

F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820

F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644

50 F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905

55 F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153

F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609  
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410  
 F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read  
 cpg13d12.rt1c.//6.8e-15:95:100//Z64565  
 5 F-NT2RP3003078  
 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315  
 F-NT2RP3003121  
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//  
 AC004510  
 10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//  
 D12646  
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//  
 U17995  
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639  
 15 F-NT2RP3003150  
 F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489  
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete  
 cds.//8.6e-06:228:65//AF064868  
 20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933  
 F-NT2RP3003197  
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 4.1e-48:640:67//AF015264  
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059  
 25 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799  
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:  
 776:74//U20286  
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064  
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460  
 30 F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200  
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153  
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//  
 4.0e-27:174:93//Z60555  
 35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983  
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:  
 71//AF004162  
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//  
 D85610  
 40 F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213  
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
 quence.//1.0:191:62//AC004527  
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107  
 F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200  
 45 F-NT2RP3003330  
 F-NT2RP3003344  
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:  
 84//AC005284  
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a  
 50 BAC end-sequence (GSS).//0.047:404:60//AL021069  
 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
 8.3e-122:632:96//AC005519  
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-  
 dered pieces.//0.0036:127:74//AC000360  
 55 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874  
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:  
 63//U90653

F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317

F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173

5 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268

10 F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124

F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347

F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234

15 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049

F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985

20 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798

F-NT2RP3003572

F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632

25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387

F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235

F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600

30 F-NT2RP3003656

F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096

35 F-NT2RP3003672

F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811

F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993

40 F-NT2RP3003701

F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975

F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300

F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785

45 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326

50 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458

F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031

55 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321

F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801

F-NT2RP3003819



F-NT2RP3003825

F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626

F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633

5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611

F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343

10 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181

F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358

15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504

F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661

F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNGC2) mRNA, complete cds.//0.021:433:58//U58837

20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692

F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726

F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400

25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317

F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939

30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089

F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433

F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038

35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973

F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560

F-NT2RP3004145

F-NT2RP3004148

40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900

F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102:82//X80434

F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374

F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009

45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052

F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084

F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181

F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385

50 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353

F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871

55 F-NT2RP3004332

F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908

F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877  
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025  
 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-  
 5 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23 :352:67//AC005653  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249  
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678  
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206  
 F-NT2RP3004451//RPC11-51J15.TK RPC11 Homo sapiens genomic clone R-51J15, genomic survey se-  
 10 quence.//8.8e-19:180:82//AQ052326  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917  
 F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458  
 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read  
 15 cpg81a11.rt1a.//7.0e-25:148:96//Z56029  
 F-NT2RP3004472//RPC11-42M5.TJ RPC11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//  
 1.6e-20:143:92//AQ052792  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925  
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//  
 20 U47024  
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851  
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//  
 4.0e-67:265:84//AC006023  
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 25 complete sequence.//1.2e-55:415:78//AC004673  
 F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260  
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//  
 AC005328  
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574  
 30 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532  
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126  
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:  
 64//AF031955  
 35 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey se-  
 quence.//5.3e-15:138:84//AQ280780  
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//  
 AF026445  
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946  
 40 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266  
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-  
 14:360:65//AC004977  
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:  
 73//AF005355  
 45 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160  
 nt].//0.046:437:57//S69350  
 F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING  
 DRAFT SEQUENCE.//1.9e-05:625:59//Z98882  
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//1.5e-155:844:92//  
 50 AC006121  
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//  
 0.012:417:59//AB012242  
 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//  
 AC005035  
 55 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761  
 F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449  
 F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538  
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952  
 5 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776  
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681  
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088  
 F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551  
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210  
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600  
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300  
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261  
 F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504  
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470  
 20 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092  
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515  
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481  
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322  
 F-NT2RP4000323  
 30 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281  
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195  
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272  
 35 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536  
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850  
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116  
 40 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966  
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086  
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101  
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194  
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183  
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982  
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499  
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483  
 F-NT2RP4000481  
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125  
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904  
 F-NT2RP4000515  
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840  
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding  
 exon 2C.//0.26:162:61//U23720  
 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498  
 5 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386  
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:  
 498:58//AC002443  
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465  
 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector  
 10 pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580  
 F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING  
 DRAFT SEQUENCE.//0.00062:253:65//AL033543  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//  
 AF067730  
 15 F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333  
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associ-  
 ated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335  
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904  
 20 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:  
 99//AB004852  
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149  
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178  
 25 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//  
 L19301  
 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey se-  
 quence.//1.1e-24:161:93//B57903  
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917  
 30 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mR-  
 NA, complete cds.//9.6e-18:259:68//U22818  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//  
 AC005189  
 35 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING  
 DRAFT SEQUENCE.//2.1e-128:644:97//AL034420  
 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey se-  
 quence.//1.5e-44:281:91//B48216  
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515  
 40 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367  
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//  
 AJ001616  
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804  
 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//  
 45 D45913  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901  
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-  
 08:609:58//AC004290  
 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:  
 50 87//U42975  
 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//  
 AF069532  
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING  
 55 DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688  
 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
 1.0e-128:673:96//AC005519  
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657

F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence.//6.5e-31:317:79//AQ015742

F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942

F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823

5 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911

F-NT2RP4000996//Panaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358

F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424

10 F-NT2RP4001004

F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176

F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140

15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086

F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170

F-NT2RP4001057

F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469

20 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124

F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018

F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164

F-NT2RP4001095

25 F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402

F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629

F-NT2RP4001122

30 F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668

F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969

F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079

35 F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095

F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067

F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952

40 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476

F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494

F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds.//0.032:453:58//U82511

45 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358

F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877

50 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251

F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569

55 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081

F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061

F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854  
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728  
 5 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250  
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119  
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870  
 10 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725  
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918  
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011  
 15 F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428  
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107  
 F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701  
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609  
 20 F-NT2RP4001375  
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153:88//AC005722  
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691  
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957  
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326  
 30 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884  
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523  
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612  
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693  
 35 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513  
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308  
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086  
 40 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663  
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335:60//AL032684  
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806  
 45 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290  
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989  
 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885  
 50 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987  
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:86//AJ223830  
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663:59//X74219  
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364  
 55 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333  
 F-NT2RP4001634  
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

clone cSRL-161FI, genomic survey sequence.//4.9e-12:144:76//B02870

F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092

F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793

F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362

F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431

F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629

F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296

F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840

F-NT2RP4001739

F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:192:98//Z96232

F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316

F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:74//AC005678

F-NT2RP4001803

F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841

F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572

F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:354:61//B26193

F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365

F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARC1000013

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARC1000058

F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617

F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-



omic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288 2.2e-22:181:83//J00345

F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003

F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

F-OVARC1000309

F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236

F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614

F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696

F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007

F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275

F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693

F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201

F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166

F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718

F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826

F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558

F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165

F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284

F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678

F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583

F-OVARC1000461

F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

124:650:93//AF023451

F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221

F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191

F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829

F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297

F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733

F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850

F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024

F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510

F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic\_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820

F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.4e-136:670:97//AL022069

F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985

F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733

F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic\_Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942

F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414

F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1 e-27:354:72//AC003973

F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775

F-OVARC1000605

F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648

F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162

F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244

F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713

F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156

F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003

F-OVARC1000700

F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661

F-OVARC1000730

F-OVARC1000746

F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic\_Sperm-Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905

F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403  
 F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552  
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542  
 5 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691  
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469  
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711  
 10 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584  
 F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963  
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125  
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086  
 15 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044  
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721  
 F-OVARC1000890  
 F-OVARC1000891  
 20 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494  
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172  
 25 F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493  
 F-OVARC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983  
 F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848  
 30 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549  
 F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276  
 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850  
 35 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181  
 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270  
 F-OVARC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841  
 40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274  
 F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858  
 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785  
 F-OVARC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910  
 45 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190  
 F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290  
 50 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021  
 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451  
 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149  
 55 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081  
 F-OVARC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//0.0017:387:6.1//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768  
 F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292  
 F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878  
 F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525  
 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657  
 F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529  
 F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153  
 F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333  
 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782  
 F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178  
 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382  
 F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052  
 F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322  
 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004069  
 F-OVARC1001162  
 F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961  
 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141  
 F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823  
 F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315  
 F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323  
 F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001  
 F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195  
 F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486  
 F-OVARC1001200  
 F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334  
 F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235  
 F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078  
 F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613  
 F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505  
 F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776  
 F-OVARC1001270  
 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543  
 F-OVARC1001282//RPCI11-60K8.TK RPCI11 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857  
 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018  
 F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061

F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986

F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504

5 F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071

F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402

F-OVARC1001342

10 F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456

F-OVARC1001357//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297

F-OVARC1001360

15 F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811

F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801

F-OVARC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819

20 F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287

F-OVARC1001399//CIT-HSP-2291I8.TR CIT-HSP Homo sapiens genomic clone 2291I8, genomic survey sequence.//1.7e-11:104:87//AQ007611

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651

25 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426

F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudo-gene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714

F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387

30 F-OVARC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687

F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482

35 F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277

F-OVARC1001480

F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140

40 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507

F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411

45 F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219

F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140

F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037

50 F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165

F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945

F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409

55 F-OVARC1001611

F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682

F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867  
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840  
 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651  
 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662  
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752  
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650  
 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522  
 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575  
 F-OVARC1001768  
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066  
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704  
 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481  
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694  
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748  
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//AC003662  
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224  
 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779  
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609  
 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361  
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611  
 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748  
 F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//U51127  
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749  
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904  
 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069  
 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979  
 F-OVARC1001928  
 F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1 a.//7.2e-12:83:98//Z60390  
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263  
 F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929  
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021  
 5 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995  
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934  
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15,  
 10 WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011  
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015  
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668  
 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483  
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.013:461:57//AC006241  
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427  
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey se-  
 20 quence.//2.3e-11:258:67//AQ055576  
 F-OVARC1002156  
 F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//1.8e-16:383:66//B11616  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568  
 25 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//AL017241  
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey se-  
 quence.//8.2e-10:158:75//AQ003859  
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585  
 30 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789  
 F-PLACE1000014  
 F-PLACE1000031//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821  
 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023  
 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177  
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508  
 40 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154  
 F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521  
 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6  
 45 unordered pieces.//5.2e-09:143:73//AC005848  
 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete se-  
 quence.//0.52:390:60//AC002389  
 F-PLACE1000094  
 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and  
 50 CpG Island, complete sequence.//4.4e-129:731:92//AL023580  
 F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291  
 F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-PLACE1000213  
 55 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504  
 F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813

F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584

F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163

F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032

F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867

F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899

F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515

F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189

F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698

F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382

F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580

F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491

F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245

F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276

F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484

F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409

F-PLACE1000564

F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877

F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449

F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276

F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967

F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896

F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219

F-PLACE1000712

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026

F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109



F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559  
 F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589  
 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey se-  
 quence.//6.5e-08:93:89//B63806  
 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548  
 F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027  
 F-PLACE1000793//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read  
 cpg13d12.rt1c.//4.6e-09:71:100//Z64565  
 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:  
 10 72//AC002310  
 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 0.013:404:60//AC006158  
 F-PLACE1000849//H.sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read  
 cpg72a10.rt1a.//3.3e-09:82:92//Z62712  
 15 F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935  
 F-PLACE1000863//H.sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpg53d2.ft1b.//  
 7.3e-37:199:98//Z55621  
 F-PLACE1000909//H.sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read  
 cpg173f8.rt1a.//1.5e-17:128:92//Z57391  
 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate  
 receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181  
 F-PLACE1000948  
 F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//  
 1.0e-26:148:99//AQ194348  
 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572  
 F-PLACE1000979//H.sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpg76e8.rt1a.//  
 2.7e-10:84:94//Z55963  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267  
 F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011  
 30 F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey se-  
 quence.//0.99:277:58//B58681  
 F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357  
 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//  
 AC004741  
 35 F-PLACE1001024  
 F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey se-  
 quence.//1.1e-80:393:98//AQ108662  
 F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//  
 8.8e-40:483:66//AB013390  
 40 F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydroge-  
 nase.//1.2e-23:224:80//AJ224761  
 F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659  
 F-PLACE1001088  
 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485  
 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:  
 62//U81400  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:  
 71//AF022158  
 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702  
 F-PLACE1001168  
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603  
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the  
 gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene  
 55 for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6  
 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:  
 102:70//AL031177  
 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:

77//D14336

F-PLACE1001241

F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219

F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476

5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282

F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181

15 F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

20 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177

25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//8.2e-121:608:97//AC006241

30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106

35 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720

40 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373

F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786

F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.7e-139:482:96//AC005669

F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261

50 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

55 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959

F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//7.7e-159:788:97//AC005971

F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.1e-149:760:96//AC005921

F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776

F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051

F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124

F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

F-PLACE1001781 1.3e-08:238:65//AC005637

F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361

F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

15 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556

F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

30 F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

35 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324

40 F-PLACE1002319

F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956

F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623

F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//5.6e-05:474:59//AC005922

45 F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928

F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801

50 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262

F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

55 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060

F-PLACE1002499

F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927  
 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING  
 DRAFT SEQUENCE.//3.7e-08:139:76//Z93930  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256  
 5 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:  
 65//AC004774  
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a  
 novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor  
 Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575  
 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314  
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//  
 AC002523  
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443  
 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109  
 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 0.0013:375:64//AC005537  
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785  
 F-PLACE1002625  
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:  
 20 92//AC005281  
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//  
 AF079765  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-  
 186:804:97//AF068180  
 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:  
 64//AF051726  
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723  
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs  
 and a GSS, complete sequence.//0.0076:161:70//AL031273  
 30 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567  
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//  
 AF084259  
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927  
 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey se-  
 quence.//1.3e-71:368:96//AQ075879  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994  
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295  
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691  
 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//  
 M27877  
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045  
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140  
 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete tran-  
 scribed region and flanks.//0.032:275:62//M10126  
 F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING  
 DRAFT SEQUENCE.//4.7e-38:355:76//Z98200  
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//  
 50 U19889  
 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120  
 F-PLACE1002962  
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558  
 F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
 DRAFT SEQUENCE.//6.8e-121:605:93//AL023755  
 55 F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey se-  
 quence.//1.9e-13:100:95//AQ054760  
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551  
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088  
 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829  
 5 F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200  
 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158  
 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875  
 10 F-PLACE1003108  
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219  
 F-PLACE1003145  
 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206  
 15 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495  
 F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934  
 20 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095  
 F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276  
 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466  
 F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954  
 25 F-PLACE1003249  
 F-PLACE1003256  
 F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317  
 30 F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429  
 F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877  
 F-PLACE1003334  
 35 F-PLACE1003342  
 F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715  
 40 F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095  
 F-PLACE1003366  
 F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558  
 F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247  
 45 F-PLACE1003375  
 F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878  
 F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680  
 F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588  
 50 F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388  
 F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470  
 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401  
 55 F-PLACE1003493  
 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859

F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729

5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

10 F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547

F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230

20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200

F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356

F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

35 F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478

F-PLACE1003669

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

40 F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

45 F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840

F-PLACE1003762

50 F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014

F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210

F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

5 F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

10 F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

15 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108

F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

20 F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

25 F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

30 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

35 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

40 F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071

F-PLACE1004197

45 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

50 F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

55 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

F-PLACE1004274//H.sapiens CpG island DNA genomic MseI fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:



97//AF084830

F-PLACE1004284//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//*Streptomyces coelicolor* cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//*Drosophila melanogaster* DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//*Mus musculus* clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//*Caenorhabditis elegans* cosmid K08F11.//8.6e-26:615:62//U70855

F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//*R.norvegicus* mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//*Dictyostelium discoideum* MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//*B.taurus* mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//*Anolis carolinensis* Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//*Mycobacterium tuberculosis* H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//*Rattus norvegicus* retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpg55h1.ft1a./12.4e-34:188:98//Z61632

F-PLACE1004664//*Caenorhabditis elegans* cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577

F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551

F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073

F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:  
 590:61//AE001373  
 F-PLACE1005026  
 F-PLACE1005027  
 5 F-PLACE1005046  
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
 QUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//  
 10 AF059569  
 F-PLACE1005077  
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)  
 complete sequence.//6.9e-29:253:77//AC004673  
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//  
 15 AC002316  
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-  
 146:734:96//AC005225  
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//  
 AC004476  
 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081  
 F-PLACE1005111  
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, com-  
 plete cds.//0.00051:287:63//L14320  
 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361  
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//  
 AC002451  
 F-PLACE1005176  
 F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey se-  
 30 quence.//0.99:211:63//AQ054651  
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey se-  
 quence.//2.7e-07:80:90//AQ074445  
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061  
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//  
 35 0.70:245:63//AC004965  
 F-PLACE1005243  
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812  
 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98//Z70695  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182  
 40 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183  
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//  
 M25757  
 F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole  
 Cg14.//1.0:128:67//AJ233621  
 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167  
 F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116  
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//  
 AC004794  
 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 5.5e-114:237:92//AC000380  
 F-PLACE1005373  
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//  
 AF017104  
 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991  
 F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6,  
 WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854  
 F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581

F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191

F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878

F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885

F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394

F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589

F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485

F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038

F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860

F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925

F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354

F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//9.3e-113:536:97//AC004707

F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504

F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517

F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126

F-PLACE1005603

F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589

F-PLACE1005623

F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840

F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255

F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618

F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667

F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422

F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147

F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635

F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-25:290:75//AQ136844

F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200

F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517

F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827

F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-126:636:96//AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482

F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150

F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-105, complete sequence.//0.00080:663:58//AL010283

5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153

F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432

F-PLACE1005851

10 F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931

F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226

F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892

15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136

F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026

F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151

20 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405

F-PLACE1005932

F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpg165g2.ft1a.//8.3e-43:247:93//Z57153

25 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719

F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236

30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070

F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925

F-PLACE1005968

35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090

F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

40 F-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521

F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023

F-PLACE1006129

F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597

F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

55 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750

F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239

5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433

F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658

10 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125

F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931

F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803

15 F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880

F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327

F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142

20 F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548

F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447

25 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320

F-PLACE1006318

F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454

30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721

F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504

F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559

35 F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082

F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232

F-PLACE1006382

F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085

40 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129

45 F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ 103347

F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496

F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118

50 F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977

F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744

F-PLACE1006492

F-PLACE1006506

55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083

F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510  
 F-PLACE1006540  
 F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998  
 F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:  
 5 77//AC006044  
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
 6.7e-167:781:99//U97670  
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete  
 sequence.//0.98:514:59//AC004470  
 10 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589  
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//  
 AC004015  
 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276  
 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
 15 DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688  
 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete  
 cds.//0.00011:184:64//AF029790  
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:  
 380:62//U67916  
 20 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-IN-  
 TERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-  
 78:520:86//Z98048  
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer/1.9e-135:378:99//  
 AC005626  
 25 F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey se-  
 quence.//0.018:147:66//AQ039246  
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:  
 823:58//AE001426  
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//  
 30 0.043:252:65//AC005487  
 F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559  
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//  
 M68513  
 35 F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete  
 sequence.//6.7e-05:391:62//AL010272  
 F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915  
 F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
 DRAFT SEQUENCE.//0.89:465:58//AL031033  
 40 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230  
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160  
 nt].//0.011:145:68//S69350  
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559  
 F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING  
 45 DRAFT SEQUENCE.//1.5e-132:643:98//AL033378  
 F-PLACE1006878  
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//  
 Z95120  
 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter se-  
 50 quence.//2.7e-19:171:81//U21672  
 F-PLACE1006904  
 F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read  
 cpg79g10.ft1a.//1.3e-21:131:98//Z63175  
 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063  
 55 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen  
 gene families.//0.85:161:63//AF029308  
 F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447  
 F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//

U23921

F-PLACE1006961//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//*H.sapiens* ir1B mRNA.//7.1e-15:202:71//X63417

5 F-PLACE1006966//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

10 F-PLACE1007014//*Rattus norvegicus* equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat\*.//6.2e-131:775:89//Z82899

15 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.3e-131:652:97//AC005224

20 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//*Mus musculus* muskelin mRNA, complete cds.//4.1e-124:687:91//U72194

25 F-PLACE1007111//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

30 F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

35 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

40 F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082

F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

45 F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//*Fugu rubripes* GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//*F.rubripes* GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//AL011743

50 F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//*Dictyostelium discoideum* gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

55 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077



F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167

F-PLACE1007386

F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117

F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302

F-PLACE1007484

F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370

F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311

F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//3.6e-139:477:98//AC004231

F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461

F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280

F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561

F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240

F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665

F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183

F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.0:386:59//AC005245

F-PLACE1007621

F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006064

F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132

F-PLACE1007649

F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755

F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120

F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452

F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483

F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662

F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243

F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510:58//AB005231

F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585

F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484

F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING

DRAFT SEQUENCE.//0.63:241:58//AL031749

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438

F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903

F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010

F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309

F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271

F-PLACE1007877

F-PLACE1007897

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956

F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097

F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529

F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758

F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695

F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628

F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840

F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719

F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883

F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883

F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163

F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867

F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586

F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199

F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849

F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397

F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450

F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-

162:791:97//AC005069

F-PLACE1008209

F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332

F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317

F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987

F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123

F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913

F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779

F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432

F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176

F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579

F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352

F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512

F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.4e-11:403:64//AC005856

F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417

F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326

F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688

F-PLACE1008424

F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864

F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317

F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479

F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589

F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526

F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014

F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494

F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778

F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555

F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997

F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571

F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077

F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373

5 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967

F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836

F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732

10 F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356

F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23 :299:64//D38595

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333

15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732

F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406

F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199

20 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260

F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25 :244:71//AC003037

25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543

F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549

F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643

30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933

F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668

F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920

35 F-PLACE1008854

F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209

F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539

40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308

F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042

45 F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312

F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309

F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences.//5.9e-15:710:60//M34651

F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727

50 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117

F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137

55 F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861

F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1.//4.7e-70:463:80//D00766

F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241

F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073

5 F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919

F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence.//0.027:630:58//AC006016

F-PLACE1009094

F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85:726:76//M36515

10 F-PLACE1009110

F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752

F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586

15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:59//D25215

F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929

F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031

20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair.//1.0:173:60//X52222

F-PLACE1009166

F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070

25 F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805

F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.//0.053:388:60//AB008266

F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242

30 F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881

F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198

F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203

35 F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945

F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024

F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192

40 F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399

F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015

F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811

45 F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311

F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:74//M27878

50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494

F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.6e-150:701:99//AC005919

F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:88//AF046700

55 F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//0.012:582:56//AL022022

F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872

F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.9e-31:264:81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I30536

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//1.9e-142:704:97//AC004531

F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:235:68//AC004601

F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.9e-83:171:92//U91321

F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160

F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//AF041862

F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587

F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869

F-PLACE1009581

F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959

F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049

F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824

F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157

F-PLACE1009621

F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248

F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308

F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159

F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534

F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011

F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109

F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024

F-PLACE1009794

F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620

F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431

F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369

F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-

QUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925

F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928

F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636

F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//2.4e-15:197:72//AC004973

F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967

F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829

F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710

F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675

F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492

F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677

F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831

F-PLACE1010579//Homo sapiens full-length insert cDNA YI23D12.//3.9e-19:147:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308

F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107

F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872

F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609

F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921

F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061

F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221

F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384

F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380

F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229

F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868



F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182  
 F-PLACE1010891  
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-  
 26:394:68//AC003997  
 F-PLACE1010900  
 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687  
 F-PLACE1010917  
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING  
 DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126  
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243  
 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247  
 F-PLACE1010947  
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey se-  
 quence.//2.1e-29:190:91//B98965  
 F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete  
 sequence.//0.00074:421:60//AL010226  
 F-PLACE1010965//CIT-HSP-2386K24:TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey se-  
 quence.//1.8e-84:412:99//AQ240696  
 F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete  
 sequence.//0.00037:257:64//AL008972  
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-  
 06:315:65//AC005348  
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669  
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636  
 F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING  
 DRAFT SEQUENCE.//3.8e-27:196:84//AL031686  
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049  
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:  
 100//S75548  
 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING  
 DRAFT SEQUENCE.//5.1e-80:479:89//AL031687  
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//  
 2.3e-24:192:84//L14684  
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249  
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//  
 0.010:345:60//B19698  
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey se-  
 quence.//0.00013:95:76//AQ109305  
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:  
 87//AC004893  
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443  
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-  
 43:447:72//AC002288  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//  
 3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965  
 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey se-  
 quence.//2.4e-20:119:100//AQ279801  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//  
 AC005014  
 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y37D8,  
 WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770

F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647

5 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.rt1b.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290

10 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310

15 F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

20 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

25 F-PLACE1011503

F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

30 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477

35 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729

40 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374

45 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

50 F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

55 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003

F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147

5 F-PLACE1011874//Homo Sapiens Chromosome X clone bW XD312, complete sequence.//2.5e-141:678:98//AC004478

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

10 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

15 F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054

20 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256

F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837

F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

25 F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

30 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

40 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

50 F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

55 F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

## EP 1 074 617 A2

F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166

5 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070

F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995

F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701

F-PLACE2000170

10 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005

F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//0.98:201:64//AC004032

F-PLACE2000187

15 F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58/B75888

F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003

20 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577

F-PLACE2000274//Anthodiaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308

25 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//US2064

F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021

F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747

30 F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554

35 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829

F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006

F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849

40 F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973

F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182

45 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776

F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909

50 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:63//X06967

F-PLACE2000399

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238

55 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984

F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792

F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949

F-PLACE2000427

F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:67//AC005821

F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999

F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492

F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025

F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300

F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740

F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037

F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602

F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187

F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075

F-PLACE3000029

F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267

F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368

F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006

F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670

F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668

F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//AC005695

F-PLACE3000136

F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520

F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662

F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053

F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474

F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:98//AC005277

F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682

F-PLACE3000157

F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878

F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130

F-PLACE3000194

F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352

F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207

F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013

F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982

F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.2e-135:721:91//AC005231

F-PLACE3000226

F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548

F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328

F-PLACE3000310

F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379

F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:68//AC005822

F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642

F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055

F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732

F-PLACE3000353

F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

0.0018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284

F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence.//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843

F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08 :692:60//I39845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131

F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926

F-PLACE4000052//M.musculus abcl mRNA.//1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311

F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158

F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430

F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673

F-PLACE4000252

F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200

F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259

F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075

F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296

F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661

F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649

F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540

F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984

F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200

F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346

F-PLACE4000450

F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065

F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//4.1e-34:351:70//AC005821

F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537

F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865

F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929

F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645

F-PLACE4000548

F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747

F-PLACE4000581

F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474

F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418

F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281

F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039

F-PLACE4000650

F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267

F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816

F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554

F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616

F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797

F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561

F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637

F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353

F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383

F-THYRO1000040

F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383

F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557

F-THYRO1000085

F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606

F-THYRO1000107



F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403

F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055

5 F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142

F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096

10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331

F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419

15 F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214

F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746

20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552

F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134

F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157

25 F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186

F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156

F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055

30 F-THYRO1000270

F-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068

F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894

35 F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233

F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091

40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080

F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

45 F-THYRO1000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

F-THYRO1000401 3.2e-116:504:80//AF051908

F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

50 F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740

F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

F-THYRO 1000505

F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYRO1000570

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-68:468:84//AC005696

F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

F-THYRO1000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPCI1-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYRO1000843

F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:

64//AF008573

F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477

F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015

F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529

F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836

F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

F-THYRO1000952

F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846

F-THYRO1000975//Plasmodium falciparum Topoll gene.//0.32:491:58//X79345

F-THYRO1000983//Mvuf9A3 exon amplification products from BACs in Mvuf region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313

F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYRO1001003

F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787

F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYRO1001173

F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953

F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496

F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086

F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693

F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114  
 F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025  
 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288  
 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:  
 74//AC004905  
 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//  
 7.6e-168:821:97//AC005660  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607  
 10 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//  
 AC005239  
 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE,  
 48 unordered pieces.//3.6e-70:360:86//AC005845  
 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852  
 15 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:  
 82//AF064635  
 F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//  
 AC006126  
 F-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chro-  
 20 mosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553  
 F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered piec-  
 es.//1.0:98:70//AC000384  
 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265  
 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 25 7.5e-42:357:80//AC006001  
 F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449  
 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3  
 unordered pieces.//4.8e-47:266:80//AC004666  
 F-THYRO1001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING  
 30 DRAFT SEQUENCE.//1.3e-79:479:89//AL031687  
 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an  
 STS and GSSs, complete sequence.//0.0034:106:77//Z96074  
 F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056  
 F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey se-  
 35 quence.//1.4e-65:384:91//AQ052105  
 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572  
 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey se-  
 quence.//1.3e-24:180:88//AQ080498  
 F-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 40 DRAFT SEQUENCE.//8.7e-145:779:93//AL023808  
 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//2.9e-26:393:68//  
 AC005863  
 F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576  
 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381  
 45 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
 6.2e-15:318:66//AC004950  
 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//  
 AC004827  
 F-THYRO1001661  
 50 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//  
 AJ225089  
 F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071  
 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857  
 F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:  
 55 75//AC004745  
 F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500  
 F-THYRO1001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING  
 DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYRO1001745

F-THYRO1001746

F-THYRO1001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021

F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626  
F-THYRO 1001809

F-THYRO1001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526

F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664

F-THYRO1001895

4.4e-13:248:68//AB012576

F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058

F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749

F-Y79AA1000013

F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027

F-Y79AA1000037//Human prot-oncogene (BML-1) mRNA, complete cds.//2.4e-19:230:66//L13689

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521

F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005

F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893

F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864

F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115

F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854

F-Y79AA1000230

F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232

F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//0.0099:547:58//U78522

F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207

F-Y79AA1000313

F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085

F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511

F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987

F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692

F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484

F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610

F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747

F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061

F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378

F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736

F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693

F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980

F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503

F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193

5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972

F-Y79AA1000574//M.musculus tex23 mRNA (5'region).//1.8e-23:291:75//X80424

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503

10 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942

F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080

F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172

F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023

F-Y79AA1000774

15 F-Y79AA1000782

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799

F-Y79AA1000794//H.sapiens CpG island DNA genomic MseI fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085

20 F-Y79AA1000802

F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642

F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538

F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING

25 DRAFT SEQUENCE.//1.5e-08:249:69//AL022315

F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757

F-Y79AA1000850

F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203

30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314

F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253

F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397

35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165

F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329

40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682

F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701

F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314

45 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452

F-Y79AA1001078

F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173

F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015

50 F-Y79AA1001167

F-Y79AA1001177//M.musculus mRNA for NfiX1-protein.//4.0e-10:398:64//Y07688

F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015

55 F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492

F-Y79AA1001216

F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//

AL021841

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497

F-Y79AA1001299//Human Ini1 mRNA, complete cds.//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183

F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151

F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267

F-Y79AA1001581//FMR1 [CGG repeats] [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583

F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468

F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743

F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136

F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943

F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017

F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.//2.6e-13:88:100//Z64565

F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654

F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186

5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184

F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340

10 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214

F-Y79AA1002089

F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548

15 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014

F-Y79AA1002115

F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693

F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358

20 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260

F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397

F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719

25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615

F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043

30 F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738

F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592

F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015

35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555

F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886

F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534

F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877

F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101

40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208

F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920

F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662

45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385

F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196

F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917

50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116

F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022

F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

55 Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

[0304] Data include



the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0305]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

**[0306]** Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953  
 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864  
 R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240  
 R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696  
 R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948  
 R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520  
 R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684  
 R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104  
 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340  
 R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060  
 R-nnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631  
 R-HEMBA1000158  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904  
 R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146  
 R-HEMBA1000193  
 R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126  
 R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655  
 R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181  
 R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526  
 R-HEMBA1000244  
 R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262  
 R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012  
 R-nnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037  
 R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270  
 R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046  
 R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223  
 R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105  
 R-nnnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131  
 R-nnnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496  
 R-nnnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505  
 R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
 5 DRAFT SEQUENCE.//2.0e-33:399:72//AL031667  
 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing  
 Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147  
 R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829  
 R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086  
 10 R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//  
 AC006012  
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene sim-  
 ilar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS  
 and a CpG island, complete sequence.//1.9e-69:355:97//AL031587  
 15 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-  
 66:410:89//AC006116  
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 un-  
 ordered pieces.//2.0e-43:363:81//AC002993  
 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//  
 20 AC005053  
 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//  
 AC004582  
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains  
 inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575  
 25 R-HEMBA1000411  
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465  
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey se-  
 quence.//4.4e-12:98:92//AQ078233  
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,  
 30 complete sequence.//2.0e-93 :526:90//Z95400  
 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 2.7e-07:452:60//AC004826  
 R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733  
 R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, com-  
 35 plete sequence.//2.6e-05:174:70//AL010226  
 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-bind-  
 ing protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane  
 protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, com-  
 plete cds; and unknown genes.//0.013:212:63//AF049236  
 40 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//  
 AC004839  
 R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220  
 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//  
 AC005104  
 45 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500  
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278  
 R-HEMBA1000491  
 R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, com-  
 plete sequence.//1.7e-08:440:60//AL009014  
 50 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858  
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chro-  
 mosome X.//1.1e-25:248:80//Z70280  
 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey se-  
 55 quence.//0.0035:293:61//B49544  
 R-HEMBA1000519  
 R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//  
 0.30:255:63//AC006232

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

5 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

10 R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

15 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

R-HEMBA1000568//RPC11-49P8.TK.1 RPC11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

R-nnnnnnnnnnnn

20 R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411AJ007509

25 R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

30 R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4, reverse read cpg155e4.r1a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

45 R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850

50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

55 R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

10 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

15 R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

20 R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-nnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

25 R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004

R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046

30 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318

R-HEMBA1001080

R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586

35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105

R-HEMBA1001099

R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527

40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833

R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551

R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511

R-HEMBA1001133

R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241

45 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077

R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304

R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398

50 R-HEMBA1001197

R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

55 R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666

R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

- R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905
- R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491
- 5 R-nnnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042
- R-HEMBA1001286
- R-HEMBA1001289
- 10 R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882
- R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222
- R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258
- 15 R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744
- R-HEMBA1001310
- R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504
- 20 R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240
- R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368
- 25 R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509
- R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
- 30 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238
- R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241
- R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542
- 35 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
- R-HEMBA1001383
- R-HEMBA1001387
- R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073
- 40 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960
- R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050
- R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380
- 45 R-HEMBA1001407
- R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981
- R-HEMBA1001413
- R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732
- 50 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146
- R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054
- 55 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527
- R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385

R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065

5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855

R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//2.7e-08:316:62//AC005324

10 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//0.57:219:60//AC005208

R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840

R-HEMBA1001478

R-HEMBA1001497

15 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337

R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753

20 R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549

R-HEMBA1001522

R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258

25 R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053

R-HEMBA1001557

R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383

R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040

30 R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453

R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506

R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276

R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012

35 R-HEMBA1001589

R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483

R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177

40 R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693

R-nnnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688

R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270

45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484

R-nnnnnnnnnnnn

R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368

50 R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808

R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740

55 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247

R-HEMBA1001675

R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593

R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801

5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598

R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886

R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577

10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250

R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781

R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261

15 R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799

R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959

20 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067

R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084

25 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153

R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//3.8e-39:331:80//AC006121

R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554

30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740

R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575

35 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222

R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506

R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977

40 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969

R-HEMBA1001809

R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025

45 R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612

R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107

R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118

50 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107

R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507

R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871

R-HEMBA1001847

55 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517

R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138



R-nnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

5 R-HEMBA1001896

R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

R-HEMBA1001913

10 R-HEMBA1001915//HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

15 R-HEMBA1001939//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

20 R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

25 R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

30 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence.//4.9e-06:153:71//AQ240461

35 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

40 R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203

45 R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

50 R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

55 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924  
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378  
 R-HEMBA1002125  
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637  
 5 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase  
 gene, complete sequence.//2.0e-26:323:70//AC005728  
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseu-  
 dogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology  
 to Phorbolins and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG  
 10 islands, complete sequence.//1.0:371:61//AL031846  
 R-HEMBA1002151  
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971  
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene,  
 similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to  
 15 URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054  
 R-HEMBA1002161//CIT-HSP-2163F10. TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey se-  
 quence.//3.1e-58:284:80//B89969  
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789  
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-  
 20 53:326:80//AC002980  
 R-HEMBA1002177  
 R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING  
 DRAFT SEQUENCE.//9.5e-37:356:76//AL033532  
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete  
 25 sequence.//3.4e-43:244:77//AC003684  
 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-  
 37:323:78//AC005077  
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498  
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete se-  
 30 quence.//1.5e-31:313:71//AC000053  
 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase  
 subunit 8.//0.0023:346:60//X57546  
 R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989  
 R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING  
 35 DRAFT SEQUENCE.//4.6e-46:375:77//AL033529  
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//  
 AF089814  
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library)  
 complete sequence.//4.3e-26:469:67//AC004242  
 40 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//  
 AC005016  
 R-HEMBA1002257  
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//  
 AF03 8127  
 45 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//  
 AC000057  
 R-HEMBA1002321  
 R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617  
 50 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, com-  
 plete cds.//3.7e-07:328:63//U23811  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314  
 R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS,  
 STS, complete sequence.//3.7e-07:587:58//AL031256  
 55 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438  
 R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:  
 661:93//AF092563  
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and

non-small cell lung cancer , segment 11/11.//1.1e-70:559:79//AB020868

R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602

R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954

R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848

R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276

R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:183:80//AC006026

R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819

R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378

R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068

R-nnnnnnnnnnnnn

R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841

R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573

R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762

R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//2.8e-22:210:78//AC004963

R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//AC003043

R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213

R-nnnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972

R-HEMBA1002515

R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923

R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792

R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658

R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378

R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957

R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409

R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634

R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587

R-HEMBA1002583

R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152

R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510

R-HEMBA1002621

R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351

R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275

R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247

R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567

R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839

R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323

R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772

R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008

R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORK-

ING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421

R-nnnnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281

R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:146:70//AC004503

R-HEMBA1002696

R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982

R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873

R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521

R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109

R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525

R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694

R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883

R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810

R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126

R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140

R-HEMBA1002777

R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139

R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344

R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560

R-HEMBA1002801//Meloiodogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185

R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043

R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041

R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:97//AC004707

R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506

R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:85//AC005562

R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557

R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261

R-HEMBA1002921

R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 7/10.//4.6e-19:139:78//AB020875

R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681

R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584

R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532

R-HEMBA1002939

R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952

R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020

R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005

R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.2e-38:300:83//AC005553

5 R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012

R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579

R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128

R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386

10 R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614

R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406

15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194

R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026

R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839

20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694

R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983

25 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182

R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962

R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302

30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136

R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975

35 R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054

R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673

40 R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798

R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039

R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213

45 R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598

R-HEMBA1003117

R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329

50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472

R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861

R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024

55 R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670

R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459  
R-HEMBA1003197  
R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162  
5 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
5.4e-44:291:83//AC005480  
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//  
AC000118  
10 R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:  
118:69//AC006148  
R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0:00014:59:91//AQ128202  
R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y43F8,  
WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393  
15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey  
sequence.//0.42:167:64//B83610  
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey se-  
quence.//3.6e-36:195:81//AQ037231  
20 R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356  
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709  
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete se-  
quence.//1.0e-32:255:84//AC002549  
25 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308  
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library)  
complete sequence.//1.1e-34:286:74//AC002395  
R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
ordered pieces.//1.8e-53:428:83//AC005840  
30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109  
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey se-  
quence.//2.9e-20:337:65//AQ003073  
R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662  
R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete se-  
35 quence.//0.00019:334:60//AB017061  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//  
AB001872  
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,  
GSS, complete sequence.//0.60:274:61//AL022153  
40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//  
AC005099  
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//  
2.2e-44:268:90//AC005081  
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//  
45 AF026029  
R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567  
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600  
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//  
AC002558  
50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alter-  
natively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a  
PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta,  
PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs,  
STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721  
55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:  
309:88//AC004651  
R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212

R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993

5 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549

R-nnnnnnnnnnnnn

R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321

10 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879

R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696

R-HEMBA1003461

15 R-HEMBA1003463

R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041

R-HEMBA1003528

R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454

20 R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701

R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453

R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153

25 R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718

R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913

R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416

30 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036

R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450

R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914

35 R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ209302

R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123

R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774

40 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715

R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480

45 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153

R-HEMBA1003615

R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139

50 R-HEMBA100362111\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599

R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980

55 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219

R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454

R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693

R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559

5 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222

10 R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872

15 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406

20 R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353

25 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699

R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634

30 R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876

35 R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259

40 R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1 e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596

45 R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781

50 R-HEMBA1003807//Bovine dinucleotide microsatellite HUII77.//5.4e-18:194:78//M96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624

55 R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929

R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300



R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

5 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

10 R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

15 R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368

R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718

R-HEMBA1003939

R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904

20 R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619

R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560

R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668

25 R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132

R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414

R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060

30 R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

35 R-HEMBA1004000

R-HEMBA1004011

R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575

40 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016

45 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

50 R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

55 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ003810, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence.//0.56:379:59//AQ277616

R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855

R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569

R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552

R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304

R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488

R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748

R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275

R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927

R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763

R-HEMBA1004241

R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011

R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903

R-HEMBA1004264

R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854

R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831

R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081

R-HEMBA1004276

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795

R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence.//2.3e-37:248:76//AQ266668

R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174

R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206

R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088

R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611

R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933

R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600

R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987

R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds.//3.3e-14:238:69//AF082024

R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.8e-

21:291:71//AC004638

R-HEMBA1004341

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667

R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002

R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611

R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949

R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811

R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540

R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124

R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057

R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030

R-HEMBA1004408

R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200

R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930

R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846

R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876

R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012

R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370

R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-08:245:66//AC005951

R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487

R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266

R-HEMBA1004509

R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230

R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330

R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329

R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457

R-HEMBA1004573

R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279

R-HEMBA1004586

R-nnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551

R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071

R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//AB007970

R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805

R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866

R-HEMBA1004632

R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534

R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076

R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171

R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432  
 R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING  
 DRAFT SEQUENCE.//4.4e-12:110:88//Z93241  
 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//  
 5 Z99291  
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//  
 0.86:309:57//AB006702  
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//  
 0.29:331:61//B97342  
 10 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559  
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-  
 49:497:76//AC004638  
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.6e-38:362:  
 79//AC005562  
 15 R-HEMBA1004725  
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:  
 79//AC002085  
 R-HEMBA1004733  
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene  
 20 for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island,  
 ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395  
 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017  
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:  
 81//AC004953  
 25 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950  
 R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING  
 DRAFT SEQUENCE.//3.3e-39:281:85//AL031121  
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//  
 30 L06498  
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains his-  
 tone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG  
 island.//1.8e-08:516:59//AL021807  
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:  
 35 72//AC004057  
 R-HEMBA1004763  
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-  
 notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
 40 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310  
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:  
 476:61//AE001371  
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete  
 sequence.//5.0e-08:113:80//AC003047  
 45 R-HEMBA1004776  
 R-HEMBA1004778//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567  
 R-nnnnnnnnnnnn/HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic  
 clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855  
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728  
 50 R-HEMBA1004806  
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-  
 20:333:69//AC005015  
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 55 Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002  
 R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//7.6e-80:297:85//  
 X53744

R-HEMBA1004850

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

R-HEMBA1004864

R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826

R-HEMBA1004889//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:7711AC005972

R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

R-HEMBA1004918//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755

R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic-clone 2021I16, genomic survey sequence.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224

R-HEMBA10050087//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548

R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),

H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179  
R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:94//AC004596

5 R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650  
R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819  
R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404

10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//AC004675  
R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030  
R-HEMBA1005075

15 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156  
R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423  
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

20 R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340  
R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336

25 R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345  
R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834

30 R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407  
R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279  
R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276  
R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205  
R-HEMBA1005219  
R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854

40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617  
R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154  
R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

45 R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548  
R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.6e-105:437:97//AC005837

50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630  
R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914  
R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887

55 R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120  
R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//

1.5e-58:445:78//AC006146

R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389

R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030

R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.9e-112:577:95//AC005803

R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722

R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412

R-HEMBA1005367//RPCI11-85E23.TV RPCI11 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915

R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997

R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142

R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379

R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722

R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524

R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320

R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384

R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.8e-84:309:99//AB020860

R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431

R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631//AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538

R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171

R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499

R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//2.2e-28:262:79//AC005746

R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446

R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13O15, genomic survey sequence.//1.0e-28:153:82//B73293

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450

R-HEMBA1005680//Homo sapiens Chr. 14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406

R-HEMBA1005705//RPCI11-13O14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13O14, genomic survey sequence.//0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.



Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

R-nnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//5.4e-79:403:97//AQ147357

R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

R-nnnnnnnnnnnn

R-HEMBA1006081

R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

R-HEMBA1006091

R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains syn-apsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113

R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

R-nnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217

R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

R-HEMBA1006259//RPC111-44N14.TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

R-HEMBA1006268

R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//AL023753

R-nnnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770

R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240

R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//0.97:447:59//AC004585

R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161

R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415

R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412

R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183

R-HEMBA1006328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429

R-HEMBA1006334

R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945

R-HEMBA1006347//Human prostaticin gene, complete cds.//1.8e-78:170:100//U33446

R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682

R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951

R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080

R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239

R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989

R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//1.5e-47:336:86//AC005914

R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609

R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence.//4.4e-37:319:76//AC002119

R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253

5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//4.1e-116:572:97//AF107885

R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:578:97//AL031781

10 R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017

R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162

15 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075

R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398

R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364

20 R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//11.1e-14:354:63//AC002052

R-HEMBA1006471

R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502

25 R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701

R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089

30 R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989

R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//4.3e-112:572:95//AC005828

35 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994

R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015

R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929

40 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566

R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304

45 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526

R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525

R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007

50 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603

R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.4e-64:551:78//U06944

R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554

55 R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421

R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357

R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032

R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875

R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709

5 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031

R-HEMBA1006612

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737

10 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudo-genes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284

R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 202O8, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848

15 R-HEMBA1006635//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572

R-HEMBA1006639

R-HEMBA1006643

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282

20 R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089

R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390

R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625

25 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776

R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551

R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608

30 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096

R-HEMBA1006696

R-HEMBA1006708

R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674

35 R-HEMBA1006717

R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828

R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108

40 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951

R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752

45 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551

R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.3e-46:305:87//AC005701

R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323

50 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317

R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.1e-43:355:801//AC006120

R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483

55 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854

R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//3.0e-08:84:90//AC004797

R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023

R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//0.70:206:65//AC005668

5 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217

R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074

R-nnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026

R-HEMBA1006885 4.2e-14:379:63//AG006839

10 R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395

R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154

R-HEMBA1006926

15 R-HEMBA1006929//HS\_3244\_A2\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500

R-HEMBA1006936

R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853

R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841

R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518

25 R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302

R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701

R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271

30 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406

R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558

R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.6e-41:437:71//AC005277

35 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088

R-HEMBA1007045

R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006

R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056

40 R-HEMBA1007062

R-HEMBA1007066

R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//2.0e-66:476:85//AC006141

R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//1.0e-38:179:82//AC005325

45 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015

R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385

R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803

50 R-HEMBA1007113//Homo sapiens (subclone 6\_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392

R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

R-HEMBA1007147//H.sapiens CpG island DNA genomic MseI fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246

55 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239

R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//

AC004875

R-nnnnnnnnnnnnn//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-103:529:94//AF062085

R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//AC005911

5 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39:262:80//AC003035

R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61:332:95//D86987

R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:436:81//Z93023

10 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96:471:97//AB018340

R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//0.011:349:62//AC004777

R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence.//2.8e-10:224:70//AC004856

15 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:362:86//AC005924

R-HEMBA1007273

R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//AJ235273

20 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.99:288:60//AJ235272

R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4e-107:554:95//AL031003

R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U39994

25 R-HEMBA1007301

R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08:524:58//Y14425

R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043

R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383:85//AC005251

30 R-HEMBA1007327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804

R-HEMBA1007341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL023513

35 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence.//1.7e-15:190:73//AC003080

R-HEMBA1007347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802

R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-62:539:79//AC006208

40 R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//1.2e-36:285:83//AC003665

R-HEMBA1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:416:79//AC004820

45 R-HEMBA1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-18:211:79//Z95113

R-HEMBA1000025//HS\_3064\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765

R-HEMBA1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.//1.5e-32:452:70//Z85986

50 R-HEMBA1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264

R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928

55 R-HEMBA1000039//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.4e-44:456:68//AC005291

R-HEMBA1000044//Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064

R-HEMBA1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-

09:330:63//AC002300

R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM BB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM BB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM BB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM BB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM BB1000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM BB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM BB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM BB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM BB1000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134

R-HEM BB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM BB1000175

R-HEM BB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM BB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM BB1000217

R-HEM BB1000218//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM BB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEM BB1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

5 R-HEM BB1000284//Homo sapiens full-length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018

R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM BB1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

10 R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

15 R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605

20 R-HEM BB1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681

R-HEM BB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

25 R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644

R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751

R-HEM BB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence.//9.0e-25:179:79//AC004067

30 R-HEM BB10003741//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199

R-HEM BB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675

R-HEM BB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080

35 R-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838

R-HEM BB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

40 R-HEM BB1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251

R-HEM BB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053

R-HEM BB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069

45 R-HEM BB1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700

R-HEM BB1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207

50 R-HEM BB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920

R-HEM BB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007

R-HEM BB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

55 R-HEM BB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849

R-HEM BB1000487



R-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423

R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023

5 R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

10 R-HEM BB1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397

R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477

15 R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079

R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//4.2e-74:428:92//AC006236

R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321

20 R-HEM BB1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824

R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786

R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914

25 R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405

R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//7.2e-52:260:80//AC003695

R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280

30 R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//1.3e-14:409:65//AC005208

R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184

35 R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831

R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381

R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717

40 R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724

R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058

45 R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176

R-HEM BB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085

R-HEM BB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112

50 R-HEM BB1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993

R-HEM BB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061

R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031

55 R-HEM BB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence.//0.98:251:63//AB005247

R-HEM BB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chro-

mosome X.//6.8e-58:296:85//Z83313

R-HEM BB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731

R-HEM BB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584

R-nnnnnnnnnnnnn/Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723

R-HEM BB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

R-HEM BB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM BB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

R-HEM BB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071

R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

R-HEM BB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046

R-HEM BB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey sequence.//3.0e-09:299:64//B63628

R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740

R-HEM BB1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM BB1000807

R-HEM BB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM BB1000821

R-HEM BB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944

R-HEM BB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043

R-HEM BB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017

R-HEM BB1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850

R-HEM BB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368

R-HEM BB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283

R-HEM BB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086

R-HEM BB1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816

R-HEM BB1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523

R-HEM BB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474

R-HEM BB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//

AC005621

R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061

R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

5 R-HEM BB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM BB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

10 R-HEM BB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEM BB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024

R-HEM BB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037

15 R-HEM BB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739

R-HEM BB1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015

R-HEM BB1000927

20 R-HEM BB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228

R-HEM BB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098

25 R-HEM BB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//0.038:377:58//AC005560

R-HEM BB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234

R-HEM BB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443

30 R-HEM BB1000985//HS\_3184\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008

R-HEM BB1000991

R-HEM BB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368

35 R-HEM BB1001004

R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056

R-HEM BB1001011//HS\_3017\_B1\_G03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944

40 R-HEM BB1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549

R-HEM BB1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475

45 R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527

R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699

R-HEM BB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586

50 R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014

R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187

55 R-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973

R-HEM BB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375

R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

R-HEM BB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735

R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577

R-HEM BB1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431

R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570

R-HEM BB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113

R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071

R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495

R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077

R-HEM BB1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222

R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564

R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904

R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766

R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070

R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055

R-HEM BB1001177

R-HEM BB1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226

R-HEM BB1001199

R-HEM BB1001208

R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098

R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199

R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158

R-HEM BB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950

R-HEM BB1001234

R-HEM BB1001242

R-HEM BB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377

R-HEM BB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089

R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461

R-HEM BB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046

R-HEM BB1001271//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544

R-HEM BB1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428

R-HEM BB1001288

R-HEM BB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-

31:301:78//AC005601

R-HEM BB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083

R-HEM BB1001302

R-HEM BB1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397

R-HEM BB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293:86//AG013777

R-HEM BB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511

R-HEM BB1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//2.3e-39:301:82//AC004585

R-HEM BB1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096

R-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850

R-HEM BB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037

R-HEM BB1001337

R-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056

R-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441

R-HEM BB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859

R-HEM BB1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207

R-HEM BB1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940

R-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876

R-HEM BB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326

R-HEM BB1001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686

R-HEM BB1001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896

R-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314

R-HEM BB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953

R-HEM BB1001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//1.4e-55:494:76//AC005549

R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204

R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370

R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350

R-HEM BB1001429//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160

R-HEM BB1001436

R-HEM BB1001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934

R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522

R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:299:84//AC005355

R-HEM BB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430

R-HEMBB1001463//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154

R-HEMBB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941

5 R-HEMBB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762

R-HEMBB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801

R-HEMBB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642

10 R-HEMBB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000

R-HEMBB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070

R-HEMBB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581

15 R-HEMBB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169

R-HEMBB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394

R-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049

R-HEMBB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267:88//AC002301

20 R-HEMBB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225

R-HEMBB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840

25 R-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677

R-HEMBB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236

30 R-HEMBB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106

R-HEMBB1001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302:59//AL010235

R-HEMBB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503:68//Z93023

35 R-HEMBB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368

R-HEMBB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062

40 R-HEMBB1001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407:69//AC004075

R-HEMBB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368

45 R-HEMBB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506

R-HEMBB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344

R-HEMBB1001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572

50 R-HEMBB1001668

R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546

R-HEMBB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429

R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:31:83//AC005411

55 R-HEMBB1001695

R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704

R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851

R-HEM BB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020

R-HEM BB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992

R-HEM BB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613

R-HEM BB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221

R-HEM BB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671

R-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829

R-HEM BB1001753//RPC11-59J22.TK RPC11 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046

R-HEM BB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130

R-HEM BB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050

R-HEM BB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157

R-HEM BB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170

R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140

R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391

R-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882

R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996

R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209

R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328

R-HEM BB1001839

R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241

R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436

R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327

R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754

R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553

R-HEM BB1001872//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027

R-HEM BB1001874

R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272

R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//1.3e-49:461:77//AC005922

R-HEM BB1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858

R-HEM BB1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345

R-HEM BB1001906

R-HEM BB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

R-HEM BB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070

R-HEM BB1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929

5 R-HEM BB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417

R-HEM BB1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422

R-HEM BB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099

10 R-HEM BB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406

R-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//8.3e-12:202:69//AB020867

R-HEM BB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544

15 R-HEM BB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408

R-HEM BB1001947//RPCI11-60L13.TJ RPCI11 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335

R-HEM BB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846

20 R-HEM BB1001952//Homo Sapiens Chromosome X clone bW XD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676

R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037

R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077

25 R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736

R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675

R-HEM BB1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617

30 R-HEM BB1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417

R-HEM BB1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420

35 R-HEM BB1001990//Homo sapiens full-length insert cDNA clone ZC33G03.//7.8e-95:456:99//AF086192

R-HEM BB1001996

R-HEM BB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055

R-HEM BB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816

40 R-HEM BB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903

R-HEM BB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904

R-HEM BB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336

45 R-HEM BB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389

R-HEM BB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612

50 R-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740

R-HEM BB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778

R-HEM BB1002049//Human Chromosome X clone bW XD187, complete sequence.1/1.9e-21:384:64//AC004383

55 R-HEM BB1002050//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//2.5e-37:368:76//AC005553

R-HEM BB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782



R-HEM BB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799

R-HEM BB1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//3.8e-45:307:87//AC005828

5 R-HEM BB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943

R-HEM BB1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279

R-HEM BB1002139//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573

10 R-HEM BB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006

R-HEM BB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881

R-HEM BB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385

15 R-HEM BB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913

R-HEM BB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846

R-HEM BB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148

R-HEM BB1002218//, complete sequence.//3.4e-17:178:82//AC005300

20 R-HEM BB1002232//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599

R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//2.9e-13:227:70//AC005829

R-HEM BB1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING

25 DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

R-HEM BB1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING

30 DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

R-HEM BB1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216

R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534

R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642

35 R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129

R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028

R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313

40 R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849

R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841

R-HEM BB1002358//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366

45 R-HEM BB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038

R-HEM BB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036

50 R-HEM BB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094

R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467

R-HEM BB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182

55 R-HEM BB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091

R-HEM BB1002415//Homo sapiens chromosome 17, clone hRPK.209\_D\_14, complete sequence.//1.4e-25:202:

79//AC005730

R-HEMBB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799

R-HEMBB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046

5 R-HEMBB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349

R-HEMBB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012

10 R-HEMBB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659

R-HEMBB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAll project).//0.42:110:74//AL021635

R-HEMBB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302

15 R-HEMBB1002492//RPC111-74F21.TK RPC111 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960

R-HEMBB1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762

R-HEMBB1002502//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//9.6e-81:538:86//AC006120

20 R-HEMBB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313

R-HEMBB1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309

25 R-HEMBB1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397

R-HEMBB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225

R-HEMBB1002531

30 R-HEMBB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009

R-HEMBB1002545//RPC111-2F3.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283

R-HEMBB1002550

35 R-HEMBB1002556//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160

R-HEMBB1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422

R-HEMBB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968

40 R-HEMBB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163

R-HEMBB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707

R-HEMBB1002600//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865

45 R-HEMBB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223

R-HEMBB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162

R-HEMBB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197

50 R-HEMBB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321

R-HEMBB1002613//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908

55 R-HEMBB1002614//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-10:512:60//AC004801

R-HEMBB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-24:486:63//AC005520

R-HEM BB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953

R-HEM BB1002635//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910

R-HEM BB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090

R-HEM BB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694

R-HEM BB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090

R-HEM BB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//1.7e-18:504:62//AC002430

R-HEM BB1002686//Homo sapiens full-length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217

R-HEM BB1002692//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206

R-HEM BB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153

R-HEM BB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511

R-HEM BB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence.//8.6e-43:351:8011859764

R-HEM BB1002705//Plasmodium yoelii rhoptyr protein, complete cds.//0.0064:454:59//L27838

R-HEM BB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052

R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037

R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720

R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163

R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058

R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090

R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054

R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicro.//0.79:63:77//AF025889

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366

R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867

R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//3.4e-39:297:85//AC003976

R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641

R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882

R-MAMMA1000133

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

5 R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476

10 R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381

15 R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic MseI fragment, clone 186c5, reverse read cpg186c5.r1b.//0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552

20 R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667

R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728

25 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideaemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266

30 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

35 R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656

40 R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549

45 R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

50 R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722

R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.1e-16:169:77//AC005553

55 R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795

R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00020:384:60//AF029779

R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence.//0.0026:310:60//AF003518

R-MAMMA1000313//Human cosmid Xq28\_IA649, complete sequence.//1.5e-26:317:67//U82694  
R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-39:277:86//AC004947  
R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180:89//AF015147  
5 R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.97:293:64//AE001388  
R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72//U85195  
R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.73:332:61//AC002493  
10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//4.6e-80:279:89//AC005189  
R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//7.8e-18:346:63//AL031676  
R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
15 ING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344  
R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING DRAFT SEQUENCE.//1.0e-28:225:84//AL031658  
R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//4.7e-60:298:99//AQ038102  
20 R-MAMMA1000395  
R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence.//1.4e-84:276:88//AC004692  
R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//6.7e-35:360:76//AC002394  
25 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//3.1e-69:327:79//AC004662  
R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains GSS (BAC end sequence), STS.//3.6e-41:180:87//AL009028  
R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.1e-59:478:77//AC005377  
30 R-MAMMA1000421//Human coxVlb gene, last exon and flanking sequence.//5.3e-53:294:82//X58139  
R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//1.0:252:59//AL031737  
R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-50:491:76//AC004816  
35 R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950  
R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484  
R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-58:564:77//AC004821  
40 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83//AC002067  
R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672  
R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//0.99:182:61//AB019236  
45 R-MAMMA1000468  
R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.//1.0e-38:142:88//AG010148  
R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015  
50 R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//4.3e-34:158:86//B54637  
R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90//AC006130  
R-MAMMA1000500//Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds.//1.2e-41:334:79//L78833  
55 R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118  
R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING

DRAFT SEQUENCE.//1.3e-43:318:83//Z82207

R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289

R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015

R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205

R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419

R-MAMMA1000576

R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//5.4e-53:297:85//AC005666

R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018

R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613

R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131

R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956

R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364

R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970

R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573

R-MAMMA1000623

R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498

R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656

R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555

R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578

R-MAMMA1000670

R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785

R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623

R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387

R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075

R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478

R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694

R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366

R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781

R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163

R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077

R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.4e-14:309:68//AC004832

R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722

R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507

5 R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115

R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence.//0.095:367:60//B20150

R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661

10 R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178

R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169

15 R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454

20 R-MAMMA1000778//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120

R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042

25 R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807

30 R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726\_O\_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323

R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985

35 R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815

R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744

40 R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461

45 R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364

50 R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301

R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653

55 R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658

R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains

ESTs STS and CpG island.//3.2e-34:354:75//Z93023

R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425

R-MAMMA1000883

R-MAMMA1000897

R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506

R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110

R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024

R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247

R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379

R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777

R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046

R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347

R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383

R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477

R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096

R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001

R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

R-nnnnnnnnnnnnn

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125



R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone NH0400O10 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWDX173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo-sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862

R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

5 R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

10 R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.5e-38:306:83//AC005703

15 R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

20 R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041

25 R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685

R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

R-MAMMA1001388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707

30 R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044

R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805

35 R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928

R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957

R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179

40 R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126

R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047

R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491

45 R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//AL024493

R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295

50 R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783

R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108\_L\_11, complete sequence.//5.1e-30:286:79//AC005206

55

R-MAMMA1001501

R-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714

R-MAMMA1001510

R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352

R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418

R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997

R-MAMMA1001575

R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764

R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027

R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216

R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238

R-MAMMA1001606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985

R-MAMMA1001620//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650

R-MAMMA1001627//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090

R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399

R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.2e-21:241:70//AC005386

R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811

R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216

R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614

R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393

R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 un-ordered pieces.//5.7e-47:533:72//AC004166

R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261

R-MAMMA1001692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345

R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324

R-MAMMA1001715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330

R-MAMMA1001730

R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:382:63//X60786

R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050

R-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//4.0e-108:566:95//AC006017

R-MAMMA1001744

R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//3.5e-113:564:97//AF070718

R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence.//3.6e-30:312:75//

AC005625

R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338

R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4\_G\_17, complete sequence.//4.7e-10:244:67//AC003688

R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432

R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60//AC005140

R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//1.6e-42:416:76//AC005332

R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.4e-13:129:83//AC004686

R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991

R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360

R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:282:86//U91319

R-MAMMA1001788

R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//9.8e-43:530:71//AC004913

R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020

R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:183:63//AE001432

R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:417:62//AC005018

R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859

R-MAMMA1001818

R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//AC004086

R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-53:291:85//AC004966

R-MAMMA1001836//HS\_3164\_B1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484

R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682

R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//AC006144

R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099

R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425

R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//6.5e-50:283:86//U80460

R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143

R-nnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:495:63//AE001417

R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117

R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKNA1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996

R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097

R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 ~complete genomic se-

quence, complete sequence.//1.7e-43:283:86//AC002303

R-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720

R-nnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373

R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008

R-MAMMA1001956//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380

R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149

R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128

R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071

R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581

R-MAMMA1002009//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879

R-MAMMA1002011

R-MAMMA1002032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284

R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954

R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865

R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318

R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318

R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506\_H\_21, complete sequence.//6.6e-48:367:82//AC005962

R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052

R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXd171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676

R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.3e-22:357:64//AC005291

R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263

R-MAMMA1002084//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602

R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey sequence.//9.7e-17:129:88//B69983

R-MAMMA1002108

R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495

R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.8e-40:313:83//AC005670

R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953

R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801

R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357

R-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447

R-MAMMA1002153//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0281M17; HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.1e-51:291:75//AC006052

R-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 608E8, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL022343

R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997

R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418

R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588

R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.2e-23:269:74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158

R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802

R-MAMMA1002230//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253

R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//2.8e-119:582:98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-33:571:67//AC006120

R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749

R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey sequence.//4.7e-05:153:69//B15590

R-MAMMA1002282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

R-MAMMA1002292//Hordeum vulgare lipooxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568

R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-35:281:82//AC004231

R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//.8e-17:296:70//AC005074

R-MAMMA1002299//HS\_3116\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979

R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054

R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042

R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991  
R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//3.4e-46:393:71//AC004973  
R-MAMMA1002333//HS\_3245\_A1\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759  
5 R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549  
R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088  
10 R-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100  
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228  
R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996  
15 R-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241  
R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//8.3e-28:187:91//AC004662  
R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 20 4p16.3 contains CpG islands.//6.3e-47:297:85//268869  
R-MAMMA1002360//HS\_2163\_B2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213  
R-MAMMA1002361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520  
25 R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196  
R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168  
R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801  
30 R-MAMMA1002385  
R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430  
R-MAMMA1002411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668  
R-MAMMA1002413//Homo sapient 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146  
35 R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997  
R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321  
40 R-MAMMA1002428//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423  
R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396  
R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387:72//B65379  
45 R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512  
R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982  
R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556  
50 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822  
R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533:93//AC005077  
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460  
55 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375  
R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859  
R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING

DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214

R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427

R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056

R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878

R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427

R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580

R-MAMMA1002590//H.sapiens CpG island DNA genomic MseI fragment, clone 8d5, forward read cpg8d5.f1g.//1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.3e-46:333:80//AC005803

R-MAMMA1002612//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067

R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598

R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//2.7e-80:344:84//AC004687

R-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727

R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmid R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006

R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-52:285:92//AC004895

R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666

R-MAMMA1002646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585

R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424

R-MAMMA1002655//Homo sapiens mini satellite cebl repeat region.//0.18:152:65//AF048727

R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870

R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:92//Z92844

R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987

R-MAMMA1002685//HS\_2052\_A1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=O, genomic survey sequence.//1.2e-23:255:75//AQ231087

R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)



complete sequence.//1.1e-38:299:83//AC004673

R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbp1 mRNA, partial cds.//3.3e-05:61:93//AF057285

R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399

R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293

R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995

R-MAMMA1002721//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826

R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710

R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037

R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629

R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//2.2e-108:544:97//AC005856

R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055

R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020

R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626

R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//AC005781

R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128

R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//0.94:260:62//Z82975

R-MAMMA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667

R-MAMMA1002782//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320

R-MAMMA1002796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394

R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331

R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487

R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//AC002073

R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295

R-MAMMA1002835

R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585

R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141

R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007

R-MAMMA1002844

R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067

R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.6e-39:288:81//AC004906

R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044

R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296

R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial

cds for thymopoietin beta.//5.1e-41:264:87//U18271

R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL022069

R-MAMMA1002887

R-MAMMA1002890

3.4e-49:376:81//AG006257

R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//AC004881

R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502

R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070

R-MAMMA1002909//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798

R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019

R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219

R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//6.3e-88:556:87//AC006120

R-MAMMA1002947

0.48:156:69//AC005469

R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997

R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200

R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt] .//0.97:305:62//S81737

R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280

R-MAMMA1002982 1.0e-27:110:85//AG005524

R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460

R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109

R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406

R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109

R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092

R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740

R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence.//2.7e-14:294:68//B71583

R-MAMMA1003026//HS\_2166\_B2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639

R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214

R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550

R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889

R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235

R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560

R-MAMMA1003047

R-MAMMA1003049

R-MAMMA1003055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//2.3e-45:317:86//Z93783

R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//AC005305

R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352  
 R-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
 DRAFT SEQUENCE.//3.1e-49:299:87//Z83826  
 R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//  
 5 AC005084  
 R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
 quence.//4.2e-44:338:82//B71494  
 R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:  
 423:79//U72634  
 10 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE,  
 100 unordered pieces.//4.8e-114:567:97//AC006087  
 R-MAMMA1003127//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
 DRAFT SEQUENCE.//1.4e-34:283:83//Z99716  
 R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776  
 15 R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//  
 AC003663  
 R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, com-  
 plete cds.//4.8e-08:438:59//M97514  
 R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 20 DRAFT SEQUENCE.//1.7e-63:149:94//AL021579  
 R-MAMMA1003166//HS\_3128\_A1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766  
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640  
 R-NT2RM4000024  
 25 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//  
 AC004993  
 R-NT2RM4000030//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//  
 U70653  
 R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//  
 30 Z26239  
 R-NT2RM4000061  
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639  
 R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey se-  
 quence.//7.2e-18:277:71//B49463  
 35 R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//  
 Z88817  
 R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:  
 336:65//AC005199  
 R-NT2RM4000155  
 40 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//3.4e-23:335:  
 72//AC005856  
 R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//  
 D12646  
 R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154  
 45 R-NT2RM4000191  
 R-NT2RM4000197//HS\_3241\_A2\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812  
 R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete se-  
 quence.//0.0047:193:63//AC006056  
 50 R-NT2RM4000200  
 R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:  
 334:76//AC004035  
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255  
 R-NT2RM4000215  
 55 R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
 2.1e-55:303:86//AC005383  
 R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735  
 R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.7e-

49:322:88//AC006116  
R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR Region, complete sequence.//  
0.97:184:66//AC000085  
R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055  
5 R-NT2RM4000290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING  
DRAFT SEQUENCE.//1.4e-05:229:65//AL023585  
R-NT2RM4000324  
R-NT2RM4000327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING  
DRAFT SEQUENCE.//3.3e-42:443:75//Z97199  
10 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
6.4e-64:433:84//AC004826  
R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630  
R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066  
R-NT2RM4000356  
15 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542  
R-NT2RM4000368  
1.6e-48:348:85//AG006257  
R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148  
R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
20 quence.//1.4e-25:207:75//871494  
R-NT2RM4000414//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
DRAFT SEQUENCE.//7.1e-17:492:64//AL031985  
R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence.//  
1.8e-40:311:82//AQ241167  
25 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-  
QUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867  
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:  
78//AF062476  
R-NT2RM4000457  
30 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952  
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461  
R-NT2RM4000496  
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829  
R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey se-  
35 quence.//1.5e-20:150:89//B95717  
R-nnnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556  
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790  
R-NT2RM4000531  
40 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:  
66//AE001391  
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//  
K00909  
R-NT2RM4000585//HS\_3252\_A2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
45 nomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890  
R-NT2RM4000590//CIT-HSP-539O24.TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey se-  
quence.//1.7e-38:226:93//B50657  
R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072  
R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey se-  
50 quence.//0.77:139:64//AQ051950  
R-nnnnnnnnnnnnn  
R-NT2RM4000616//HS\_3107\_A2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034  
R-NT2RM4000674  
55 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823  
R-NT2RM4000698  
R-nnnnnnnnnnnnn  
R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039

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R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560  
R-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.0e-107:566:95//AL034379  
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303  
R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence.//5.2e-41:244:93//AQ006361  
R-NT2RM4000751//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//2.7e-28:416:67//AL034405  
R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217  
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//0.00060:241:62//AC002980  
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2.9e-104:546:94//AB007920  
R-NT2RM4000787//Homo sapiens, clone hRPK.3\_A\_1, complete sequence.//5.3e-32:321:77//AC006198  
R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//AC005306  
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//U58675  
R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF086348  
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868  
R-NT2RM4000813  
R-NT2RM4000820//, complete sequence.//2.0e-104:432:97//AC005406  
R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence.//2.0e-07:166:68//AB012248  
R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013  
R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709  
R-NT2RM4000855  
R-nnnnnnnnnnnn//HS\_3189\_B2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597  
R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-46:207:91//AF077058  
R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.0:336:60//AC002530  
R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//7.1e-09:259:64//AF011889  
R-NT2RM4000979  
R-NT2RM4000996//HS\_3164\_A1\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence.//2.0e-82:443:94//AQ141622  
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.2e-112:545:97//AB018272  
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.9e-113:556:97//AB014539  
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:120:82//AJ224639  
R-NT2RM4001047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//1.0:158:67//AL008733  
R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey sequence.//5.8e-19:118:97//AQ004096  
R-nnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//1.0e-05:271:64//M10296  
R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey sequence.//1.0:186:63//AQ277294  
R-NT2RM4001116  
R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//3.6e-79:468:90//AC004593  
R-NT2RM4001151//HS\_2270\_B1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence.//5.5e-62:312:98//AQ163739  
R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.4e-107:536:97//AC005841  
R-NT2RM4001160//HS\_3015\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712

R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201  
 R-NT2RM4001191//HS\_3002\_A1\_F05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791  
 R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857  
 5 R-NT2RM4001203  
 R-NT2RM4001204  
 R-NT2RM4001217  
 R-NT2RM4001256  
 R-NT2RM4001258  
 10 R-NT2RM4001309  
 R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPCI1-71H24 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//0.00055:183:63//AC004551  
 R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117\_K\_16, complete sequence.//4.5e-21:212:79//  
 AC004757  
 15 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey se-  
 quence.//3.8e-30:86:89//AQ021084  
 R-NT2RM4001340  
 0.0027:493:60//AC005133  
 R-NT2RM4001344  
 20 R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey se-  
 quence.//6.5e-16:1.01:99//AQ262797  
 R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey  
 sequence.//0.063:140:65//AQ265776  
 R-NT2RM4001382//HS\_3044\_A1\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668  
 R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000  
 R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920  
 R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete  
 cds.//1.7e-55:235:83//U57391  
 30 R-NT2RM4001412  
 R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library)  
 complete sequence.//1.7e-80:489:89//U69730  
 R-NT2RM4001437//RPCI11-56D2.TJ RPCI11 Homo sapiens genomic clone R-56D2, genomic survey sequence.//  
 3.8e-43:250:93//AQ081969  
 35 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library)  
 complete sequence.//0.0034:224:63//AC005926  
 R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//2.4e-33:360:68//  
 AC004075  
 R-NT2RM4001455//HS\_3229\_B1\_E04\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289  
 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
 2.2e-51:451:79//AC005282  
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585  
 R-NT2RM4001519//HS\_2208\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 45 nomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836  
 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336  
 R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970  
 R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910  
 50 R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811  
 R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel  
 (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein)  
 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ri-  
 55 bosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix  
 Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific  
 protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core'  
 domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//  
 AL031663

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317

R-nnnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120

5 R-NT2RM4001597//HS\_2059\_A1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334

R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936

10 R-NT2RM4001629//RPC111-54G14.TJ RPC111 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575

15 R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685

R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775

20 R-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153

25 R-nnnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430

R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709

30 R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483

R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.9e-18:202:78//Z83868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270

35 R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence.//4.4e-106:551:95//AC006017

R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099

R-NT2RM4001813

R-NT2RM4001823

40 R-NT2RM4001828//HS\_3073\_A2\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence.//1.6e-46:255:96//AQ121030

R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077

45 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633

R-nnnnnnnnnnnn//Hs\_3244\_B1\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5.0e-119:592:97//Y17711

R-NT2RM4001876//Megastigmus wachtli dinucleotide microsatellite, clone

50 MWA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS\_2016\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877

55 R-NT2RM4001922//HS\_2228\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498

R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34\_M\_24, complete sequence.//0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//2.9e-85:421:

98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353

R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659

R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742

R-NT2RM4002067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504

R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960

R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448

R-NT2RM4002251

R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H.sapiens CpG island DNA genomic MseI fragment, clone 179f11, forward read cpg179f11.ft1a.//0.72:97:69//Z57487

R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//HS\_2028\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262

R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-



gene similar to GPIISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822  
 R-ntnt2rm4002344//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317  
 R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 5 DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709  
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549  
 R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417  
 R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316  
 10 R-NT2RM4002390  
 R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411  
 R-NT2RM4002438  
 15 R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008  
 R-NT2RM4002452  
 R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034  
 20 R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545  
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255  
 25 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591  
 R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882  
 R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711  
 30 R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368  
 R-ntnt2rm4002532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING  
 DRAFT SEQUENCE.//3.4e-17:171:79//Z97985  
 35 R-NT2RM4002534  
 R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271  
 R-NT2RM4002571  
 R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579  
 40 R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862  
 R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422  
 45 R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205  
 R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090  
 R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098  
 50 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749  
 R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163  
 55 R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758  
 R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//6.0e-10:137:79//D42148

R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754

R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372

5 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97+++F050079

R-NT2RP2000079//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338

10 R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048

R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873

R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015

R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973

15 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356

R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909

R-nnnnnnnnnnnnn

20 R-nnnnnnnnnnnnn/Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827

R-NT2RP2000147

R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626

25 R-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924

R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728

R-NT2RP2000175

R-NT2RP2000183

30 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//4.3e-39:306:83//AC005325

R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

35 R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382

R-NT2RP2000232

R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401

40 R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066

R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726

R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894

45 R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077

R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179

50 R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409

R-NT2RP2000288

R-NT2RP2000289

R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165

55 R-NT2RP2000298

R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE

pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398

R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039

R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993

R-NT2RP2000414//Mouse DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828

R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640\_L\_15, complete sequence.//0.99:150:62//AC005324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142:90//AF102265

R-NT2RP2000438//RPC111-62I13.TK RPC111 Homo sapiens genomic clone R-62I13, genomic survey sequence.//3.1e-06:103:79//AQ199572

R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.0e-22:276:73//AC004691

R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//853940

R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234

R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48:201:64//D10170

R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07:472:59//AF033929

R-nnnnnnnnnnnnn

R-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318

R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.6e-29:167:97//AB005543

R-NT2RP2000617

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514

R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796

R-NT2RP2000668

R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590

R-NT2RP2000764

R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002

R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey se-

quence.//9.5e-32:176:97//B99575

R-nnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init. region.//0.0077:418:57//K00916

R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//AL011013

R-NT2RP2000819

R-NT2RP2000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504

R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370

R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//0.0022:200:68//AC005703

R-NT2RP2000863

R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412

R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//0.0028:221:62//AB020875

R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266

R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336

R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298

R-NT2RP2000965

R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393

R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.4e-93:484:95//AC005277

R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372

R-NT2RP2001036//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732

R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029

R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973

R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140

R-NT2RP2001119

R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348

R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394

R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838

R-NT2RP2001168

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949

R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134

R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153

R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110

R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353  
 R-NT2RP2001277//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8,  
 WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870  
 R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 5 DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709  
 R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//  
 AC006041  
 R-NT2RP2001312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//0.12:117:64//AL033520  
 10 R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212  
 R-NT2RP2001328//HS\_2213\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874  
 R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560  
 R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404  
 15 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433  
 R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//  
 L19301  
 R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands  
 and polymorphic CA repeat.//3.4e-60:351:90//Z93242  
 20 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294  
 R-NT2RP2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108D11, WORKING  
 DRAFT SEQUENCE.//1.0e-44:246:85//AL034419  
 R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs  
 and a GSS, complete sequence.//3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid  
 25 cSRL34e5, complete sequence.//0.94:287:59//U73643  
 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702  
 R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//  
 D17447  
 R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Li-  
 30 brary) complete sequence.//1.0e-06:452:59//AC004801  
 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 5.1e-08:218:67//AC004846  
 R-NT2RP2001450  
 R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//3.8e-31:254:83//AC002465  
 35 R-NT2RP2001506//C.barati p-47, ntnt, bonT genes.//1.2e-06:415:60//Y12091  
 R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559  
 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.1e-104:545:95//Y14494  
 R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.0e-16:283:68//  
 AC004596  
 40 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, ge-  
 nomic sequence, complete sequence.//7.7e-16:108:96//AF037222  
 R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey se-  
 quence.//0.052:112:66//B73597  
 R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey se-  
 45 quence.//6.0e-78:383:98//AQ042029  
 R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322  
 R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407  
 R-NT2RP2001597//HS\_3016\_B2\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854  
 50 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.015:445:58//  
 AC006079  
 R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:  
 413:63//AF009326  
 R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, com-  
 55 plete cds.//0.11:190:63//AF034626  
 R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:  
 157:81//AC004125  
 R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//

AC004472

R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107:66//AC002385

R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758

5 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352:97//AC004079

R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914

10 R-NT2RP2001740//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104

R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583

R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435:97//AC004783

15 R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261:60//M23468

R-NT2RP2001861

R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//I34189

R-NT2RP2001876

20 R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.0e-111:485:97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563

25 R-NT2RP2001926//HS\_3180\_B2\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504

R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280

30 R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033

R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575

35 R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAll project).//0.031:282:61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715

R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389:61//D88270

40 R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429:61//AC004011

R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239:62//X83707

45 R-NT2RP2002058//HS\_2183\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792

R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183

50 R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178

55 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191:64//AQ266779

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.0065:294:61//AC005913

R-NT2RP2002154

R-NT2RP2002172//RPC11-90C20.TJ RPC11 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591

R-NT2RP2002185//CIT-HSP-2341115.TF CIT-HSP Homo sapiens genomic clone 2341115, genomic survey sequence.//6.0e-36:230:90//AQ053355

R-NT2RP2002192//HS\_2222\_B1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491

R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872

R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785

R-NT2RP2002219//HS\_2058\_A1\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380

R-NT2RP2002231//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557

R-nnnnnnnnnnnn//Sequence 11 from patent US 5624818.//3.3e-91:553:87//I41141

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e14:132:84//AF005418

R-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527

R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.1e-06:391:60//AC004605

R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532

R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389:59//AE001408

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093668

R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323:73//L23204

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958

R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308

R-NT2RP2002408//HS\_2212\_A1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence.//9.6e-35:231:88//AQ184632

R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877

R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225

R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z99289

R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013

R-NT2RP2002475

R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289

R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047

R-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.0e-86:429:98//AC006213

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334

R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//0.14:406:58//AJ223323

R-NT2RP2002537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314  
 R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316  
 R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878  
 5 R-NT2RP2002595  
 R-NT2RP2002606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529  
 R-NT2RP2002609  
 R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551  
 10 R-NT2RP2002621//Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs.//1.1e-38:348:78//Z97352  
 R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030  
 R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384  
 15 R-NT2RP2002701  
 R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778  
 R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983  
 20 R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815  
 R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138  
 R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674  
 25 R-NT2RP2002741//HS\_3051\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283  
 R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395  
 R-NT2RP2002752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494  
 30 R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882  
 R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917  
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537  
 35 R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850  
 R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078  
 R-NT2RP2002857//HS\_3026\_B2\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ 128697  
 40 R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//1.5e-44:270:85//AQ052700  
 R-NT2RP2002880//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318  
 45 R-NT2RP2002891  
 R-NT2RP2002925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395  
 R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556  
 R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140  
 50 R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//1.0:275:61//AC005701  
 R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483  
 55 R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132  
 R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140



R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542

R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//1.3e-51:283:88//AC005968

5 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21.1:4.3e-11:430:63//AL021307

R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887

R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870

10 R-NT2RP2003073

R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914

R-NT2RP2003108

R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378

15 R-NT2RP2003121//HS\_2238\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=1, genomic survey sequence.//0.00055:324:61//AQ293058

R-NT2RP2003125

R-NT2RP2003129

R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084

20 R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879

R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581

R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018\_N\_14, complete sequence.//2.2e-71:467:86//AC005823

25 R-NT2RP2003177

R-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597

R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877

R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551

30 R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888

R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738

R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481

35 R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525

R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831

40 R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261

R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079

45 R-NT2RP2003295//HS\_2053\_B1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251

R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332

R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960

50 R-NT2RP2003329//C.reinhardtii psbB 5' flanking region.//0.79:161:59//X59731

R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039

R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357

55 R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321

R-NT2RP2003391//HS\_2255\_B2\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937  
 R-NT2RP2003393//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 3.9e-31:290:79//AQ0202481  
 R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//  
 5 X14910  
 R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, par-  
 tial cds.//0.32:174:66//U81429  
 R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536  
 R-NT2RP2003445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 10 DRAFT SEQUENCE.//4.4e-99:585:89//AL023808  
 R-NT2RP2003446  
 R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559  
 R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540  
 R-NT2RP2003499  
 15 R-NT2RP2003506  
 R-NT2RP2003511  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460  
 R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:  
 518:79//M12783  
 20 R-NT2RP2003522//HS\_2182\_A1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304  
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE,  
 31 unordered pieces.//1.5e-37:328:80//AC005841  
 R-NT2RP2003543//HS\_3028\_A2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957  
 R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055  
 R-NT2RP2003564  
 R-NT2RP2003581  
 R-NT2RP2003596//HS\_2163\_B1\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 30 nomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143  
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067  
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507  
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//  
 35 AJ006215  
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chro-  
 mosome X contains ESTs.//0.0053:395:58//Z76735  
 R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385  
 R-NT2RP2003691//HS\_3252\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783  
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey se-  
 quence.//3.9e-43:431:75//AQ035000  
 R-NT2RP2003704  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097  
 45 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X \*.//0.64:169:67//Z84470  
 R-NT2RP2003714//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//  
 4.6e-11:152:73//295704  
 R-nnnnnnnnnnnnn/H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631  
 R-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 50 2.2e-109:547:96//AC004951  
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-  
 109:545:97//AC004626  
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019  
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468  
 55 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete  
 cds.//0.96:446:58//D87956  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437  
 R-NT2RP2003777

R-NT2RP2003781//HS\_3109\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749

R-NT2RP2003793

R-NT2RP2003840

5 R-NT2RP2003857//HS\_2205\_A2\_H12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299

R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850

10 R-NT2RP2003871//HS\_3210\_A1\_C08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028

R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214

R-NT2RP2003912//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693

15 R-NT2RP2003952

R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458

R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916

R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347

20 R-NT2RP2003984

R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC0003 82

R-NT2RP2003988

R-NT2RP2004014

25 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780

R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389

R-NT2RP2004043//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555

30 R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308

R-NT2RP2004098//H.sapiens CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpg133h3.rt1a.//7.9e-25:140:100//Z64530

35 R-NT2RP2004124

R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964

R-NT2RP2004152//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

40 R-NT2RP2004165//Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021

R-NT2RP2004170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064

R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047

45 R-NT2RP2004187//RPCI11-59E12.TK RPCI11 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120

R-NT2RP2004194

R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601

50 R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//0.19:175:64//AC005023

R-NT2RP2004226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808

55 R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524

R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718

R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280

5 R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662

10 R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPC11-90N11.TJ RPC11 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548

15 R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433

20 R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

25 R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164

30 R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS\_3238\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514

35 R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

40 R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591

R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547

R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890

45 R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184

50 R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976

55 R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605

R-NT2RP2004600//Homo sapiens full-length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522

R-NT2RP2004602//Homo sapiens full-length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033



R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//I25644

R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475:67//AF009326

R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.4e-104:518:97//AB014564

R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//X98743

R-NT2RP2005139

R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101

R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911

R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100:75//AC004971

R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence.//0.90:113:71//AQ262104

R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence.//5.0e-14:183:75//AC003041

R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5e-100:513:95//AJ007509

R-NT2RP2005204

R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-119:583:97//AC005189

R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial.//8.4e-62:312:98//AJ010952

R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328:62//Z99297

R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355:61//AL034560

R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541:58//AC000107

R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335

R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.4e-124:594:98//AF060219

R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590

R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101

R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//9.5e-15:218:77//AL022069

R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804

R-NT2RP2005336//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567

R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.//0.094:451:60//297629

R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841

R-NT2RP2005360//Homo sapiens clone RG023I15, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266:60//AC005049

R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//6.0e-41:226:86//AC005695

R-NT2RP2005407

R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835

R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548

R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845

R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2.//2.0e-42:315:82//X71342

R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816

R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence.//01251288:62//AC005457

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510

5 R-NT2RP2005476//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030

10 R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722

15 R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//7e-29:252:76//AC005828

20 R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563

25 R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911

R-NT2RP2005539//Homo sapiens mRNA for NSI-binding protein (NSI-BP).//2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963

30 R-NT2RP2005549//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//AC004996

35 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148

R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126

40 R-NT2RP2005620

R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538

R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996

45 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937

R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398

R-NT2RP2005651

50 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908

R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814

55 R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B13538

R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478

R-NT2RP2005694//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-106, complete sequence.//0.0026:414:57//AL010210

R-NT2RP2005701

5 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342

R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277

R-NT2RP2005722//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985

R-NT2RP2005723

10 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842

R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384

R-NT2RP2005748//RPCI11-64K11.TK RPCI11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313

15 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516

R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098

20 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672

R-NT2RP2005773//HS\_2168\_B1\_G12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414

R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310

25 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623

R-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423

R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//6.3e-16:481:63//AC005332

30 R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696

R-NT2RP2005815

R-NT2RP2005835

R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873

R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047

35 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308

R-NT2RP2005859//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-83, complete sequence.//0.0097:363:59//AL010152

40 R-NT2RP2005868//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971

R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316

R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661

45 R-NT2RP2005908

R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840

R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289

50 R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616

R-NT2RP2006023//HS\_2176\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148

55 R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369

R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835

R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING



DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS\_2020\_A2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:199:79//M85300

R-NT2RP2006141

R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045

R-NT2RP2006184//RPCI11-6O16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6O16, genomic survey sequence.//0.52:273:61//B49539

R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554

R-NT2RP2006196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981

R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057

R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484

R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707

R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318

R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008

R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630

R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262

R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768

R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761

R-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//AC004660

R-nnnnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532

R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:

448:64//U22015

R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U-23155

R-NT2RP3000109//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514

R-NT2RP3000220//RPCI11-63O7.TJ RPCI11 Homo sapiens genomic clone R-63O7, genomic survey sequence.//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.025:131:66//AC005726

R-NT2RP3000252

R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879

R-NT2RP3000267

R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766

R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970

R-NT2RP3000320//HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064

R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090

R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551

R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544

R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177

R-NT2RP3000350

R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039

R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124

R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634

R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence.//0.015:184:63//B31814

5 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185

R-NT2RP3000418//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510B21, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885

R-NT2RP3000433

R-NT2RP3000439

10 R-NT2RP3000441

R-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K<sup>+</sup> channel protein.//0.71:101:66//E13519

R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889

15 R-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847

R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//I16692

20 R-NT2RP3000512//RPC11-60F15.TK RPC11 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516

R-NT2RP3000526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783

R-NT2RP3000527//HS\_3228\_A1\_H07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence.//4.5e-30:184:93//AQ209131

25 R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538

R-NT2RP3000542//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316

30 R-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.1e-107:548:95//AC006012

R-NT2RP3000562//HS\_2041\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.6e-55:279:98//AQ230207

R-NT2RP3000578//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.00060:356:58//AL010212

35 R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377

40 R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505

R-nnnnnnnnnnnn//HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452

45 R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128

R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414

50 R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115

R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379

55 R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092

R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//

AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645

R-NT2RP3000685//HS\_3007\_A2\_F02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655

R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

R-NT2RP3000759//HS\_2055\_A2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

R-NT2RP3000836//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.20:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

R-NT2RP3000847//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572

R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153 R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

R-NT2RP3000869//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens /Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.36:186:62//AC006079

R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

R-NT2RP3001007//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

R-NT2RP3001081//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107

R-nnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316  
R-NT2RP3001111  
R-NT2RP3001113  
5 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189  
R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.000.13.160:69//AQ002011  
R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
10 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.9e-99:497:96//AL031864  
R-NT2RP3001120  
R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559  
R-NT2RP3001133  
15 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305  
R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448  
R-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379  
20 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266  
R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688  
R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785  
R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey  
25 sequence.//7.0e-29:167:97//B88077  
R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827  
R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326  
30 R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003  
R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237  
35 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398  
R-NT2RP3001253//HS\_3002\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=O, genomic survey sequence.//0.98:190:63//AQ251982  
R-NT2RP3001260  
40 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936  
R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589  
R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341  
45 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811  
R-NT2RP3001307//HS\_2058\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868  
R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848  
50 R-NT2RP3001325  
R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367  
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920  
R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105  
55 R-NT2RP3001355  
R-NT2RP3001374//HS\_2184\_A2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence.//3.7e-10:101:84//AQ024647  
R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:

R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785

R-NT2RP3001392//HS\_3078\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587

R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544

R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046

R-NT2RP3001399

R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160

R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158

R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152

R-nnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668

R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029

R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903

R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630

R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906

R-NT2RP3001457

R-NT2RP3001459

R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030

R-NT2RP3001490//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395

R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.  
2.1e-110:549:97//AF064801

R-NT2RP3001527//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549

R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420

R-NT2RP3001538

R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292

R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688

R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337

R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//0.066:360:60//AC005410

R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490

R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c oxidase subunit I, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase (EC 2.3.1.37), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64/Z83821

R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21:31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808

R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10.//0.99:137:63//X76572

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149

R-NT2RP3001642

R-NT2RP3001646//HS\_3218\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A. genomic survey sequence.//2.6e-32:215:91//AQ303003

R-NT2RP3001671//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-88, complete sequence.//0.018:262:61//AL010157

R-NT2RP3001672

R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905  
 R-NT2RP3001678//RPCI11-50C17.TK RPCI11 Homo sapiens genomic clone R-50C17, genomic survey se-  
 quence.//0.15:232:62//AQ116359  
 5 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer , segment 3/11.//7.8e-104:549:95//AB020860  
 R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//  
 AC006019  
 R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:  
 433:59//AE001415  
 10 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//  
 AF053523  
 R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey se-  
 quence.//1.5e-95:456:99//AQ279562  
 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//  
 15 AC004617  
 R-NT2RP3001724//Human HepG2 3' region MboI cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273  
 R-NT2RP3001730//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING  
 DRAFT SEQUENCE.//7.6e-43:409:76//Z98200  
 R-NT2RP3001739  
 20 R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279  
 R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey se-  
 quence.//8.8e-06:102:78//AQ113378  
 R-NT2RP3001764  
 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232  
 25 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928  
 R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//  
 U13262  
 R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962  
 R-NT2RP3001819  
 30 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410  
 R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),  
 CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein  
 (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694  
 R-NT2RP3001855  
 35 R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey  
 sequence.//0.0012:68:82//AQ116409  
 R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2  
 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950  
 R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486  
 40 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142  
 R-NT2RP3001929  
 R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969  
 R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//  
 Z95328  
 45 R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:  
 61//AC004500  
 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836  
 R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE,  
 72 unordered pieces.//7.0e-109:552:96//AC005844  
 50 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029  
 R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987  
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779  
 R-NT2RP3002007  
 R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA  
 55 CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//  
 AL022322  
 R-NT2RP3002033  
 R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877

R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006

R-NT2RP3002057

R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002  
R-nnnnnnnnnnnnn

R-NT2RP3002081//HS\_3082\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25 :344:73//AQ122260

R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210

R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//AC004746

R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071

R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077

R-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710

R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:80//AB003503

R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857

R-NT2RP3002165

R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z48711

R-NT2RP3002173

R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980

R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF100669

R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs.//0.30:217:63//Z82189

R-NT2RP3002255

R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//0.84:463:57//AF070717

R-NT2RP3002276//HS\_2260\_A1\_MF\_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491

R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546

R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115

R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688

R-NT2RP3002343

R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.20:489:56//AC004617

R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164

R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578

R-NT2RP3002484

R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359

R-NT2RP3002512

R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272

R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479

R-NT2RP3002566//HS\_2036\_A1\_D08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627

R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956

R-NT2RP3002590//Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MXK3, complete sequence.//0.00010:431:59//AB019236

R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522

R-NT2RP3002603



R-NT2RP3002631//Homo sapiens chromosome 21 PAC  
 RPCIP704A9190Q2.//1.0:241:59//AJ006997  
 R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//6.8e-24:  
 331:76//M85300  
 5 R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//  
 Z49816  
 R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA,  
 partial sequence.//0.60:300:59//U82072  
 R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704  
 10 R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 4.7e-09:122:77//AQ202481  
 R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276  
 R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037  
 R-NT2RP3002701  
 15 R-NT2RP3002713//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE.//0.95:334:59//AL031427  
 R-NT2RP3002763//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567  
 R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710  
 R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//  
 20 AC004822  
 R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flank-  
 ing repeat regions.//1.1e-20:161:77//AF003528  
 R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972  
 R-NT2RP3002818//HS\_3053\_A2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025  
 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276  
 R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//  
 AC005256  
 R-NT2RP3002876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
 30 DRAFT SEQUENCE.//2.6e-59:311:96//AL034380  
 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//4.6e-24:422:63//AC003035  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314  
 R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//  
 35 AC005014  
 R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500  
 R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:  
 566:96//AC005754  
 R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:  
 40 58//AE001391  
 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666  
 R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482  
 R-NT2RP3002978//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 DRAFT SEQUENCE.//4.8e-05:249:63//AL031733  
 45 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATI-  
 DYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//  
 0.0097:246:67//Z97195  
 R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,  
 G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:  
 50 188:78//AF109905  
 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site.//5.3e-07:376:  
 63//L47211  
 R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-13:323:66//  
 AC005669  
 55 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hll-10).//3.8e-42:  
 265:91//Y16708  
 R-NT2RP3003068//HS\_3214\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-NT2RP3003078//T26A1 TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013

5 R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153

R-NT2RP3003121//Homo sapiens full-length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348

R-NT2RP3003133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985

10 R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646

R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995

R-NT2RP3003150

15 R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence.//5.5e-42:289:74//AC005294

R-NT2RP3003185//HS\_2058\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298

R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//4.8e-40:349:79//AC005701

20 R-NT2RP3003197//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319

R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904

25 R-NT2RP3003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183

R-NT2RP3003212//Homo sapiens full-length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173

R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307

R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272

30 R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083

R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862

R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022

35 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983

R-NT2RP3003290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662

R-NT2RP3003301

40 R-NT2RP3003302//CIT-HSP-2319H19.TF CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950

R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660

45 R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287

R-NT2RP3003330//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015

R-NT2RP3003344//HS\_3235\_B2\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203

R-NT2RP3003346

50 R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519

55 R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820

R-NT2RP3003385

R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-40:496:

72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635

5 R-NT2RP3003427//RPC111-45J23.TJ RPC111 Homo sapiens genomic clone R-45J23, genomic survey sequence.//0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:61//AC006031

10 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:495:59//AE001398

R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene.//0.0074:514:59//X77238

15 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(GTG)n repeat-containing mRNA.//1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019

R-NT2RP3003564

20 R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:59//AL008638

R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:79//AC003007

R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560

25 R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the AD-SL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.8e-44:448:77//AL022238

30 R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//0.34:257:62//AC005291

R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701

R-NT2RP3003665//HS\_3078\_B2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580

R-NT2RP3003672

35 R-NT2RP3003686

R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//AC002452

R-NT2RP3003716//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL034410

40 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300

R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-07:217:66//AC003009

R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1e-26:456:68//Z98052

45 R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736

R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:95//AF077754

R-NT2RP3003805

50 R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107

R-NT2RP3003819//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487

R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404

R-NT2RP3003828

55 R-NT2RP3003831//\*\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567

R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611

R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-46:457:74//AC002980

R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-06:356:62//Z98547  
 R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11.//8.2e-09:68:98//AF086402  
 R-NT2RP3003876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORK-  
 ING DRAFT SEQUENCE.//0.0027:180:66//AL031650  
 5 R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array.//0.029:234:62//  
 X53439  
 R-NT2RP3003918  
 R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds.//0.00087:164:  
 67//AF029215  
 10 R-NT2RP3003989  
 R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465  
 R-NT2RP3004013//HS\_3018\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3018 Col=17 Row=M, genomic survey sequence.//0.00026:421:60//AQ119904  
 R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), com-  
 15 plete sequence.//4.8e-12:308:62//AC004532  
 R-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE.//0.42:190:64//AL021579  
 R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//  
 AC006130  
 20 R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308  
 R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//  
 AC005784  
 R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//  
 25 AC002525  
 R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-  
 93:551:92//AC005038  
 R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence.//1.6e-104:317:100//AC006064  
 30 R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2  
 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532  
 R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542  
 R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//  
 0.013:134:70//U78721  
 35 R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//  
 AC004081  
 R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533  
 R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763  
 R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052  
 40 R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498  
 R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:  
 407:60//AE001415  
 R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//  
 2.8e-105:534:97//AC005385  
 45 R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey se-  
 quence.//4.0e-64:382:90//AQ281324  
 R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967  
 R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536  
 R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.4e-06:435:  
 50 62//AC004231  
 R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey se-  
 quence.//0.0018:210:65//AQ263365  
 R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//7.1 e-46:340:83//  
 AC005695  
 55 R-NT2RP3004349//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117O3, WORKING  
 DRAFT SEQUENCE.//9.4e-29:263:79//AL020995  
 R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoam-  
 ine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125



6.2e-26:163:93//AQ200049

R-NT2RP4000185

R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505 :96//AB014600

R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300

R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261

R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081

R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470

R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727

R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092

R-NT2RP4000263//CIT-HSP-2336N24. TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515

R-nnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368

R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524

R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311

R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195

R-NT2RP4000370//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//9.9e-25 :348:72//AC005154

R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901

R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//0.066:197:63//AC006080

R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527

R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313

R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026

R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505

R-NT2RP4000449//HS\_2037\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047

R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271

R-nnnnnnnnnnnn

R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082

R-nnnnnnnnnnnn

R-NT2RP4000500

R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140

R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007

R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068

R-NT2RP4000519

R-NT2RP4000524

R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078

5 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013

R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3

10 unordered pieces.//6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-2300I7.TR CIT-HSP Homo sapiens genomic clone 2300I7, genomic survey sequence.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443

15 R-NT2RP4000704//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080

R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669

20 R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503

25 R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5)

30 of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098

R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

35 R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

40 R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698

45 R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633O19, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302

50 R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS\_3009\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957

55 R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011 TIN.01\_di1PD, partial cds.//0.11:219:62//U44882

R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//I25669

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),

CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694

R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003

5 R-NT2RP4001004//HS\_3163\_A2\_H02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515

R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023

R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247

10 R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086

R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859

R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

15 R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213

R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial.//2.4e-118:574:98//AJ010953

R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429

20 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164

R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626

R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021

25 R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629

R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298

R-NT2RP4001126//HS\_3146\_A1\_805\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093

R-NT2RP4001138

30 R-NT2RP4001143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095

35 R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996

40 R-nnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772

45 R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593

R-NT2RP4001219//HS\_2190\_A1\_A06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635

R-NT2RP4001228//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745

50 R-NT2RP4001235//HS\_3047\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918

R-NT2RP4001256//HS\_3007\_A2\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389

55 R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426

R-NT2RP4001274//RPCI11-24O21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24O21, genomic survey sequence.//3.9e-25:142:99//AQ013887



R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334  
 R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:  
 466:66//AF009326  
 R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey se-  
 5 quence.//0.98:305:62//AQ018036  
 R-NT2RP4001339  
 R-NT2RP4001345  
 R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//  
 AB003097  
 10 R-NT2RP4001353//RPCI11-55N17.TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey se-  
 quence.//0.74:106:66//AQ081821  
 R-NT2RP4001372  
 R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//1.5e-09:473:  
 60//AC006080  
 15 R-NT2RP4001375  
 R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey se-  
 quence.//9.4e-41:441:75//AQ040083  
 R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//  
 AC004691  
 20 R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140  
 R-NT2RP4001414  
 R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272  
 R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 25 DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308  
 R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone  
 cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220  
 R-NT2RP4001474  
 R-NT2RP4001483  
 30 R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:  
 61//L34027  
 R-NT2RP4001502//HS\_2187\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108  
 R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE,  
 35 4 unordered pieces.//0.15:333:62//AC005916  
 R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226  
 R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086  
 R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING  
 DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710  
 40 R-nnnnnnnnnnnn//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119  
 R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//  
 Z82212  
 R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence.//  
 0.0072:180:60//AQ200771  
 45 R-NT2RP4001568  
 R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11),  
 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit  
 III (COIII) gene, complete cds.//1.6e-09:555:58//U14181  
 R-NT2RP4001574//HS\_2247\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 50 nomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345  
 R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the  
 BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18  
 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseu-  
 dogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6  
 55 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type  
 XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG  
 islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228  
 R-NT2RP4001592//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING

DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384

R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380

R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735

R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316

R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020

R-NT2RP4001803//HS\_3087\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

R-NT2RP4001822

R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540

R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523

R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157

R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023

R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region.//1.0e-46:242:98//U25276

R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536

R-NT2RP4002047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353

R-NT2RP4002058//RPCI11-69O1.TJ RPCI11 Homo sapiens genomic clone R-69O1, genomic survey sequence.//0.23:163:64//AQ268418

R-NT2RP4002071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386

R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon

of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375  
R-NT2RP4002078//RPC111-79116.TV RPC111 Homo sapiens genomic clone R-79116, genomic survey sequence.//  
3.3e-87:452:95//AQ283131  
R-nnnnnnnnnnnnn  
5 R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619  
R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey se-  
quence.//6.8e-62:320:96//AQ111163  
R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476  
R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//  
10 AC002383  
R-NT2RP4002905//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete  
sequence.//0.0017:533:57//AL008972  
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934  
R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:  
15 74//AC005510  
R-OVARC1000006//HS\_2253\_B1\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124  
R-OVARC1000013//HS\_2212\_A2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584  
20 R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:  
62//Z80232  
R-OVARC1000017  
R-OVARC1000035//RPC111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.//  
3.3e-05:236:63//AQ237194  
25 R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains  
an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga  
and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721  
R-OVARC1000060//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING  
DRAFT SEQUENCE.//5.0e-21:297:70//AL033397  
30 R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276  
R-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING  
DRAFT SEQUENCE.//5.1e-110:599:93//AL031387  
R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413  
R-nnnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey se-  
35 quence.//0.80:285:59//B94391  
R-OVARC1000091  
R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey se-  
quence.//1.4e-17:141:85//AQ111520  
R-OVARC 1000106  
40 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-  
100:495:97//AF069250  
R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342  
R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:  
65//U95740  
45 R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//  
1.8e-16:370:67//AC005385  
R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey  
sequence.//1.1e-05:55:98//AQ240492  
R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642  
50 R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey se-  
quence.//0.050:176:62//AQ042932  
R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING  
DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506  
R-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07;  
55 HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604  
R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501  
R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484  
R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//6.2e-38:193:82//

AC005670

R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194

R-OVARC1000288//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131

R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//1.7e-10:100:88//AC005971

R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574

R-OVARC 1000309

R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236

R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614

R-OVARC1000335//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690

R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308

R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588

R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812

R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720

R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388

R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378

R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382

R-OVARC1000431//HS\_2199\_A2\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722

R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662

R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043

R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381

R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583

R-OVARC1000461//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417

R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-81:489:91//AF023451

R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526

R-OVARC1000473//Homo sapiens full-length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851

R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671

R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984

R-OVARC1000496

R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005

R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024

R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510

R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831

R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069

R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197

R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//AC004223

R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit

(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC 1000605

R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162.

R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130\_H\_16, complete sequence.//6.9e-48:525:73//AC005585

R-OVARC1000730//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

R-OVARC1000862//M.musculus Fit mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS\_3082\_A2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS\_2195\_A2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

R-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp).//2.2e-07:223:70//X91255

R-OVARC1000984

R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca<sup>2+</sup>/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//5.8e-71:332:87//AC003957

R-OVARC1001000//HS\_3032\_B1\_G11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190

R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813

R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345

R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//9.7e-17:180:78//AC005410

R-OVARC1001044

R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237

R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657

R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276

R-OVARC1001074//HS\_2205\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272

R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270

R-OVARC1001161//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680

R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781

R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//

1.3e-28:427:70//AC004963

R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859

R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549

R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213

R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907

R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796

R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462

R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794

R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//1.4e-41:284:87//AC006071

R-OVARC1001243//HS\_2055\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142

R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148

R-OVARC1001268

R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551

R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494

R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062

R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018

R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142

R-OVARC1001329//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402

R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862

R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242

R-OVARC1001341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818

R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874

R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350

R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297

R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//0.20:335:60//AC005863

R-OVARC 1001369

R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210

R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491

R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//9.3e-20:422:60//AC005821

R-OVARC1001391

R-nnnnnnnnnnnn

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB00665

R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668

R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157

R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341

R-OVARC1001442

R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086

R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655

R-OVARC1001480//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676

R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507

R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039

R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488

R-OVARC1001547

R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165

R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418

R-OVARC1001610//HS\_3070\_A2\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523

R-OVARC1001611//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423

R-OVARC1001615//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658

R-OVARC1001668//HS\_3228\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379

R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965

R-OVARC1001703

R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194

R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145

R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276

R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257

R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575

R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279

R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066

R-OVARC1001795

R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337

R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694

R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585

R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046

R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086

R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688

R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905



R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350  
 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611  
 R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 5 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 complete sequence.//9.1e-20:206:80//AL031864  
 R-OVARC1001880//RPC111-42I15.TJ RPC111 Homo sapiens genomic clone R-42I15, genomic survey se-  
 quence.//3.9e-50:287:88//AQ052700  
 R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//6.1e-13:457:63//  
 AC003950  
 10 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 2.5e-86:346:90//AF061749  
 R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//  
 7.2e-89:421:100//AF072246  
 R-OVARC1001911//Homo sapiens full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315  
 15 R-OVARC1001916  
 R-OVARC1001928  
 R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166  
 R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region  
 (env) gene, partial cds.//0.14:173:64//U58826  
 20 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:  
 63//M99593  
 R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//8.2e-38:385:  
 75//AC005666  
 R-OVARC1001987  
 25 R-OVARC1001989//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11,  
 WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841  
 R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island,  
 complete sequence.//5.0e-42:298:86//AL031286  
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934  
 30 R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//  
 0.23:210:61//AC004411  
 R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 5.4e-99:546:92//AC006015  
 R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glypican-3  
 35 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174  
 R-OVARC1002127  
 R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP Homo sapiens genomic clone 2290O18, genomic survey se-  
 quence.//2.4e-07:316:62//AQ003988  
 R-OVARC1002143//RPC111-54M8.TJ RPC111 Homo sapiens genomic clone R-54M8, genomic survey sequence.//  
 40 2.3e-35:220:90//AQ083241  
 R-OVARC1002156  
 R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey se-  
 quence.//1.6e-12:140:79//AQ265720  
 R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey se-  
 45 quence.//5.0e-59:291:99//AQ020420  
 R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060  
 R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981  
 R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507  
 50 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557  
 R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING  
 DRAFT SEQUENCE.//2.8e-44:405:77//D83253  
 R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//  
 AC006162  
 55 R-PLACE1000040//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5,  
 WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855  
 R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462  
 R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505

R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154

R-PLACE1000066

R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848

R-PLACE1000081

R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619

R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746\_E\_8, complete sequence.//1.8e-06:420:57//AC005358

R-PLACE1000142

R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291

R-PLACE1000185

R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//8.2e-80:410:97//AQ022149

R-PLACE1000214//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989

R-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818

R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122

R-PLACE1000292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200

R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281\_F\_24, complete sequence.//1.8e-16:598:62//AC004706

R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326

R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:492:58//AC005278

R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:59//AE001364

R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//AF073997

R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015

R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//0.51:346:58//AB020742

R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009

R-PLACE1000421//HS\_2251\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807

R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073

R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724

R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.0e-54:429:81//AC005899

R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.66:103:72//AF059580

R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166

R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//U35245

R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308

R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790

R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799\_N\_11, complete sequence.//1.5e-37:414:74//AC005323

5 R-nnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506

10 R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059

15 R-PLACE1000610//HS\_3071\_A1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341

R-PLACE1000636//HS\_3220\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157

20 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408

25 R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791

30 R-PLACE1000755//HS\_2183\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548

35 R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970

R-nnnnnnnnnnnn

R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081

40 R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272

45 R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505

R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489

50 R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//8.3e-20:223:76//AC005553

55 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506

R-PLACE1000979

R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey se-

quence.//7.0e-07:64:95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664

R-PLACE1001076

R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07 :302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS\_2036\_A1\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399

R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030

R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319

R-PLACE1001387

R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355

R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087

R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.12:53:84//AC006241

R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28u1 gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111

5 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130

R-PLACE1001468//HS\_3050\_A2\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920

R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368

10 R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401

R-PLACE1001503//HS\_2183\_A1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613

R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969

15 R-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667

R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.6e-18:171:82//AC 005669

R-PLACE1001551

20 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135

R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860

R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605

R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037

25 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174

R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878

R-PLACE1001634//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791

30 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//2.6e-83:441:95//AC005971

R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253

R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250

35 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077

R-PLACE1001705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716

R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349

40 R-PLACE1001720

R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120

R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261

45 R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027

R-PLACE1001745

R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509

50 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243

R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463

R-PLACE1001761

R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426

R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711

55 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//

4.1e-92:463:95//AF058953

R-PLACE1001821//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011

R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.

Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939

R-PLACE1002433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542  
 R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey  
 sequence.//0.70:247:61//AQ242104  
 R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.//  
 0.00060:471:59//AJ229041  
 R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//  
 2.5e-10:98:81//AC004854  
 R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262  
 R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-  
 53:307:91//AF042273  
 R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551  
 R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey se-  
 quence.//3.2e-42:297:85//AQ037614  
 R-PLACE1002514//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING  
 DRAFT SEQUENCE.//7.8e-16:221:73//Z95114  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256  
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//  
 AC004774  
 R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//  
 0.0042:489:60//D16253  
 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178  
 R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:  
 292:84//AC006084  
 R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete  
 cds.//3.1e-17:517:61//AF045555  
 R-PLACE1002591  
 R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626  
 R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:  
 65//U63313  
 R-PLACE1002625//HS\_2233\_B2\_H04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663  
 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//  
 AF079765  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-  
 77:390:97//AF068180  
 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656  
 R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723  
 R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library)  
 complete sequence.//0.0098:197:64//AC005185  
 R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:  
 82//AC006145  
 R-PLACE1002782  
 R-PLACE1002794  
 R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey se-  
 quence.//6.0e-50:250:100//AQ034981  
 R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279  
 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC li-  
 brary) complete sequence.//6.3e-59:339:93//AC004466  
 R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.4e-78:413:95//  
 M27877  
 R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74//  
 AC004819  
 R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey se-  
 quence.//0.0011:210:61//AQ040519  
 R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

R-PLACE1002881

R-PLACE1002908//HS\_3064\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985

R-PLACE1002941

R-PLACE1002962

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921

R-PLACE1002996//HS\_2064\_A1\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS\_2244\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616

R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479

R-PLACE1003176

R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095

R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551

R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139

R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11.//7.6e-114:567:96//AF086432

R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416

R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099

R-PLACE1003258

R-PLACE1003296//Diphoropria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952

R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9.//1.7e-91:458:96//M27877

R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243

R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460

R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153

R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715

R-PLACE1003361



R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805  
 R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174  
 R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//1.2e-62:434:83//AC004771  
 R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350  
 R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878  
 R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//2.4e-13:175:76//AC005695  
 R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587  
 R-PLACE1003454//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//0.47:411:58//AL009014  
 R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125  
 R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.6e-37:319:81//AC006080  
 R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480  
 R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859  
 R-PLACE1003521//HS\_3252\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562  
 R-PLACE1003528//HS\_2041\_B1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483  
 R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404  
 R-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297  
 R-PLACE1003566  
 R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965  
 R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571  
 R-PLACE1003584  
 R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032  
 R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066  
 R-PLACE1003596//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597  
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200  
 R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081  
 R-nnnnnnnnnnnnn  
 R-PLACE1003618//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451  
 R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688  
 R-PLACE1003638//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312  
 R-PLACE1003669//HS\_3054\_A2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713  
 R-PLACE1003704//HS\_3213\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784  
 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067  
 R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607  
 R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-

44:505:73//AL022336

R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357

R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023

R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//AC003070

R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//5.4e-12:189:71//AC005919

R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160

R-PLACE1003783

R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659

R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933

R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558

R-PLACE1003850

R-PLACE1003858

R-nnnnnnnnnnnnn

R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete sequence.//8.7e-33:285:81//AC000072

R-nnnnnnnnnnnnn

R-PLACE1003886

R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//AC004069

R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810

R-PLACE1003903//Homo sapiens full-length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422

R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520

R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281

R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:342:85//Z74022

R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030

R-PLACE1003968//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-62, complete sequence.//1.3e-07:245:65//AL010247

R-PLACE1004104

R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485

R-PLACE1004118//HS\_3092\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151

R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085

R-PLACE1004149//HS\_2253\_A2\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711

R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295

R-PLACE1004161

R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071

R-PLACE1004197//RPCI11-69N15.TK RPCI11 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515

R-PLACE1004203//Homo sapiens semaphorin L (SEMA) mRNA, complete cds.//3.4e-105:501:98//AF030698

R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//AL021326

R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:61//AC006031

R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470

R-PLACE1004258//HS\_3034\_A1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936

R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234

5 R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308

R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//5.8e-31:340:75//AC005920

10 R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095

R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588

R-PLACE1004336//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383

15 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817

20 R-PLACE1004388//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027

25 R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532

R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296

R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283

30 R-PLACE1004451//HS\_2258\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189

R-PLACE1004460

R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621

35 R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333:70//AC004389

R-PLACE1004473

R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584

40 R-PLACE1004506

R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427

R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071

45 R-PLACE1004518

R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666

R-PLACE1004550

50 R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931

R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800

R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136

55 R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876

R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343

R-nnnnnnnnnnnn//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey se-

quence.//2.2e-81:433:94//AQ283692

R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606

R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860

R-PLACE1004686

R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859

R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448

R-PLACE1004716//CITBI-E1-2519C14. TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965

R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507

R-PLACE1004736

R-PLACE1004740

R-nnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556

R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//AC002523

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367

R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010

R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178

R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250

R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126

R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666

R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669

R-PLACE1004836//HS\_2270\_A2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110

R-PLACE1004838//CIT-HSP-2343E10. TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544

R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820

R-PLACE1004868//Human Chromosome X clone bWDX342, complete sequence.//0.57:344:59//AC004072

R-PLACE1004885//HS\_3235\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193

R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577

R-PLACE1004902

R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209

R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605

R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936

R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683

R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788

R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494

R-PLACE1004972

R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970

5 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308

R-PLACE1004985//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522

10 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925

R-PLACE1005027

R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775

R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SE-

15 QUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867

R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584

R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556

20 R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//2.1e-42:384:69//AC005495

R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401

25 R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476

R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195

R-PLACE1005111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845

30 R-PLACE1005128

R-PLACE1005146

R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140

R-nnnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018

35 R-PLACE1005181//HS\_2182\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787

R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161

R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043

40 R-PLACE1005232//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476

R-PLACE1005243

R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132

R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067

45 R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720

R-PLACE1005287//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744

R-PLACE1005305//HS\_3180\_B2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443

50 R-PLACE1005308

R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383

R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960

55 R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794

R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380

R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195  
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//3.0e-44:434:77//  
AC005291  
R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991  
5 R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//  
AC002477  
R-PLACE1005467//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE.//1.1e-40:328:81//Z93014  
R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
10 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-  
notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310  
R-PLACE1005477//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING  
DRAFT SEQUENCE.//0.020:216:66//AL023693  
15 R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//  
2.8e-44:327:70//AC005392  
R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164\_O\_3, complete sequence.//4.2e-23:284:  
74//AC004703  
R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631  
20 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185  
R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468  
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SE-  
QUENCE.//2.3e-76:395:96//AP000038  
R-PLACE1005530//C.familiaris CA repeat sequence (isolate ).//0.023:90:75//X86184  
25 R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:  
64//AL025928  
R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.069:305:60//  
AC005969  
R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//4.3e-105:587:  
30 91//AC004707  
R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971  
R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:  
77//AC004991  
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//  
35 AC004126  
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//  
U72788  
R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599  
R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405  
40 R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1  
ordered pieces.//5.6e-79:270:94//AC005840  
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382  
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//  
AF083255  
45 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//8.6e-08:505:  
58//AC005701  
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and  
polymorphic CA repeat.//3.2e-27:307:72//Z82203  
R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey se-  
50 quence.//0.030:91:70//B15144  
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II  
(COL2A1) gene.//5.2e-10:587:59//L10171  
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810  
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635  
55 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601  
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//D42087  
R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024  
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//

AC004827

R-PLACE1005803

R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75//AC002530

5 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150

R-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745

R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763 R-PLACE1005850

10 R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-06:318:63//AC004887

R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931

R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281

15 R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139

R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21,-genomic survey sequence.//4.8e-84:494:89//AQ261347

R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243

20 R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719

R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654

R-PLACE1005934

25 R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//0.00021:272:62//AF069716

R-PLACE1005951

R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429

R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131

30 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863

R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086

35 R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866

R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177

R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375

R-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266:83//AF072521

40 R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete sequence.//1.8e-17:164:82//AC000077

R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139

R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906

45 R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-18:220:74//AC004885

R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63//AJ005122

R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454

50 R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68//AC004849

R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455:59//Z98551

R-PLACE1006157//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557

55 R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01\_124\_D\_3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006103

R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-

28:342:75//U91328

R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555

R-nnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433

5 R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410

R-PLACE1006196

R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398

10 R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362

R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877

R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970

R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142

15 R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034

R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548

R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087

20 R-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320

R-PLACE1006318

R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560

R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987

25 R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276

R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398

R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630

30 R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232

R-PLACE1006382

R-PLACE1006385//Mus musculus intersectin-EH binding protein lbp2 mRNA, partial cds.//1.4e-50:350:86//AF057286

35 R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854

R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804

R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985

40 R-PLACE1006445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726

R-PLACE1006469

R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152

R-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977

45 R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//0.78:44:95//AC005972

R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100

R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158

50 R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197

R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934

R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209

55 R-PLACE1006552//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865

R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710

R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//



2.9e-116:590:95//U97670

R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050

R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331

R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128

R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038

R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882

R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024

R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154

R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172

R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626

R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622

R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984

R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865

R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599

R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083

R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793

R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507

R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174

R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062

R-PLACE1006829

R-PLACE1006860

R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378

R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155

R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232

R-nnnnnnnnnnnnn

R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203

R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184

R-PLACE1006932

R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061

R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482

R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//6.7e-42:295:86//AC005544

R-PLACE1006962//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349

R-PLACE1006966//HS\_2219\_B2\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequencer.//0.019:180:63//AQ145873

R-PLACE1006989

R-PLACE1007014

R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845

R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693

R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895

R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368

R-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//2.7e-32:379:73//U72194

R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688

R-PLACE1007112//Cynops cornifex cytb gene.//0.020:427:58//AJ228479

R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09.//5.7e-107:535:96//AF074987

R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050

R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283

R-PLACE1007226

R-PLACE1007238

R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495

R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454

R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970

R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908

R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.4e-10:135:74//AC006080

R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291

R-PLACE1007282//B.garinii (strain TIs1) p83/100 gene (partial).//0.95:183:60//X81533

R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158

R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195

R-PLACE1007317//Drosophila dasyncemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253

R-PLACE1007342

R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870

R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507

R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709

R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261

R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081

R-PLACE1007460

R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-

brary) complete sequence.//7.0e-08:335:60//AC004241

R-PLACE1007484

R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373

R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559

R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-79:387:96//AC004231

R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682

R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381

R-PLACE1007544

R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds.//4.0e-17:108:97//U77706

R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465

R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179

R-PLACE1007618

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176

R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840

R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408

R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149

R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367

R-PLACE1007688

R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044

R-PLACE1007697

R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243

R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854

R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//3.8e-53:415:81//U60269

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585

R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169

R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560

R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820

R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z37981

R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116

R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104

R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//0.00052:455:61//AC002379

R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275

R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010

R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309

R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:551:70//AL022162

R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754

R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905  
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956  
R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095  
R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157  
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530  
R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529  
R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262  
R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933  
R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346  
R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628  
R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840  
R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592  
R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232  
R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036  
R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157  
R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919  
R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955  
R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939  
R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849  
R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748  
R-PLACE1008198  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102  
R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549  
R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688  
R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562  
R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611  
R-nnnnnnnnnnnnn  
R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272  
R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308  
R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886  
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176  
R-PLACE100833//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226  
R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR.//2.5e-98:556:90//AF036145  
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011

R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244

5 R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417

R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604

R-nnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326

10 R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177

R-PLACE1008424

R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864

15 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576

R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335

R-PLACE1008455

20 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526

R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696

R-PLACE1008488

25 R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778

R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555

R-PLACE1008532

30 R-PLACE1008533

R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623

R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074

35 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120

R-nnnnnnnnnnnnn

R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297

R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836

40 R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826

R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096

R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001

45 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333

R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742

R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406

50 R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147

R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841

55 R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864

R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088  
 R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366O14, genomic survey se-  
 quence.//3.5e-35:223:89//AQ079210  
 5 R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//  
 AF030933  
 R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
 R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 un-  
 ordered pieces.//2.9e-28:207:87//AC004581  
 10 R-nnnnnnnnnnnnn//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey se-  
 quence.//8.9e-30:166:97//B93289  
 R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//  
 AC005058  
 R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-  
 37:585:67//AC004932  
 15 R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G\_17, complete sequence.//0.0022:409:60//  
 AC005820  
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
 R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4,  
 WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
 20 R-PLACE1008934  
 R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//9.8e-84:429:  
 92//AC005495  
 R-PLACE1008947  
 R-PLACE1009020  
 25 R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like pro-  
 tease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
 R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs,  
 GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
 R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//2.9e-06:160:  
 30 70//AC004707  
 R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last  
 coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene  
 downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:  
 339:66//AL023694  
 35 R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
 R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//  
 0.00075:79:83//AJ005074  
 R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-  
 13:212:73//AC004783  
 40 R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
 R-PLACE1009099  
 R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete se-  
 quence.//5.1e-17:301:66//AC004025  
 R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 45 DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
 R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551  
 R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* , WORKING DRAFT SEQUENCE.//2.3e-  
 118:614:95//AJ011929  
 R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SE-  
 50 QUENCE.//1.4e-107:584:93//AP000031  
 R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876  
 R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//2.8e-44:360:71//  
 AC005972  
 R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
 55 R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//  
 AC004925  
 R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5')  
 two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and

STSs, complete sequence.//1.9e-46:572:69//Z84480  
 R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070  
 R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560  
 R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248  
 5 R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392  
 R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818  
 R-PLACE1009308  
 10 R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801  
 R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:85//AC006120  
 R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176  
 15 R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140  
 R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989  
 R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915  
 20 R-PLACE1009388  
 R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61//AC002427  
 R-nnnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038  
 25 R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:96//AC005919  
 R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598  
 30 R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151  
 R-PLACE1009459  
 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531  
 35 R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213  
 R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321  
 R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160  
 40 R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427  
 45 R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614  
 R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146  
 R-PLACE1009581  
 50 R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006  
 R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051  
 R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230  
 55 R-PLACE1009613//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266  
 R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222  
 R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109

R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024

R-PLACE1009794

R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116

R-nnnnnnnnnnnnn

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874

R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482

R-PLACE1010076//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699

R-PLACE1010083



R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59//B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cpg85a61rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein varI.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370

R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

5 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467

10 R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

15 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

20 R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682

25 R-PLACE1010802//Phoebeis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524

30 R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507:90//AB020868

35 R-PLACE1010870//RPCI11-59K21:TK RPCI11 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

40 R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

45 R-PLACE1010917

R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243

50 R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522

55 R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//

AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//0.99:267:60//

AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

5 R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

10 R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

15 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

20 R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

25 R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

30 R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

35 R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478

40 R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

45 R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

50 R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

55 R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299:86//  
 5 AC006236  
 R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey se-  
 quence.//4.5e-54:295:94//AQ058140  
 R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907  
 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-  
 10 34:200:79//AC005628  
 R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//  
 AC003083  
 R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey se-  
 quence.//1.8e-48:389:79//AQ112243  
 15 R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING  
 DRAFT SEQUENCE.//0.0027:95:76//AL022315  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147  
 R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
 5.9e-40:310:84//AC004832  
 20 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219  
 R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910  
 R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part  
 of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-  
 25 38:285:84//AL031730  
 R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING  
 DRAFT SEQUENCE.//4.3e-113:559:97//AL031848  
 R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricle light chain, exon 1.//0.00041:347:61//  
 X16325  
 30 R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067  
 R-PLACE2000132  
 R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete  
 sequence.//0.0032:310:61//AL008974  
 R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING  
 35 DRAFT SEQUENCE.//1.1e-111:566:96//AL020995  
 R-PLACE2000164  
 R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598  
 R-PLACE2000172  
 40 R-PLACE2000176  
 R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
 DRAFT SEQUENCE.//8.7e-45:298:87//AL008718  
 R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897  
 R-PLACE2000223  
 45 R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271  
 R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58  
 unordered pieces.//9.1e-41:282:86//AC005902  
 R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 50 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181  
 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:  
 67//AC002394  
 R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//  
 AC003043  
 55 R-PLACE2000305//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING  
 DRAFT SEQUENCE.//1.2e-43:295:85//Z93015  
 R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-  
 threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147

5 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963

10 R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734

15 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917

R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059

20 R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216

R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273

R-PLACE2000419

25 R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379

R-PLACE2000435

30 R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521

R-PLACE2000450 4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence.//5.1e-116:570:97//AC005740

35 R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460

R-PLACE2000477//M.musculus tex264 mRNA (3'region).//7.5e-06:117:76//X80427

R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976

40 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648

R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156

45 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026

R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200

R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645

50 R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735

R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237

55 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//6.9e-106:549:94//AC005277

R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

R-PLACE3000157

R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500

R-PLACE3000160

R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//AC006130

R-PLACE3000194

R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//7.2e-61:394:89//AC005291

R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.23:309:57//U52112 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//1.1e-15:156:81//B54637

R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594

R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720

R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363:80//AC004167

R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786

R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626

R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I35489

R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169

R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307

R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379

R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081

R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328

R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884

R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037

R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006

R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:230:84//AC005480

R-PLACE3000339

R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055

R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL022323

R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142

R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712

R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197

R-PLACE3000363

R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487:76//AC002465

R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699

R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722

R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00098:444:60//AC005231

R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506

R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023

R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003

R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//2.4e-44:466:74//AF104455

R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718

R-PLACE3000413

R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612

R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627

R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899

R-PLACE3000477

R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352

R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984

R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379

R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557

R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356

R-PLACE4000089//RPCI11-15I1.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-15I1, genomic survey sequence.//3.2e-07:284:60//B82414

R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506

R-PLACE4000100

R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010

R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969

R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034

R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939

R-PLACE4000192

R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631

R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981

R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//5.7e-59:558:76//AC005821

R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381

R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.5e-39:311:83//AC005920

R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410

R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510

R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675

R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339

R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete



sequence.//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829

R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342

R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//2.9e-44:465:75//AC002996

R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844

R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422

R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157

R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573

R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528

R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300

R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318

R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142

R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114

R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//3.4e-37:425:73//AC005703

R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536

R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

70:553:81//Z83841

R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732

R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271

R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//AC004139

R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698

R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552

R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482

R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115

R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039

R-THYRO 1000242

R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152

R-THYRO1000270

R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664

R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068

R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091

R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777

R-nnnnnnnnnnnnn

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523

R-THYRO 1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO 1000569

R-THYRO1000570//Homo sapiens full-length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408

R-nmmmmnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587

R-THYRO 000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675  
 R-THYRO 1000605  
 R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//  
 AC005546  
 5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs  
 and GSSs, complete sequence.//4.0e-06:249:63//AL022323  
 R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998  
 R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572  
 R-nnnnnnnnnnnnn  
 10 R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains  
 endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005  
 R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:  
 64//AC004069  
 R-THYRO1000684  
 15 R-THYRO1000699  
 R-THYRO1000712  
 R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460  
 R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
 R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660  
 20 R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558  
 R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey se-  
 quence.//1.2e-81:391:99//AQ038226  
 R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//  
 AC004617  
 25 R-THYRO1000793  
 R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
 DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
 R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered piec-  
 es.//4.7e-40:362:76//AC002555  
 30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
 DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
 R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788  
 R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angel-  
 man Syndrome region, complete sequence.//3.3e-57:522:76//AC004738  
 35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE,  
 9 unordered pieces.//4.2e-17:291:69//AC005849  
 R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs,  
 complete sequence.//1.1e-41:419:75//AL031592  
 R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-  
 40 ING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
 R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING  
 DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
 R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 1.0e-97:554:92//AC006015  
 45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:  
 566:94//AF079529  
 R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
 R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 un-  
 ordered pieces.//8.9e-61:479:81//AC004229  
 50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//  
 AF047440  
 R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//  
 AC006126  
 55 R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//0.99:71:78//  
 AC005562  
 R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
 WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727

R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677

R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070

R-THYRO1001120

R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO 1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

R-THYRO 1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-nnnnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPCI11-69F22.TK RPCI1 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece.//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnnnn

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-

56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

5 R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

10 R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cyttauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225

15 R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA10003131//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

20 R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

25 R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171:65//B88000

30 R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033

35 R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

40 R-Y79AA1000540//Z.diploperemnis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

45 R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

50 R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

55 R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

R-nnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

5 R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

10 R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

15 R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

20 R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

25 R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259

R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

30 R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

35 R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112

40 R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110i133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

45 R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

50 R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221

55 R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,

complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336

R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic MseI fragment, clone 72f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PIUS mRNA, complete cds.//2.3e-90:557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey sequence.//8.5e-21:147:91//B75354

R-Y79AA1002139

R-Y79AA1002204

R-nnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:59//U13616

R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415

R-Y79AA1002210



R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133  
 R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//5.9e-07:535:57//AL034557  
 R-Y79AA1002229  
 5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592  
 R-Y79AA1002246  
 R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384  
 R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331  
 10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534  
 R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//  
 1.1e-07:368:61//AC005887  
 R-Y79AA1002351  
 R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65b9, reverse read cpg65b9.rt1a.//  
 15 0.57:59:79//Z62206  
 R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//2.0e-98:385:99//  
 AC005920  
 R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:  
 76//AC004662  
 20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
 quence.//6.3e-08:103:80//AC004087  
 R-Y79AA1002431  
 R-nnnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284  
 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-  
 25 103:525:96//AC006116  
 R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//9.7e-38:302:  
 83//AC006238  
 R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

#### 30 Homology Search Result Data 4.

**[0307]** The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

**[0308]** Data include

35 the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

40 **[0309]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069  
 F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
 L40157  
 45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668  
 F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
 F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
 F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
 myces cerevisiae]//0.00019:192:65//Hs.7900:W22411  
 50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
 F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
 F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
 F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
 342:61//Hs.14207:U86453  
 55 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:  
 AB018340  
 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200  
 F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

Hs.135552:AI215187

F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309

F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079

5 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802

F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133

F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847

10 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529

F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984

F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231

15 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377

F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703

F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460

F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562

F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568

20 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186

F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406

F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664

F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095

F-HEMBA1000303

25 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946

F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898

F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965

F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961

30 F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712

F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503

F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548

F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802

F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087

35 F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010

F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520

40 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008

F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253

F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875

45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893

50 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875

F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853

F-HEMBA1000469

55 F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561

F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551

F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:  
 D13666  
 F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093  
 F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646  
 5 F-HEMBA1000518  
 F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881  
 F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:  
 84//Hs.155871:AA533783  
 F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:  
 10 87//Hs.22383:R51067  
 F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:  
 AA455706  
 F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080  
 F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809  
 15 F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389  
 F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:  
 K00629  
 F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684  
 F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729  
 20 F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:  
 AB018303  
 F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977  
 F-HEMBA1000568//EST//0.12:270:61//Hs.134833 :AI091046  
 F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042  
 25 F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681  
 F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//  
 Hs.55084:AA479162  
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:  
 AJ007509  
 30 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241  
 F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.0e-68:574:  
 79//Hs.159176:U92019  
 F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535  
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925  
 35 F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333  
 F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:  
 AA643235  
 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:  
 AB014590  
 40 F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174  
 F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582  
 F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912  
 F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073  
 F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878  
 45 F-HEMBA1000686  
 F-HEMBA1000702  
 F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309  
 F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850  
 F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630  
 50 F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881  
 F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491  
 F-HEMBA1000747  
 F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568  
 F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716  
 55 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239  
 F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803  
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216  
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843  
 5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237  
 10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154  
 F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
 15 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
 nomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046  
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537  
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142  
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:  
 20 AB011119  
 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//  
 Hs.111445:H00596  
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:  
 AA609476  
 25 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phos-  
 phoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199  
 F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//  
 0.080:128:71//Hs.118972:AA761369  
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161  
 30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903  
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775  
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314  
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.  
 159564:AF061936  
 35 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.  
 127338:AB007961  
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895  
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835  
 40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.  
 46468:U45984  
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:  
 AB007937  
 45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572  
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.  
 159897:AB007970  
 50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142  
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515  
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881  
 F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971  
 F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:  
 55 U06088  
 F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813  
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420  
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750

F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497

F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940

F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917

F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341

F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582

F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457

F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226

F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499

F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463

P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717

F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694

F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058

F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046

F-HEMBA1001265

F-HEMBA1001281

F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117

F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017798

F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726  
 5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499  
 10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390  
 15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144  
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451  
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219  
 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054  
 20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503  
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902  
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869  
 F-HEMBA1001526  
 25 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476  
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580  
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652  
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205  
 30 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814  
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449  
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184  
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228  
 35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988  
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918  
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210  
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400  
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870  
 40 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536  
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899  
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204  
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560  
 45 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283  
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121  
 F-HEMBA1001661  
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943  
 50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953  
 F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788  
 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060  
 F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760  
 55 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995  
 F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836  
 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114  
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

vegicus//3.0e-30:195:92//Hs.132948:AA194452  
 F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554  
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197  
 F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363  
 5 F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415  
 F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250  
 F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924  
 F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328  
 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:  
 10 N41598  
 F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622  
 F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:  
 AB007943  
 F-HEMBA1001791  
 15 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570  
 F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817  
 F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233  
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.5e-175:809:98//Hs.  
 118164:AB007969  
 20 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305  
 F-HEMBA1001815  
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.  
 158174:U66561  
 F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845  
 25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:  
 AF064244  
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:  
 AF071309  
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078  
 30 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.I55243:N70293  
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324  
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:  
 AB014517  
 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121  
 35 F-HEMBA1001866//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922  
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036  
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.  
 158095:AB007953  
 40 F-HEMBA1001896  
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346  
 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633  
 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:  
 200:62//Hs.9573:AF027302  
 45 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511  
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141  
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:  
 855:99//Hs.154934:AF000145  
 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295  
 50 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221  
 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882  
 F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943  
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360  
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//  
 55 Hs.25674:AF072242  
 F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930  
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803 :W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867: M93426

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26: 223:81//Hs.105292:AA504776

F-HEMBA1002084

F-HEMBA1002092

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21: 124:96//Hs.101842:L32832

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263

F-HEMBA1002151

F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs. 158241:AB007976

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245

F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589

F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs. 159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696

F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767

F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906: AA001281

F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs. 67619:AB007957

F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394

F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455

F-HEMBA1002241

F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs. 159564:AF061936

F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420

F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60// Hs.150926:AF017445

F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404

F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60// Hs.77729:AB010710

F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982



- F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
 F-HEMBA10023481/EST//1.0e-19:285:70//Ms.121860:AA776692  
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563  
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
 10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289  
 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561  
 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490  
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783  
 20 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133  
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
 F-HEMBA1002495  
 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972  
 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951  
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
 F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587  
 40 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351  
 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 55 F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142  
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497  
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368  
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457  
 5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164  
 F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221  
 10 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924  
 F-HEMBA1002712  
 F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800  
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521  
 15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811 :AB007867  
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596  
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372  
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786  
 20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817  
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126  
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947  
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809  
 25 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392  
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326  
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756  
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938  
 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185  
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744  
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119  
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904  
 35 F-HEMBA1002833  
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550  
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823  
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730  
 40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429  
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679  
 F-HEMBA1002921  
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001  
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915  
 45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148  
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053  
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703  
 50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460  
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925  
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099  
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092  
 55 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828  
 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219  
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) //1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564  
 F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525  
 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219  
 5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486  
 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080  
 F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454  
 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003  
 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514  
 10 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182  
 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438  
 F-HEMBA1003067  
 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164  
 15 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865  
 F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454  
 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461  
 F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881  
 20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721  
 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872  
 F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721  
 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802  
 25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575  
 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314  
 F-HEMBA1003136  
 F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279  
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670  
 30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588  
 F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740  
 F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895  
 35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523  
 F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135  
 F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412  
 F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080  
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765  
 40 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784  
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310  
 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012  
 F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694  
 45 F-HEMBA1003250  
 F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292  
 F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991  
 F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020  
 50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864  
 F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867  
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662  
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:AB011109  
 55 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912  
 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160  
 F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872  
 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459  
 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254  
 5 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328  
 F-HEMBA1003330  
 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329  
 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092  
 10 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159  
 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819  
 F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637  
 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017  
 F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552  
 15 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488  
 F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813  
 F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959  
 F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309  
 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546  
 20 F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962  
 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696  
 F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378  
 F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632  
 25 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578  
 F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600  
 F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443  
 F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067  
 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811  
 30 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559  
 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311  
 F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833  
 F-HEMBA1003556  
 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122  
 35 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327  
 F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113  
 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972  
 F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546  
 40 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232  
 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285  
 F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405  
 F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827  
 45 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916  
 F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782  
 F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344  
 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954  
 50 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750  
 F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159  
 F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591  
 55 F-HEMBA1003640//ESTs//1.1e-11:267:661//Hs.34359:AI122791  
 F-HEMBA1003645  
 F-HEMBA1003646  
 F-HEMBA1003656

F-HEMBA1003662  
 F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381  
 F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906  
 F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204  
 5 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072  
 F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691  
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187  
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116  
 10 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995  
 F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760  
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317  
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921  
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839  
 15 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503  
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid  
 R31180//0.16:242:62//Hs.153325:AC005390  
 F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946  
 20 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984  
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920  
 F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327  
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172  
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064  
 25 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815  
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239  
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108  
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721  
 30 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516  
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.I45447:AI204220  
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314  
 F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167  
 35 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367  
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U52840  
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002  
 F-HEMBA1003880  
 40 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295  
 F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675  
 F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236  
 F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097  
 45 F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875  
 F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389  
 F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562  
 F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0.0029:222:61//Hs.I44236:W52380  
 F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055  
 50 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580  
 F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230  
 F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567  
 F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965  
 55 F-HEMBA1003978  
 F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009  
 F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456  
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

0.022:349:58//Hs.104640:AF000561  
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573  
 5 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.I5519:AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930  
 F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI312281  
 10 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.I62529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.46328:D87942  
 15 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.46468:U45984  
 20 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957  
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064  
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759  
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260  
 25 F-HEMBA1004143  
 F-HEMBA1004146  
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056  
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341  
 30 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427  
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.10092:AI189282  
 35 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040  
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748  
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514  
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.I63588:AI073878  
 F-HEMBA1004238  
 40 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571  
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522  
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876  
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112  
 45 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:AB014588  
 F-HEMBA1004272  
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444  
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331  
 50 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795  
 F-HEMBA1004289  
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484  
 55 F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047  
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314  
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367  
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612  
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062  
 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888  
 5 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606  
 F-HEMBA1004341  
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667  
 F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968  
 10 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376  
 F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928  
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800  
 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019  
 15 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250  
 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818  
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199  
 F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:AI246426  
 20 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531  
 F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219  
 F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080  
 F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606  
 25 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984  
 F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450  
 F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600  
 F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431  
 F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503  
 30 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492  
 F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800  
 F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416  
 F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381  
 35 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552  
 F-HEMBA1004554  
 F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331  
 F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802  
 F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825  
 40 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238  
 F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661  
 F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370  
 45 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606  
 F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198  
 F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178  
 F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416  
 50 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891  
 F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780  
 F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522  
 F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083  
 F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796  
 55 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582  
 F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141  
 F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252  
 F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235  
 25 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971  
 30 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 55 F-HEMBA1004972  
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946



F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548  
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560  
 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193  
 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381  
 20 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561  
 25 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547  
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144  
 40 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs,128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723  
 55 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581  
 F-HEMBA1005353//EST//5.4e-09:2:22:68//Hs.119508:AA485732  
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:

AF071787

F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452

5 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951

10 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807

F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347

F-HEMBA1005411

15 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248

F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687

F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

20 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219

25 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694

F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957

30 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

35 F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280

40 F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471

F-HEMBA1005530

F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376

45 F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

50 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

55 F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA

FORMS//0.54:439:591//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
 F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280  
 5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845  
 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
 F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
 10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956  
 F-HEMBA1005666  
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142  
 F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
 15 F-HEMBA1005680  
 F-HEMBA1005685  
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406  
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
 20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697  
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 25 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
 30 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984  
 40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880  
 45 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
 F-HEMBA1005963  
 F-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
 50 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
 F-HEMBA1006002  
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151  
 55 F-HEMBA1006031  
 F-HEMBA1006035  
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422  
 F-HEMBA1006081  
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788  
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313  
 5 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799  
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741  
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968  
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222  
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372  
 10 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734  
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881  
 F-HEMBA1006155  
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575  
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627  
 15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117  
 F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540  
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557  
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046  
 F-HEMBA1006252  
 20 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706  
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341  
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631  
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140  
 25 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770  
 F-HEMBA1006283  
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964  
 F-HEMBA1006291  
 F-HEMBA1006293  
 30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285  
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174  
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350  
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789  
 35 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142  
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220  
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287  
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244  
 40 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026  
 F-HEMBA1006377//Homo sapiens RaiBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233  
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922  
 45 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531  
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503  
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477  
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881  
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830  
 50 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835  
 F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264  
 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194  
 F-HEMBA1006445  
 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889  
 55 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369  
 F-HEMBA1006467  
 F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453  
 F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:

AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

5 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

10 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

15 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898

20 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778

25 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

30 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

35 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282

40 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

45 F-HEMBA1006676

F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198

F-HEMBA1006708

50 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

55 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-  
 SOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC  
 15 REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214  
 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065 :366:621//Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:  
 AJ010841  
 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.  
 14934:AF004828  
 F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447:89//  
 Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:  
 35 70//Hs.43003:AF035812  
 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:  
 M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:  
 57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085  
 F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-  
 39:248:90//Hs.157148:AA311921  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:  
 D86987  
 F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252  
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:  
 5 AB018340  
 F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.  
 82314:M31642  
 F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204  
 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575  
 10 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:  
 U13695  
 F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836  
 F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475  
 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529  
 15 F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637  
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062  
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615  
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506  
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634  
 20 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241  
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]/3.5e-09:144:76//Hs.20597:  
 W58370  
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130  
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006  
 25 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561  
 F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568  
 F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073  
 F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.  
 83428:M58603  
 30 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307  
 F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392  
 F-HEMBA1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z46788  
 F-HEMBA1000036  
 F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:  
 35 98//Hs.20815:AF084928  
 F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358  
 F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319  
 F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131  
 F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717  
 40 F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503  
 F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923  
 F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304  
 F-HEMBA1000083  
 F-HEMBA1000089//EST//0.0016:192:661//Hs.137093:AA917621  
 45 F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645  
 F-HEMBA1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627  
 F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763  
 F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521  
 F-HEMBA1000136//ESTs//112.3e-101:507:96//Hs.12659:AA195207  
 50 F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044  
 F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881  
 F-HEMBA1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715  
 F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646  
 F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457  
 55 F-HEMBA1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:  
 AB011129  
 F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277  
 F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013

F-HEM BB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEM BB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEM BB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483  
 5 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981//Hs.151411:AF075587  
 F-HEM BB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEM BB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEM BB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 10 F-HEM BB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684  
 F-HEM BB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEM BB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEM BB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEM BB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326  
 15 F-HEM BB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEM BB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEM BB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEM BB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 20 F-HEM BB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEM BB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEM BB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219  
 F-HEM BB1000341  
 F-HEM BB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 25 F-HEM BB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874  
 F-HEM BB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970  
 F-HEM BB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEM BB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEM BB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 30 F-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEM BB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEM BB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEM BB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEM BB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735AF010144  
 35 F-HEM BB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEM BB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEM BB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEM BB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 40 F-HEM BB1000472  
 F-HEM BB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEM BB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEM BB1000491  
 45 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEM BB1000510//Glucocorticoid receptor alpha {alternative products}//1.6e-46:409:77//Hs.102761:U25029  
 F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEM BB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 50 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996  
 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 55 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293  
 F-HEM BB1000564  
 F-HEM BB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001



F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEMBB10005891//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 5 F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990  
 F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323  
 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589  
 F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481  
 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 15 F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924  
 F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 20 F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 25 F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703  
 F-HEMBB1000709//EST//0.99:110:651//Hs.162437:AA577510  
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 30 F-HEMBB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216  
 F-HEMBB1000763  
 F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390  
 35 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577  
 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 40 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA66887  
 F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
 45 F-HEMBB1000827  
 F-HEMBB1000831  
 F-HEMBB1000835//EST//4.3e-27:201:851//Hs.141451:N29915  
 F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503  
 50 F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
 55 F-HEMBB1000887  
 F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290  
 F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433  
 F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834

F-HEM BB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
 F-HEM BB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEM BB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEM BB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
 5 F-HEM BB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEM BB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEM BB1000947  
 F-HEM BB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEM BB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 10 F-HEM BB1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEM BB1000981  
 F-HEM BB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEM BB1000991//EST//0.12:125:66//Hs.22945:R43713  
 15 F-HEM BB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055  
 F-HEM BB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEM BB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310  
 20 F-HEM BB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEM BB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEM BB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970  
 F-HEM BB1001037//EST//0.0057:192:66//Hs.149987:AI291177  
 25 F-HEM BB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721  
 F-HEM BB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEM BB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 30 F-HEM BB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942  
 F-HEM BB1001063  
 F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEM BB1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEM BB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 35 F-HEM BB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84:75//Hs.112434:U50529  
 F-HEM BB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEM BB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 40 F-HEM BB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEM BB1001119  
 F-HEM BB1001126  
 F-HEM BB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEM BB1001137  
 45 F-HEM BB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329  
 F-HEM BB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854  
 F-HEM BB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716  
 F-HEM BB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863  
 F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334  
 50 F-HEM BB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEM BB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129  
 F-HEM BB1001199  
 F-HEM BB1001208//ESTs//0.12:120:69//Hs.130093:AA928802  
 55 F-HEM BB1001209//EST//0.00028:215:65//Hs.118276:W15258  
 F-HEM BB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452  
 F-HEM BB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157  
 F-HEM BB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

158241:AB007976

F-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790

F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754

F-HEM BB1001249//EST//0.26:203:63//Hs.140791:AA935909

F-HEM BB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEM BB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

F-HEM BB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828

F-HEM BB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEM BB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:U13045

F-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021

F-HEM BB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEM BB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEM BB1001302

F-HEM BB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEM BB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEM BB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219

F-HEM BB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEM BB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222

F-HEM BB1001335

F-HEM BB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135

F-HEM BB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

F-HEM BB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEM BB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

F-HEM BB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEM BB1001364

F-HEM BB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEM BB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219

F-HEM BB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEM BB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

F-HEM BB1001384

F-HEM BB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

F-HEM BB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

F-HEM BB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEM BB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEM BB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174

F-HEM BB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175

F-HEM BB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEM BB1001443

F-HEM BB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEM BB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEM BB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEM BB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEM BB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740

F-HEM BB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303

F-HEM BB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942  
 F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815  
 F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735  
 5 F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093  
 F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748  
 F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306  
 10 F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315  
 F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240  
 F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953  
 F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080  
 15 F-HEMBB1001585  
 F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708  
 F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289  
 F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414  
 F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680  
 20 F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314  
 F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713  
 F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077  
 F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172  
 F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279  
 25 F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480  
 F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407  
 F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519  
 F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546  
 30 F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496  
 F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430  
 F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664  
 F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398  
 35 F-HEMBB1001706  
 F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219  
 F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064  
 F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219  
 F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578  
 40 F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244  
 F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144  
 F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263  
 F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077  
 45 F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639  
 F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976  
 F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102  
 F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370  
 50 F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951  
 F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956  
 F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017  
 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209  
 55 F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190  
 F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067  
 F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858  
 F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219  
 F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752  
 F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371  
 5 F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503  
 F-HEMBB1001872  
 F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478  
 F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743  
 10 F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868  
 F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEMBB1001905  
 F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155  
 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742  
 15 F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEMBB1001911  
 F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113  
 20 F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245  
 F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398  
 F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875  
 25 F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053  
 F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:Z48051  
 35 F-HEMBB1001983  
 F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEMBB1002044  
 F-HEMBB1002045  
 F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512  
 F-HEMBB1002069  
 F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 55 F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080  
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027  
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

F-HEM BB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254  
 F-HEM BB1002189//EST//0.26:81:70//Hs.147726:AI220208  
 F-HEM BB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350  
 F-HEM BB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934  
 5 F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332  
 F-HEM BB1002218//EST//0.015:241:61//Hs.105298:AA489813  
 F-HEM BB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219  
 F-HEM BB1002247  
 F-HEM BB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 10 6.8e-47:418:77//Hs.125231:AF068006  
 F-HEM BB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:  
 AB011166  
 F-HEM BB1002255//ESTs//0.017:255:61//Hs.126786:U74314  
 F-HEM BB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//  
 15 Hs.58169:AF017790  
 F-HEM BB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998  
 F-HEM BB1002300  
 F-HEM BB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.  
 46468:U45984  
 20 F-HEM BB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083  
 F-HEM BB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054  
 F-HEM BB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188  
 F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:  
 AJ010841  
 25 F-HEM BB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991  
 F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:  
 U00943  
 F-HEM BB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838  
 F-HEM BB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796  
 30 F-HEM BB1002381  
 F-HEM BB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566  
 F-HEM BB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784  
 F-HEM BB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456  
 F-HEM BB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.  
 35 159897:AB007970  
 F-HEM BB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150  
 F-HEM BB1002442  
 F-HEM BB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087  
 F-HEM BB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101  
 40 F-HEM BB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274  
 F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885  
 F-HEM BB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//  
 Hs.74304:AF001691  
 F-HEM BB1002492//EST//0.24:149:62//Hs.146790:AI149051  
 45 F-HEM BB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:  
 M89796  
 F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494  
 F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725  
 F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354  
 50 F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503  
 F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719  
 F-HEM BB1002531  
 F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219  
 F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102  
 55 F-HEM BB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648  
 F-HEM BB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191  
 F-HEM BB1002579//EST//1.0:77:68//Hs.147935:AI250286  
 F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:  
 AF089749  
 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711  
 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811  
 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504  
 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//  
 0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC  
 25 REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922  
 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750  
 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:  
 AA001281  
 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-  
 50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:  
 40 AB011174  
 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//  
 Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:  
 AB011792  
 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:  
 AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:  
 219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050  
 55 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695  
 F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.  
 158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:  
 98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:  
 117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME  
 III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:  
 AF061573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:  
 AF034546  
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:  
 AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:  
 93//Hs.9043:W21827  
 55 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete  
 cds//0.58:311:63//Hs.66721:D49818  
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080



F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete  
 cds//5.8e-51:404:80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
 15 cds//8.8e-45:390:78//Hs.159523:AF001622  
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494  
 20 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:  
 25 AF023674  
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:  
 K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:  
 U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//  
 Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:  
 AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.  
 158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:  
 AF100141  
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580  
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:  
 50 AB011147  
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:  
 Z48051  
 55 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//  
 9.8e-19:131:76//Hs.118972:AA761369  
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 10 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.  
 35 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968  
 55 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:  
 61//Hs.98384:AF062006  
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038

F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178  
 F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882  
 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719  
 5 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503  
 F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749  
 10 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
 F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
 F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254  
 15 F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627  
 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045  
 F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915  
 20 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
 F-MAMMA1001133  
 F-MAMMA1001139  
 F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534  
 F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217  
 25 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
 F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147  
 F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
 F-MAMMA1001181  
 30 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171  
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
 F-MAMMA1001198  
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348  
 35 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776  
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087  
 40 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534  
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
 F-MAMMA1001244  
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476  
 45 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561  
 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
 50 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
 F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
 F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426  
 55 F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305  
 F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087  
 F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147  
 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806  
 F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197  
 5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267  
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258  
 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981  
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR//4.6e-09:415:58//Hs.839:M86826  
 10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402  
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763  
 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928  
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394  
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.  
 15 46328:D87942  
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108  
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321  
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590  
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040  
 20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053  
 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:  
 D78335  
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:  
 AA524909  
 25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366  
 F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269  
 F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795  
 F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506  
 F-MAMMA1001547  
 30 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:  
 AB007931  
 F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:  
 AI017072  
 F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764  
 35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339  
 F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132  
 F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375  
 F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266  
 F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152  
 40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727  
 F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc  
 Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-  
 67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger  
 protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and  
 45 DXS1055//1.4e-40:447:73//Hs.154353:AL022165  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796  
 F-MAMMA1001635  
 F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524  
 F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:  
 50 68//Hs.59829:AB014602  
 F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:  
 AB007917  
 F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 55 F-MAMMA1001671  
 F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317  
 F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889  
 F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549  
 F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984  
 F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548  
 5 F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926  
 F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634  
 F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098  
 F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768  
 10 F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245  
 F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503  
 F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632  
 F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822  
 15 F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109  
 F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.102576:AJ010230  
 F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072  
 F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832  
 20 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080  
 F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:U38276  
 F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940  
 25 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549  
 F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:K00627  
 F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869  
 F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987  
 30 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884  
 F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096  
 F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582  
 F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589  
 F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293  
 35 F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742  
 F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691  
 F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827  
 40 F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665  
 F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028  
 F-MAMMA1001854  
 F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218  
 F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060  
 45 F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209  
 F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687  
 F-MAMMA1001878  
 F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944  
 50 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576  
 F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078  
 F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521  
 F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874  
 F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529  
 55 F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859  
 F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317  
 F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878  
 F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:

N91115

F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915

5 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159

F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.158095:AB007953

F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580

F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225

10 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256

F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305

F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503

F-MAMMA1002078

F-MAMMA1002082

15 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012

F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:AJ010840

F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932

20 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219

F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963

F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638

F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338

F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837

25 F-MAMMA1002153

F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385

F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999

F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206

30 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

35 F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986

40 F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172

45 F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

50 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935

55 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776

F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481

F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956  
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291  
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908  
 5 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536  
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515  
 F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026  
 F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627  
 10 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254  
 F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633  
 F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591  
 15 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907  
 F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086  
 F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539  
 F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901  
 20 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733  
 F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818  
 F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830  
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923  
 F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345  
 25 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677  
 F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022  
 F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362  
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624  
 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632  
 30 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737  
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745  
 F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788  
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030  
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087  
 35 F-MAMMA1002446  
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809  
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707  
 F-MAMMA1002470  
 40 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779  
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059  
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460  
 45 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628  
 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920  
 F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392  
 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214  
 50 F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788  
 F-MAMMA1002554  
 F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822  
 F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421  
 55 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368  
 F-MAMMA1002573//ESTs//2.1e-4:8:265:94//Hs.155128:AI224516  
 F-MAMMA1002585  
 F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107  
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958  
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220  
 5 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895:  
 AA428463  
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357  
 F-MAMMA1002618  
 F-MAMMA1002619  
 10 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449  
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300  
 F-MAMMA1002625  
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.  
 158241:AB007976  
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:  
 15 AB006626  
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335  
 20 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:  
 25 D86987  
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915  
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697  
 30 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs.  
 46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165  
 35 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccha-  
 romyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312  
 F-MAMMA1002748  
 40 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902  
 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293  
 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782  
 F-MAMMA1002769  
 45 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//  
 7.6e-84:417:97//Hs.77705:U07563  
 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988  
 F-MAMMA1002782  
 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710  
 50 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919  
 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514  
 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:  
 AB011135  
 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067  
 55 F-MAMMA1002835  
 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta mi-  
 gratoria]//7.7e-38:179:78//Hs.141344:H29951  
 F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590



F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:AB018353

F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:AI357868

F-MAMMA1002858

5 F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643

F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284

F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423

F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632

10 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:D45027

F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270

F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657

F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666

F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265

15 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658

F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952

F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125

F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730

F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.102928:AI346344

20 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:AB014598

F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389

F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418

25 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884

F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400

F-MAMMA1002972

F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932

F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944

30 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645

F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931

F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.159897:AB007970

F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979

35 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:AF054174

F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372

F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062

F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951

40 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137

F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549

F-MAMMA1003035

F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391

F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750

45 F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639

F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336

F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742

F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518

50 F-MAMMA1003056

F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.96500:AI206781

F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618

F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531

55 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045

F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634  
 F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:AF105424  
 F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786  
 5 F-MAMMA1003140  
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062  
 F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087  
 F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632  
 10 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782  
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:AB014590  
 15 F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204  
 F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067  
 F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//Hs.46465:U45285  
 20 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210  
 F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:AB014561  
 F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689  
 25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:AF007155  
 F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054  
 F-NT2RM1000127  
 F-NT2RM1000131  
 30 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF5 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959  
 F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.110099:AB010419  
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:AF007155  
 35 F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382  
 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458  
 F-NT2RM1000242  
 F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105  
 40 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190  
 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516  
 F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:AI037879  
 45 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920  
 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047  
 F-NT2RM1000272  
 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144  
 50 F-NT2RM1000300  
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880  
 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205  
 F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976  
 F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798  
 55 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608  
 F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691  
 F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.163707:AA137181

F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507  
 F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353  
 F-NT2RM1000399  
 F-NT2RM1000421  
 5 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//  
 Hs.20815:AF084928  
 F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382  
 F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660  
 F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847  
 10 F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957  
 F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204  
 F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625  
 F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.ele-  
 gans]//6.2e-51:254:98//Hs.132096:AA314601  
 15 F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:  
 AF038957  
 F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297  
 F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279  
 F-NT2RM1000672  
 20 F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348  
 F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101  
 F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706  
 F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832  
 F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:  
 25 AB011139  
 F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208  
 F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465  
 F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885  
 F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 :  
 30 U39067  
 F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503  
 F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845  
 F-NT2RM1000800  
 F-NT2RM1000802  
 35 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208  
 F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957  
 F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422  
 F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726  
 F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148  
 40 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:  
 AJ010840  
 F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643  
 F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619  
 F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239  
 45 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1  
 gene//4.0e-155:750:97//Hs.132898:AC004770  
 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.  
 26285:AF082516  
 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:  
 50 AB014561  
 F-NT2RM1000894  
 F-NT2RM1000898  
 F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701  
 F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679  
 55 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350  
 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440  
 F-NT2RM1000978  
 F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//

Hs.58488:U97067

F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200

F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395

F-NT2RM1001044//ESTs, Weakly similar to C43E11.9[C.elegans]//3.0e-98:491:96//Hs.102173:AA045270

F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204

F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703

F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822

F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846

F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198

F-NT2RM1001085

F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244

F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331

F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564

F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495

F-NT2RM1001115

F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074

F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113

F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563

F-NT2RM2000030

F-NT2RM2000032//ESTs//7.1 e-18:138:68//Hs.114031:AA700958

F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243

F-NT2RM2000092

F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085

F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428

F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:97//Hs.18953:AF067223

F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999

F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:AB011162

F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520

F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500

F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981

F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:AB011132

F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251

F-NT2RM2000371

F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866

F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006

F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568

F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290

F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.76669:U08021

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812:AF061243

F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487

F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:

AI141736

F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220

F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108

F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508

5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128

F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [*Saccharomyces cerevisiae*]//1.4e-33:214:92//Hs.55609:W37993

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987

10 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220

F-NT2RM2000594

F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963

F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313

15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548

F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093

F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258

F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272

20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558

F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576

F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371

25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984

F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342

F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244

30 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [*Saccharomyces cerevisiae*]//4.2e-85:464:91//Hs.161551:W24286

F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750

F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338

F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701

35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046

F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [*D.melanogaster*]//6.2e-94:441:99//Hs.59075:AI023761

F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433

40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831

F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [*Saccharomyces cerevisiae*]//2.9e-48:282:93//Hs.17035:AI080471

F-NT2RM2001065

F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258

45 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153

F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190

F-NT2RM2001141

50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042

F-NT2RM2001177

F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [*C.elegans*]//2.4e-23:149:93//Hs.10618:AI288739

F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959

F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630

55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349

F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766

F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928

F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

AF039694

F-NT2RM2001256

F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845

F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601

F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800

F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902

F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729

F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431

F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518

F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952

F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725

F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301

F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195

F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907

F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129

F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356

F-NT2RM2001675

F-NT2RM20016811//ESTs//0.16:197:63//Hs.20585:R10305

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216

F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937

F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415

F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817

F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826

F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788

F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650

F-NT2RM2001718

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931

F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132

5 F-NT2RM2001743

F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399

F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742

10 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933

F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698

F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens I kappa B kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

20 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080

25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610

30 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931

F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840

35 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080

40 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392

F-NT2RM2001982

F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816

F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778

45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538

F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398

F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274

F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729

F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516

50 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427

F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154

F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377

F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840

55 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435

F-NT2RM2002128

F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274

F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:AB007936

F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.99936:X14487

F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563

F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074

F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464

F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674

F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511

F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H. sapiens]//1.6e-30:369:70//Hs.114623:AI204280

F-NT2RM4000086

F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865

F-NT2RM4000139

F-NT2RM4000155

F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632

F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853

F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044

F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190

F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744

F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147

F-NT2RM4000200

F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:AB006626

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:AB018255

F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651

F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458

F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582

F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439

F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.93841:AA442297

F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.46328:D87942

F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.31305:M99438

F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:AB000712

F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707

F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.12796:W27884

F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630

F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:M023761

F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542

F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745

F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718

F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029



F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046  
 F-NT2RM4000421  
 5 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166  
 F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820  
 F-NT2RM4000457  
 F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631//Hs.66369:U95040  
 10 F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004  
 F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632  
 F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915  
 F-NT2RM4000514  
 F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409  
 15 F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305  
 F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967  
 F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987  
 F-NT2RM4000534  
 20 F-NT2RM4000585  
 F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938  
 F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227  
 25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390  
 F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068  
 F-NT2RM4000616  
 F-NT2RM4000674  
 F-NT2RM4000689  
 30 F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529  
 F-NT2RM4000700  
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789  
 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181  
 35 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605  
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:AB018303  
 F-NT2RM4000741  
 40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.112361:R99396  
 F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815  
 F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731  
 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:AB007920  
 45 F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186  
 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306  
 F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:AI337820  
 50 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676  
 F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301  
 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387  
 F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568  
 55 F-NT2RM4000833  
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322  
 F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934  
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

ens]//4.4e-29:164:95//Hs.115095:AI392943

F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004

F-NT2RM4000950

F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546

F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875

F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:AB014539

F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:AB018254

F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:AI247543

F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//0.79:142:69//Hs.77424:M63835

F-NT2RM4001084

F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758

F-NT2RM4001116

F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701

F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730

F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145

F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351

F-NT2RM4001187

F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220

F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.14934:AF004828

F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205

F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70//Hs.104925:AF059611

F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.26676:AA033997

F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:AB007950

F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003

F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973

F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335

F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016

F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988

F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTER-GENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714

F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818

F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799

F-NT2RM4001384

F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575

F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520

F-NT2RM4001412

F-NT2RM4001414//ESTs, Moderately similar to 18547\_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817

F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087

F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914  
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784  
 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585  
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619  
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247  
 F-NT2RM4001557  
 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487  
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453  
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859  
 F-NT2RM4001582  
 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566  
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094  
 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077  
 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334  
 F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739  
 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946  
 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339  
 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320  
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323  
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638  
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957  
 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905  
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903  
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318  
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306  
 F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719  
 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270  
 F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677  
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105  
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547  
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712  
 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442  
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687  
 F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824  
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204  
 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814  
 F-NT2RM4001856  
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711  
 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984  
 F-NT2RM4001880  
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633  
 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875  
 F-NT2RM4001938  
 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162  
 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087  
 F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493  
 10 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341  
 F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082  
 F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936  
 15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271  
 F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601  
 F-NT2RM4002034  
 F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048  
 F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912  
 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540  
 F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802  
 F-NT2RM4002063  
 25 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309  
 F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040  
 F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569  
 30 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.146459:X66975  
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743  
 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542  
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877  
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158  
 F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879  
 40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535  
 F-NT2RM4002174  
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998  
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276  
 45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454  
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182  
 F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984  
 F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966  
 50 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764  
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118  
 F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180  
 F-NT2RM4002281  
 F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979  
 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457  
 F-NT2RM4002301  
 F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331  
 F-NT2RM4002339

F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549  
 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263  
 5 F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293  
 F-NT2RM4002390  
 F-NT2RM4002398  
 F-NT2RM4002409  
 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.26676:AA033997  
 10 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151  
 F-NT2RM4002452  
 F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783  
 F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780  
 15 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255  
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591  
 F-NT2RM4002493  
 20 F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347  
 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219  
 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020  
 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075  
 25 F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176  
 F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004  
 F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273  
 30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054  
 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394  
 F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151  
 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275  
 35 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402  
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587  
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449  
 40 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907  
 F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647  
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834  
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924  
 45 F-NT2RP1000111  
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699  
 F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025  
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901  
 50 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792  
 F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535  
 F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499  
 55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703  
 F-NT2RP1000243  
 F-NT2RP1000259  
 F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.

4214:AF067730

F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551

5 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231

F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204

F-NT2RP1000357

F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807

10 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594

F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031

15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159

F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.3e-177:857:97//Hs.6823:W18181

20 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815

F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603

F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862

F-NT2RP1000460

25 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634

F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102

F-NT2RP1000493

30 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977

F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992

F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418

35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770

40 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475

F-NT2RP1000630

F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576

F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553

45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736

F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148

F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612

F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045

50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434

F-NT2RP1000746

F-NT2RP1000767

55 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023

F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401

F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

2.7e-23:147:91//Hs.102336:Z83838

F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF067223

F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903

F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990

F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838

F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875

F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094

F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683

F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435

F-NT2RP1001011

F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150

F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523

F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094

F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231

F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724

F-NT2RP1001294

F-NT2RP1001302

F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341

F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815

F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770

F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-rus]//6.8e-101:480:94//Hs.75017:AA166853

F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859

F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673

F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081

F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
 F-NT2RP1001466  
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
 F-NT2RP1001482  
 5 F-NT2RP1001494  
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400  
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277  
 F-NT2RP1001569  
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913  
 10 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081  
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390  
 15 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763  
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359  
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290  
 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749  
 F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433  
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134  
 25 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609  
 30 F-NT2RP2000076//H.sapiens mRNA for TFIIA/0.00023:356:62//Hs.121686:D14887  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078  
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338  
 35 F-NT2RP2000091  
 F-NT2RP2000097  
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963  
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390  
 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356  
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177  
 45 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195  
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475  
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910  
 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291  
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713  
 55 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208



F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:  
 243:61//Hs.143641:AB009462  
 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990  
 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669  
 5 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378  
 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719  
 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846  
 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691  
 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011  
 10 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599  
 F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.  
 15 37138:U35376  
 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467  
 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:  
 80//Hs.58218:U82381  
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006  
 20 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905  
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:  
 X60673  
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:  
 25 97//Hs.76556:U83981  
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530  
 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010  
 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779:  
 30 AA626790  
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:  
 96//Hs.5819:AF102265  
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381  
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918  
 35 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747  
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293  
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702  
 F-NT2RP2000510  
 F-NT2RP2000516  
 40 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus]  
 //3.2e-15:167:75//Hs.10984:AA806768  
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144  
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:  
 242:57//Hs.114001:Z20656  
 45 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514  
 F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174  
 F-NT2RP2000656  
 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602  
 F-NT2RP2000668  
 50 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453  
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN  
 CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442  
 F-NT2RP2000710  
 F-NT2RP2000715  
 55 F-NT2RP2000731  
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242  
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:  
 445:89//Hs.21421:AA911739

F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182  
 5 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.75794:U80811  
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850  
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:AB018284  
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65//  
 15 Hs.46146:AA418097  
 F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266  
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014  
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:AB018298  
 20 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494  
 F-NT2RP2000970  
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700  
 25 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944  
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292  
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117  
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957  
 30 F-NT2RP2001065  
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-NT2RP2001081  
 F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560  
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219  
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191  
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362  
 F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582  
 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361  
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949  
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011  
 F-NT2RP2001196  
 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598  
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053  
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367  
 F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813  
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353  
 F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277  
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412  
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287  
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387  
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783  
 F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522  
 55 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883  
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244  
 F-NT2RP2001378  
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558

F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:  
 225:62//Hs.159402:AC005609  
 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767  
 F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088  
 5 F-NT2RP2001420  
 F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018  
 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875  
 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966  
 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//  
 10 9.8e-56:603:72//Hs.75544:Z82248  
 F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218  
 F-NT2RP2001449  
 F-NT2RP2001450  
 F-NT2RP2001467  
 15 F-NT2RP2001506  
 F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779  
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:  
 Y14494  
 F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134  
 20 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 5.2e-105:384:94//Hs.99742:AF035586  
 F-NT2RP2001560  
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.  
 67619:AB007957  
 25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389  
 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876  
 F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268  
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:  
 AB018340  
 30 F-NT2RP2001613  
 F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229  
 F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//  
 Hs.58488:U97067  
 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-  
 35 NA, complete cds//1.3e-145:687:97//Hs.159558:AF058718  
 F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328  
 F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936  
 F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314  
 F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 :  
 40 U52840  
 F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091  
 F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:  
 AI197870  
 F-NT2RP2001721  
 45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991  
 F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstrans-  
 ferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697  
 F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete\_cds//5.2e-34:191:96//Hs.47504:  
 AF091754  
 50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180  
 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250  
 F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610  
 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:  
 AF027219  
 55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768  
 F-NT2RP2001883  
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:  
 90//Hs.142189:M74161

F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650  
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757  
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754  
 F-NT2RP2001936  
 5 F-NT2RP2001943  
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797  
 F-NT2RP2001947  
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489  
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892  
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:  
 AB011117  
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:  
 AB018299  
 15 F-NT2RP2002032  
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543  
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336  
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509  
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198  
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284  
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:  
 66//Hs.44553:AF055634  
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183  
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014  
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:  
 AJ007509  
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.  
 30 122755:AF032986  
 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286  
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363  
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112  
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314  
 35 F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:  
 C06057  
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:  
 M58460  
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//  
 40 6.8e-15:228:67//Hs.111323:AF077954  
 F-NT2RP2002208  
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628  
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318  
 F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439  
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:  
 AF005418  
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720  
 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373  
 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.  
 24812:AF069532  
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445  
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:  
 55 95//Hs.31034:AB015594  
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637  
 F-NT2RP2002373  
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

97//Hs.109051:AF038958

F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289

F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433

F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

F-NT2RP2002442//ESTs, Weakly similar to similar to molybdopter biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265

F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045

10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289

F-NT2RP2002498

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044

15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334

F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212

F-NT2RP2002537

F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

20 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503

25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805

F-NT2RP2002621

30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385

35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572

F-NT2RP2002727

F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217

40 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297

F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016

F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329

F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709

F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705

45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204

F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407

F-NT2RP2002800

F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763

F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142

50 F-NT2RP2002862

F-NT2RP2002880

F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573

F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392

55 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317  
 F-NT2RP2002979  
 F-NT2RP2002980

5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569  
 F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740  
 F-NT2RP2002993

10 F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219  
 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741  
 F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019  
 F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190  
 F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050

15 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633  
 F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379  
 F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161  
 F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544

20 F-NT2RP2003137  
 F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520  
 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025  
 F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170

25 F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944  
 F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353  
 F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123  
 F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223  
 F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594

30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794  
 F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947  
 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696  
 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153

35 F-NT2RP2003265  
 F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:C06057  
 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525

40 F-NT2RP2003280  
 F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159  
 F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334

45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572  
 F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312  
 F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752  
 F-NT2RP2003308

50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227  
 F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765  
 F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963  
 F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

55 F-NT2RP2003391  
 F-NT2RP2003393  
 F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023  
 F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647

5 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106

10 F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136

F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270

F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

15 F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513

20 F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947

25 F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252

30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561

35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097

F-NT2RP2003713

40 F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbCH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318

F-NT2RP2003751

45 F-NT2RP2003760

F-NT2RP2003764

F-NT2RP2003769

F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677

F-NT2RP2003777

50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689

F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

55 F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-

113:632:92//Hs.50072:AI378221

F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458

F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347

F-NT2RP2003984

F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036

F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369

F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:AI380378

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780

F-NT2RP2004042

F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573

F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942

F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828

F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292

F-NT2RP2004142

F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872

F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666

F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966

F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501

F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:AA626790

F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317

F-NT2RP2004196

F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756

F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270

F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756

F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680

F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536

F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487

F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:N25951

F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263

F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544

F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416

F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735

F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510

F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632

F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202

F-NT2RP2004365

F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986

F-NT2RP2004373

F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916

F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164

F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468



F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367  
 F-NT2RP2004412  
 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944  
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687  
 5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823  
 F-NT2RP2004490  
 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203  
 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//  
 10 Hs.73614:U83460  
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:AB011163  
 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891  
 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:  
 15 AF039694  
 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219  
 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309  
 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898  
 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895  
 20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835  
 F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908  
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291  
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:  
 25 AB007929  
 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839  
 F-NT2RP2004681  
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525  
 30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942  
 F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780  
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947  
 F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242  
 35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183  
 F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504  
 F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451  
 40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157  
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953  
 F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043  
 45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179  
 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161  
 F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258  
 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111  
 50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144  
 F-NT2RP2004936  
 F-NT2RP2004959  
 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763  
 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478  
 55 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735  
 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927  
 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//  
 Hs.124161:AF065164  
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:  
 AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200  
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141  
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600  
 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433  
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067  
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035  
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612  
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:  
 15 AF055917  
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:  
 AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.  
 20 100555:X98743  
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803  
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:  
 AF045583  
 25 F-NT2RP2005147  
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582  
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:  
 AJ007509  
 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189  
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783  
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439  
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341  
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.  
 81452:AF030555  
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932  
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//  
 Hs.27007:AF060219  
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590  
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:  
 AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.  
 45 1569:U11701  
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds//0.016:353:62//Hs.113265:AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138  
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958  
 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:  
 489:96//Hs.107254:AC005943  
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122  
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.  
 113252:U80761  
 55 F-NT2RP2005407  
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133  
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068  
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-  
rus]//8.5e-48:295:90//Hs.75017:AA166853

F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243

F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656

F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412

F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:  
AB018315

F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573

F-NT2RP2005491

F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164

F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324

F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:  
M64930

F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669

F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:  
291:59//Hs.89709:L35546

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:  
444:92//Hs.119023:AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:  
AB018307

F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]//3.5e-50:366:83//Hs.  
61833:AA036735

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:  
AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:  
AB007963

F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME  
III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407

F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822

F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839

F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436

F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627

F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071

F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085

F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702

F-NT2RP2005635

F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905

F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145

F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440

F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:  
AB006626

F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//  
Hs.25664:AF089814

F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702

F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496:  
55//Hs.79326:L76703

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:  
AB018342

F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527

F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367

F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017

F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191

F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086

F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769

F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//  
 Hs.159651:AF068868  
 5 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.  
 26285:AF082516  
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853  
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836  
 10 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:  
 Z50115  
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556  
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.  
 34853:U28368  
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820  
 15 F-NT2RP2005812  
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595  
 F-NT2RP2005835  
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//  
 Hs.59829:AB014602  
 20 F-NT2RP2005853  
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:  
 98//Hs.50758:AF092564  
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567  
 F-NT2RP2005868  
 25 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:  
 L16782  
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943  
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360  
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399  
 30 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:  
 AA292186  
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770  
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339  
 F-NT2RP2006023  
 35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382  
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664  
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093  
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469  
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416  
 40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970  
 F-NT2RP2006100  
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135  
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349  
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240  
 45 F-NT2RP2006166  
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910  
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:  
 AB014554  
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:  
 50 AB018315  
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484  
 F-NT2RP2006237  
 F-NT2RP2006238  
 55 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970  
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630  
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:  
 60//Hs.75111:D87258

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262  
 F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.  
 36794:AI038407  
 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371  
 5 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344  
 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:  
 AF076974  
 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174  
 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501  
 10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341  
 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.  
 95838:AF059734  
 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934  
 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509  
 15 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266  
 F-NT2RP2006467  
 F-NT2RP2006472  
 F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048  
 20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete  
 cds//2.1e-115:669:90//Hs.31218:AF038966  
 F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.  
 73864:U22029  
 25 F-NT2RP2006573  
 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223  
 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180  
 F-NT2RP30000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:  
 AJ011972  
 30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:  
 AF000560  
 F-NT2RP3000047  
 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.  
 37138:U35376  
 35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961  
 F-NT2RP3000068  
 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769  
 F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670  
 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608  
 40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140  
 F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595  
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189  
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:  
 AB011164  
 45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503  
 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.  
 127338:AB007961  
 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779  
 F-NT2RP3000207  
 50 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.  
 122967:AF059569  
 F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972  
 55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733  
 F-NT2RP3000252  
 F-NT2RP3000255  
 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821  
 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863  
 5 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153  
 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242  
 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097  
 10 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390  
 F-NT2RP3000348  
 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754  
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673  
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921  
 15 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016  
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639  
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873  
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185  
 20 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503  
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948  
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487  
 F-NT2RP3000441  
 25 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562  
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705  
 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068  
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822  
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058  
 30 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667  
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379  
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966  
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308  
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412  
 35 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404  
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723  
 F-NT2RP3000578  
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277  
 F-NT2RP3000584  
 40 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904  
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914  
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811  
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492  
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980  
 45 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203  
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683  
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162  
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333  
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904  
 50 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219  
 F-NT2RP3000661  
 F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789  
 F-NT2RP3000685  
 55 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001  
 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884  
 F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854  
 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765  
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937  
 F-NT2RP3000815  
 5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132  
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700  
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476  
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012  
 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630  
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520  
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219  
 F-NT2RP3000852  
 15 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918  
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445  
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204  
 20 F-NT2RP3000875  
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101  
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374  
 F-NT2RP3000917  
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277  
 25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407  
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212  
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411  
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198  
 F-NT2RP3001007  
 30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707  
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:AI244662  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219  
 35 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325  
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:AJ006470  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969  
 40 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050  
 F-NT2RP3001111  
 F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088  
 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023  
 F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779  
 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384  
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367  
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318  
 F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297  
 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305  
 F-NT2RP3001147  
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266  
 F-NT2RP3001176  
 55 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859  
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981  
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866  
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756  
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237  
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132  
 F-NT2RP3001253//Human prepromulimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109  
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:AB018269  
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847  
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566  
 10 F-NT2RP3001274  
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457  
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060  
 15 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010  
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966  
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920  
 20 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164  
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831  
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487  
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022  
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451  
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332  
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595  
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783  
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847  
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567  
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658  
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP3001426  
 F-NT2RP3001427  
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397  
 40 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393  
 F-NT2RP3001447  
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508  
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212  
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:AF072836  
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877  
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500  
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328  
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074  
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291



F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302  
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686:  
 M69013  
 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:  
 5 AF057280  
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688  
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349  
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435  
 F-NT2RP3001629  
 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149  
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:  
 AJ012449  
 15 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027  
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]/9.0e-53:  
 375:85//Hs.41127:AA555184  
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071  
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 20 [*Caenorhabditis elegans*]/4.0e-111:518:99//Hs.20364:AI420022  
 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198  
 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329  
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219  
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [*D.mela-*  
 25 *nogaster*]/1.4e-31:191:94//Hs.131279:AA486291  
 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862  
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]  
 //7.6e-159:747:98//Hs.6823:W18181  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:  
 30 565:97//Hs.159273:AF054177  
 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III  
 [*Caenorhabditis elegans*]/3.5e-116:554:98//Hs.144332:AA046836  
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918  
 F-NT2RP3001739  
 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172  
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete  
 cds//0.10:528:56//Hs.22138:U49250  
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:  
 U27193  
 40 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.  
 57783:U78525  
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:  
 AB007928  
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532  
 45 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361  
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162  
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634  
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729  
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:  
 50 U68727  
 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706  
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [*C.elegans*]/2.9e-94:452:98//Hs.54952:  
 AA872675  
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326  
 55 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896  
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185  
 F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247  
 F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398  
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:AB014575  
 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335  
 5 F-NT2RP3001969  
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180  
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219  
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779  
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946  
 10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821  
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153  
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:AA993745  
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155  
 15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806  
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503  
 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710  
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//  
 20 0.91:194:65//Hs.1298:J03779  
 F-NT2RP3002081  
 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:297:61//Hs.102732:U88153  
 F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256  
 25 F-NT2RP3002108  
 F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018  
 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260  
 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with  
 some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative  
 30 CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009  
 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644  
 F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985  
 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //3.0e-61:340:93//Hs.11379:AA594140  
 35 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046  
 F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME  
 III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915  
 F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643  
 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:  
 40 242:57//Hs.114001:Z20656  
 F-NT2RP3002248  
 F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261  
 F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.  
 110637:AC004080  
 45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139  
 F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386  
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910  
 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871  
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383  
 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:  
 Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200  
 55 F-NT2RP3002399  
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:  
 AB014578

F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310  
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108  
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.  
 5 57738:U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:  
 AB018272  
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.  
 96759:AA469984  
 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706  
 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054  
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919  
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508  
 F-NT2RP3002603  
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888  
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900  
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.  
 20 151518:U38847  
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308  
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//  
 Hs.41086:AI337400  
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991  
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584  
 F-NT2RP3002687  
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200  
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657  
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514  
 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291  
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//  
 Hs.129736:AF040753  
 F-NT2RP3002785  
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713  
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:  
 AF004715  
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070  
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582  
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895  
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314  
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765  
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//  
 45 Hs.3826:U69560  
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:  
 AB011160  
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262  
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870  
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997  
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703  
 F-NT2RP3002985//Human TFIIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:  
 U28838  
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308  
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083  
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446  
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749  
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928

F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079

F-NT2RP3003078

F-NT2RP3003101

5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700

F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740

F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061

10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975

F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944

F-NT2RP3003150

15 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376

F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093

F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933

F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854

20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308

F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325

F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525

F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497

25 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200

F-NT2Rp3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225

30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983

F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953

F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947

35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503

F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947

F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058

F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200

F-NT2RP3003330

40 F-NT2RP3003344

F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339

F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833

F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542

F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791

45 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363

F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850

F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653

F-NT2RP3003411//Human metallothionein-Ie gene (hMT-Ie)//0.99:116:62//Hs.74170:M10942

50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830

F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268

55 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330

F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302

F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169

F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322

F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

5 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311

F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247

F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741

F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:D14012

10 F-NT2RP3003625

F-NT2RP3003656

F-NT2RP3003659

F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586

F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184

15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:63//Hs.44585:U58334

F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000

F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848

F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865

20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:AB018300

F-NT2RP3003746

F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230

F-NT2RP3003799

25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:M19722

F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656

30 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832

F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315

F-NT2RP3003825

F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481

35 F-NT2RP3003831

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611

F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268

40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343

F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576

F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659

45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358

F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396

F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006

F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498

50 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.142151:AA984061

F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317

55 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317

F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875

F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

100007:X76091

F-NT2RP3004093

F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258

F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390

F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900

F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706

F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523

F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835

F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361

F-NT2RP3004242

F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240

F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140

F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871

F-NT2RP3004332

F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:X97249

F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113

F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403

F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:AB007917

F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564

F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219

F-NT2RP3004472

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925

F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851

F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718

F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948

F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046

F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110

F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126

F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:AI364967

F-NT2RP3004569

F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445

F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923

5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266

F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336

F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232

F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204

10 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436

F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919

F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668

F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495

15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761

F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470

F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449

20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538

F-NT2RP4000111

F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952

25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069

F-NT2RP4000150

F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356

F-NT2RP4000159

F-NT2RP4000167

30 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946

F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600

F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006

F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731

35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984

F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470

F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298

40 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092

F-NT2RP4000263

F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580

45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481

F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732

F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112

F-NT2RP4000355

50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195

F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073

55 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678

F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368  
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688  
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156  
 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984  
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087  
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468  
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853  
 10 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499  
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535  
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742  
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995  
 15 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293  
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594  
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904  
 F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840  
 20 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372  
 F-NT2RP4000524  
 F-NT2RP4000528  
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154  
 25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026  
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351  
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730  
 30 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513  
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396  
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907  
 35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848  
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783  
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622  
 40 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178  
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440  
 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058  
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162  
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123  
 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189  
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833  
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603  
 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278  
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367  
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803  
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843  
 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901  
 F-NT2RP4000918  
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865



F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//  
 Hs.24812:AF069532  
 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371  
 5 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542  
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888  
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058  
 F-NT2RP4000979  
 F-NT2RP4000984  
 10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913  
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068  
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204  
 F-NT2RP4001004  
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718  
 15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.  
 113287:AF009204  
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494  
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:  
 L40157  
 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157  
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497  
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.4e-131:634:98//Hs.  
 25 106778:AJ010953  
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.  
 146459:X66975  
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164  
 F-NT2RP4001095  
 30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054  
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//2.2e-26:171:92//Hs.14038:R06800  
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142  
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:  
 35 100//Hs.126925:AA931237  
 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266  
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261  
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207  
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171  
 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734  
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324  
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264  
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324  
 F-NT2RP4001207  
 45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636  
 F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251  
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262  
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.  
 122967:AF059569  
 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778  
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463  
 F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//  
 Hs.31121:U40571  
 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578  
 55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736  
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250  
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110  
 F-NT2RP4001339  
 F-NT2RP4001343  
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39;686:64//Hs.112125:M12625  
 5 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds//2.0e-31:784:62//Hs.15432:U53445  
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356  
 F-NT2RP4001372  
 10 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194  
 F-NT2RP4001375  
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190  
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918  
 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957  
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:  
 AB018326  
 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.  
 20 26676:AA033997  
 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523  
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.  
 63220:AA522707  
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395  
 25 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260  
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863  
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494  
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:  
 U13220  
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534  
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174  
 F-NT2RP4001567  
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836  
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410  
 F-NT2RP4001574  
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228  
 F-NT2RP4001592  
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903  
 40 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952  
 F-NT2RP4001634  
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC  
 REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436  
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409  
 45 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECUR-  
 SOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629  
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:  
 67//Hs.30250:AF055376  
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080  
 50 F-NT2RP4001696  
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927  
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.  
 92614:M62302  
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198  
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878  
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656  
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:  
 AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 cds//0.028:580:58//Hs.2363:L36069  
 F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131  
 F-NT2RP4001823//Human facio-genital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:  
 5 U11690  
 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888  
 F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:  
 10 AB014572  
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:  
 84:94//Hs.140232:AA705170  
 F-NT2RP4001889  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014  
 15 F-NT2RP4001896  
 F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848  
 F-NT2RP4001927  
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:  
 AI379442  
 20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894  
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063  
 F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868  
 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene  
 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribos-  
 25 omal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:  
 788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete  
 cds//0.0019:279:65//Hs.159439:AF092047  
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.  
 30 3826:U69560  
 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139  
 F-NT2RP4002052  
 F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873  
 F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//  
 Hs.100030:AF002999  
 35 F-NT2RP4002075  
 F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:  
 AA325104  
 F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654  
 F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684  
 40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284  
 F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204  
 F-NT2RP4002888  
 F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960  
 F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995  
 45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071  
 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067  
 F-NT2RP5003492  
 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//  
 Hs.132884:AB006179  
 50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:  
 AC004131  
 F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542  
 F-NT2RP5003522  
 F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943  
 55 F-NT2RP5003534  
 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:  
 AB007934  
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:  
 AI051983  
 F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304  
 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922  
 5 F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060  
 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603  
 F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549  
 F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:  
 H50008  
 10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798  
 F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543  
 F-OVARC1000085  
 F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442  
 F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778  
 15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600  
 F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174  
 F-OVARC1000109  
 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-  
 135:663:96//Hs.3688:AF069250  
 20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:  
 AB011134  
 F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010  
 F-OVARC1000139  
 F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293  
 25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414  
 F-OVARC1000151  
 F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305  
 F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth  
 and development factor)//0.10:504:59//Hs.154083:U70136  
 30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131  
 F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840  
 F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834  
 F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]  
 //2.7e-31:264:79//Hs.151895:AA196379  
 35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984  
 F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868  
 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306  
 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287  
 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECUR-  
 40 SOR [Felis catus]//0.51:193:66//Hs.6194:AI378579  
 F-OVARC1000321  
 F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//  
 Hs.122359:AF051946  
 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444  
 45 F-OVARC1000347  
 F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1)  
 mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450  
 F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930  
 F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162  
 50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682  
 F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930  
 F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082  
 F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615  
 F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416  
 55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284  
 F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423  
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:  
 AB014583

F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524  
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640  
 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854  
 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926  
 5 F-OVARC1000479  
 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036  
 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850  
 F-OVARC1000526//ESTs//2.9e-08:368:611//Hs.42771:N26740  
 10 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492  
 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475  
 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667  
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410  
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:  
 15 66//Hs.85302:U76421  
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358  
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200  
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729  
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725  
 20 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722  
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881  
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
 plete cds//1.6e-78:424:93//Hs.86859:D43772  
 25 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:  
 AB011162  
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106  
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279  
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639  
 30 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.  
 125315:AF027156  
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306  
 F-OVARC 1000700  
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320  
 35 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//  
 1.2e-110:451:91//Hs.13476:AF038661  
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:  
 AI141736  
 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411  
 40 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196  
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//  
 Hs.157059:W28130  
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793  
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835  
 45 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584  
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032  
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:  
 AB014543  
 50 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584  
 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155  
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.  
 159234:U89995  
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143  
 55 F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323  
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777  
 F-OVARC 1000890  
 F-OVARC1000891

F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818  
 F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691  
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456  
 5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119  
 F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078  
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843  
 10 F-OVARC 1000948  
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986  
 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952  
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288  
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069  
 15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661  
 F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317  
 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219  
 20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114  
 F-OVARC1001004  
 F-OVARC1001010  
 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866  
 F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584  
 25 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149  
 F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074  
 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385  
 30 F-OVARC1001051  
 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020  
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873  
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451  
 35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657  
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013  
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937  
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248  
 40 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF051782  
 45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102  
 F-OVARC1001118  
 F-OVARC1001129  
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008  
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725  
 50 F-OVARC1001162  
 F-OVARC1001167  
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279  
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287  
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159  
 55 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581  
 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551  
 F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

C06057

F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675

F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

5 F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837

10 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835

15 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.152455:AF044209

F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

20 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054

F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493

F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251

25 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715

F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633

F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777

30 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554

F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819

35 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242

F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426

40 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651

F-OVARC1001436

F-OVARC1001442

F-OVARC1001453

45 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823

F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568

F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507

50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243

F-OVARC1001525

F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

55 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299

F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398  
 F-OVARC1001611  
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500  
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144  
 5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867  
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229  
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858  
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807  
 10 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863  
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825  
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588  
 F-OVARC1001762  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 15 1.4e-150:706:98//Hs.155377:U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575  
 F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697  
 F-OVARC1001791  
 20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830  
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102  
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287  
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172  
 25 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825  
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453  
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567  
 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537  
 30 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973  
 F-OVARC1001861  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611  
 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-  
 35 unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709  
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127  
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 40 2.6e-57:300:96//Hs.6216:AF061749  
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834  
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261  
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263  
 F-OVARC1001928  
 45 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204  
 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794  
 F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251  
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228  
 50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639  
 F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776  
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934  
 55 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865  
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063  
 F-OVARC1002107



F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174  
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913  
 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022  
 5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795  
 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097  
 F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568  
 10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517  
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230  
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928  
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789  
 15 F-PLACE1000014  
 F-PLACE1000031  
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088  
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494  
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755  
 20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499  
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771  
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366  
 25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082  
 F-PLACE1000094  
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378  
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135  
 30 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291  
 F-PLACE1000185  
 F-PLACE1000213  
 35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255  
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226  
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022  
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202  
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294  
 40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047  
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675  
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197  
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153  
 45 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024  
 F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516  
 F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260  
 50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174  
 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053  
 F-PLACE1000424  
 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590  
 55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531  
 F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638  
 F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353  
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573  
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289  
 5 F-PLACE1000562  
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538  
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179  
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542  
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449  
 10 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751  
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542  
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986  
 F-PLACE1000636  
 15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265  
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896  
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353  
 20 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949  
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447  
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288  
 F-PLACE1000749//Human MAGe-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694  
 25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
 F-PLACE1000769  
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548  
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215  
 30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079  
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180  
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736  
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
 35 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428  
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
 F-PLACE1000948  
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821  
 40 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789  
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267  
 45 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432  
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633  
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876  
 50 F-PLACE1001024  
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741  
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204  
 F-PLACE1001062  
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859  
 55 F-PLACE1001088  
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485  
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

71//Hs.150406:AF022158  
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704  
 F-PLACE1001168  
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135  
 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741  
 F-PLACE1001238  
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494  
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929  
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476  
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283  
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:  
 58//Hs.124161:AF065164  
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.  
 16533:D87930  
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052  
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385  
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342  
 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:  
 AF009615  
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748  
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:  
 117:84//Hs.21301:AF093419  
 25 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE  
 EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646  
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete  
 CDS//0.0038:496:57//Hs.97681:AJ223333  
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.  
 30 154069:U06452  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:  
 AF091087  
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232  
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987  
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510  
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455  
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716  
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529  
 F-PLACE1001503  
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914  
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753  
 F-PLACE1001545  
 F-PLACE1001551  
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835  
 45 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233  
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987  
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230  
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005  
 F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690  
 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:  
 AB018341  
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198  
 F-PLACE1001640  
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927  
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-  
 148:726:96//Hs.3688:AF069250  
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN  
 [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869  
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776  
 F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686  
 5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094  
 F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052  
 F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159  
 F-PLACE1001745  
 F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361  
 10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243  
 F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750  
 F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283  
 F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050  
 15 F-PLACE1001781  
 F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115  
 F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138  
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 20 3.6e-110:546:96//Hs.40820:AF058953  
 F-PLACE1001821  
 F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494  
 F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214  
 F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906  
 25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257  
 F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220  
 F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936  
 F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837  
 30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778  
 F-PLACE1001989  
 F-PLACE1002004  
 F-PLACE1002046  
 F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108  
 35 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555  
 F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707  
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178  
 F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765  
 40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637  
 F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831  
 F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747  
 F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631  
 45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390  
 F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891  
 F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627  
 F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674  
 F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289  
 50 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989  
 F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442  
 F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935  
 F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503  
 F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675  
 55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279  
 F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291  
 F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710  
 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.  
 40993:AF000148  
 F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947  
 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:  
 5 66//Hs.150406:AF022158  
 F-PLACE1002465  
 F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581  
 F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523  
 F-PLACE1002493  
 10 F-PLACE1002499  
 F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.  
 111967:U76010  
 F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:  
 15 AB018256  
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:  
 AC004774  
 F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369  
 F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866  
 20 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627  
 F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725  
 F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:  
 D44497  
 F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187  
 25 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915  
 F-PLACE1002625  
 F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412  
 F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:  
 30 804:97//Hs.124903:AF068180  
 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903  
 F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:  
 U92971  
 F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080  
 35 F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728  
 F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827  
 F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:  
 AF082516  
 F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926  
 40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994  
 F-PLACE1002815  
 F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691  
 F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163  
 F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167  
 45 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405  
 F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024  
 F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627  
 F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029  
 F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056  
 50 F-PLACE1002962  
 F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815  
 F-PLACE1002991  
 F-PLACE1002993  
 F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959  
 55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:  
 AB007979  
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:  
 AB011088

F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567  
 F-PLACE1003045  
 F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491  
 5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875  
 F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419  
 F-PLACE1003136  
 F-PLACE1003145  
 F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590  
 10 F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997  
 F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797  
 F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209  
 F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532  
 15 F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770  
 F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208  
 F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:X57025  
 F-PLACE1003256  
 F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802  
 20 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106  
 F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376  
 F-PLACE1003334  
 F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308  
 25 F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715  
 F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277  
 30 F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575  
 F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858  
 F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009  
 F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069  
 F-PLACE1003383  
 35 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546  
 F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178  
 F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846  
 F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912  
 40 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874  
 F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635  
 F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627  
 F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145  
 F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633  
 45 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248  
 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428  
 F-PLACE1003553  
 F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780  
 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367  
 50 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932  
 F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194  
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620  
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965  
 55 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961  
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200  
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104

F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896  
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503  
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105  
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762  
 5 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413  
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299  
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305  
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101  
 10 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553  
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344  
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648  
 15 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983  
 F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629  
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944  
 F-PLACE1003783  
 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308  
 20 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169  
 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786  
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165  
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124  
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359  
 25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257  
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770  
 F-PLACE1003886  
 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108  
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050  
 30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944  
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142  
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069  
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585  
 35 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537  
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536  
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412  
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812  
 40 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940  
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516  
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.153045:X52056  
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526  
 45 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779  
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552  
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785  
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666  
 50 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201  
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493  
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722  
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273  
 55 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689  
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128  
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914

F-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830

5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884

F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588

F-PLACE1004336

10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108

F-PLACE1004388

15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283

20 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867

F-PLACE1004460

F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363

F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085

F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416

25 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163

F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680

F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445

F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150

30 F-PLACE1004518

F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314

F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854

F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371

35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299

F-PLACE1004645

F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991

F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590

F-PLACE1004664

40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606

F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589

45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561

F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131

F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542

F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891

50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148

F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680

F-PLACE1004743

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470

55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367

F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391

F-PLACE1004793

F-PLACE1004804



F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340  
 F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus lae-  
 vis]//2.4e-78:415:95//Hs.80965:AA493284  
 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362  
 5 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047  
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943  
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669  
 F-PLACE1004838  
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910  
 10 F-PLACE1004868  
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772  
 F-PLACE1004900  
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382  
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929  
 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.  
 118910:U82130  
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:  
 AF099936  
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592  
 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851  
 F-PLACE1004969  
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:  
 235:60//Hs.27610:U34605  
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:  
 25 AB011147  
 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520  
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831  
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459  
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159  
 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943  
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:  
 AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.  
 35 122967:AF059569  
 F-PLACE1005077//EST//0.79:283:591//Hs.89276:AA283899  
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740  
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:  
 AB011147  
 40 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401  
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//  
 8.9e-18:538:62//Hs.104640:AF000561  
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366  
 F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227  
 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661  
 F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:  
 H11741  
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087  
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:  
 50 AB014541  
 F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:  
 AI138605  
 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417  
 F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009  
 55 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//  
 Hs.47334:W72370  
 F-PLACE1005243  
 F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182  
 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947  
 5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673  
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534  
 F-PLACE1005313  
 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650  
 10 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794  
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297  
 F-PLACE1005373  
 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348  
 15 F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751  
 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951  
 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433  
 F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925  
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503  
 20 F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323  
 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973  
 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029  
 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105  
 F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747  
 25 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572  
 F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335  
 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385  
 F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144  
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR  
 30 [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261  
 F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278  
 F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436  
 F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594  
 F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851  
 35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057  
 F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234  
 F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867  
 F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991  
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255  
 40 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618  
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917  
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457  
 45 F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437  
 F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944  
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258  
 F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302  
 50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696  
 F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493  
 F-PLACE1005802  
 F-PLACE1005803  
 55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156  
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482

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F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:  
327:81//Hs.138404:R70986

F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870

F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497

5 F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905

F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242

F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487

F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300

10 F-PLACE1005898

F-PLACE1005921

F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504

F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274

F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:  
M18391

15 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142

F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978

F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357

F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468

20 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868

F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:  
U13948

F-PLACE1005968

F-PLACE1005990

25 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981

F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256

F-PLACE1006011

F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743

F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:  
AB018332

30 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906

F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:  
AF039023

35 F-PLACE1006129

F-PLACE1006139

F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353

F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:  
R92857

40 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868

F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433

45 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608

F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.  
135623:AA134719

F-PLACE1006205

F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]  
//0.0089:166:63//Hs.127179:AI279486

50 F-PLACE1006225

F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668

F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185

F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802

55 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:  
AB014548

F-PLACE1006262

F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

F-PLACE1006318

F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503

F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492

F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249

5 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481

F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581

F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715

F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693

10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085

F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

15 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

25 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

35 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088

F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858

F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396

F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473

40 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917

F-PLACE1006678

F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403

F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612

F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354

45 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152

F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252

F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783

F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228

50 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941

F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017

F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892

F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518

55 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503

F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876

F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773

F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273

F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601  
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187  
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443  
 F-PLACE1006917  
 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913  
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211  
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565  
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723  
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [*Saccharomyces cerevisiae*]//3.2e-07:67:98//Hs.  
 10 21806:AA630312  
 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417  
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:  
 191:67//Hs.8813:AF032922  
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753  
 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//  
 3.1e-05:594:58//Hs.32951:AF034102  
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971  
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503  
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957  
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243  
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987  
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type III)//0.18:268:63//Hs.904:U84010  
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385  
 25 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669  
 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//  
 Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:  
 L06133  
 F-PLACE1007282  
 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412  
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//  
 Hs.144877:AF029403  
 F-PLACE1007342  
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:  
 567:98//Hs.76596:AF096870  
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173  
 F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642  
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287  
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//  
 Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436  
 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391  
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714  
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975  
 F-PLACE1007488  
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385  
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503  
 5 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296  
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979  
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080  
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755  
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:  
 10 AB014561  
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863  
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257  
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163  
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533  
 15 F-PLACE1007621  
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867  
 F-PLACE1007645  
 F-PLACE1007649  
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266  
 20 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055  
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503  
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812  
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953  
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:  
 25 AF061243  
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:  
 AA476815  
 F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:  
 64//Hs.104129:AA923278  
 30 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:  
 AB014585  
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424  
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030  
 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469  
 35 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656  
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504  
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107  
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841  
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635  
 40 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503  
 F-PLACE1007852  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:  
 AB018309  
 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387  
 45 F-PLACE1007877  
 F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.  
 92381:AB007956  
 F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002  
 50 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.  
 5671:AF084530  
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:  
 730:98//Hs.78106:AF079529  
 55 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:  
 W28567  
 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043  
 F-PLACE1008000//Homo sapiens vcl 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031  
 F-PLACE1008044  
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382  
 5 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:  
 U44060  
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:  
 U60975  
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.  
 10 100431:AF044197  
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769  
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874  
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683  
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-  
 20:124:95//Hs.146238:AI263135  
 15 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427  
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524  
 F-PLACE1008201  
 F-PLACE1008209  
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856  
 20 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385  
 F-PLACE1008273  
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113  
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.  
 159897:AB007970  
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.  
 4076:AF081287  
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071  
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:  
 AB011129  
 30 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579  
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:  
 AF059569  
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911  
 35 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171  
 F-PLACE1008398  
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:  
 62//Hs.25674:AF072242  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326  
 40 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943  
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene cod-  
 ing for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel  
 gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653  
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499  
 45 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431,  
 mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487  
 F-PLACE1008437  
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335  
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901  
 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381  
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:  
 U10886  
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.0:304:  
 60//Hs.24040:AF006823  
 55 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697  
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081  
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997  
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334  
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326  
 5 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794  
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560  
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458  
 F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211  
 10 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394  
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535  
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333  
 F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728  
 15 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406  
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741  
 F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080  
 20 F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503  
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543  
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772  
 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542  
 25 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905  
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883  
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858  
 30 F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728  
 F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563  
 F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503  
 F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323  
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308  
 35 F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771  
 F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026  
 F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937  
 F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308  
 40 F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950  
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112  
 F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762  
 F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689  
 45 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585  
 F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698  
 F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525  
 F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800  
 50 F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091  
 F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031  
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011  
 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890  
 F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788  
 55 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586  
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215  
 F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108



F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953

F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302

5 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250

F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821

F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100

10 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396

F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689

F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131

F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540

F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575

15 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735

F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192

20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630

30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872

F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678

35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A//4.1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

40 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

45 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

50 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789  
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024  
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989  
 5 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-  
 130:600:95//Hs.16411:AL030996  
 F-PLACE1009845  
 10 F-PLACE1009861  
 F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021  
 F-PLACE1009886  
 F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889  
 F-PLACE1009908  
 15 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717  
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379  
 F-PLACE1009925  
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153  
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446  
 20 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345  
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114  
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540  
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:  
 AB014529  
 25 F-PLACE1010023  
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878  
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.  
 142151:AA984061  
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596  
 30 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:  
 AF065482  
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424  
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925  
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus  
 35 musculus]//1.8e-38:212:95//Hs.98067:AA236822  
 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:  
 U69567  
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:  
 AF020761  
 40 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.  
 122967:AF059569  
 F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682  
 F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889  
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740  
 45 F-PLACE1010152  
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792  
 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582  
 F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:  
 H69637  
 50 F-PLACE1010231  
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:  
 AB007917  
 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590  
 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540  
 55 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813  
 F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433  
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248  
 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659  
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117  
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855  
 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648  
 5 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986  
 F-PLACE1010401  
 F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824  
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:  
 AF039081  
 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500  
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100  
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:  
 64//Hs.159273:AF054177  
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472  
 15 F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979  
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148  
 F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06  
 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661  
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete  
 20 cds//9.9e-148:707:97//Hs.19851:AF045186  
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394  
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858  
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778  
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200  
 25 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461  
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225  
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102  
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076  
 F-PLACE1010662  
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.  
 37138:U35376  
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027  
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:  
 96//Hs.50758:AF092564  
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:  
 AJ131244  
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391  
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus lae-  
 vis]//5.1e-80:407:96//Hs.80965:AA493284  
 40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]  
 //6.0e-45:251:94//Hs.11379:AA594140  
 F-PLACE1010786  
 F-PLACE1010800  
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157  
 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085  
 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.  
 132736:AA583494  
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048  
 F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.  
 50 130135:AA905493  
 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:  
 AB011182  
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671  
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169  
 F-PLACE1010900  
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981  
 F-PLACE1010917

F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126  
 5 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:AF064244  
 F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985  
 F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154  
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506  
 10 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632  
 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721  
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931  
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032  
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886  
 15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678  
 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194  
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//Hs.153640:U56998  
 20 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320  
 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663  
 F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037  
 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317  
 F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857  
 25 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949  
 F-PLACE1011160  
 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443  
 F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664  
 30 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:AA283057  
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221:88//Hs.101821:W27452  
 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751  
 35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014  
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803  
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:AF070637  
 40 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915  
 F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160  
 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310  
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265  
 45 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970  
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535  
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053  
 50 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868  
 F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102  
 55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503  
 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204  
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482  
 F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264  
 F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997  
 5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319  
 F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476  
 F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333  
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180  
 10 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462  
 F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778  
 F-PLACE1011641  
 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631  
 15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661  
 F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086  
 F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745  
 F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640  
 F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234  
 20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366  
 F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350  
 F-PLACE1011725  
 F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853  
 F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891  
 25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240  
 F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693  
 F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660  
 F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664  
 F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775  
 30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152  
 F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913  
 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868  
 F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817  
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617  
 35 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763  
 F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514  
 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591  
 F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514  
 40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256  
 F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956  
 F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503  
 45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330  
 F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627  
 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831  
 F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627  
 F-PLACE2000017  
 50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557  
 F-PLACE2000030  
 F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512  
 F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179  
 55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204  
 F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128  
 F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966  
 F-PLACE2000061

F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457  
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219  
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333  
 5 F-PLACE2000100  
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219  
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:U56417  
 F-PLACE2000115  
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353  
 F-PLACE2000132  
 F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911  
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645  
 15 F-PLACE2000164  
 F-PLACE2000170  
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179  
 F-PLACE2000176  
 F-PLACE2000187  
 20 F-PLACE2000216  
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933  
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296  
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338  
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958  
 25 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522  
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560  
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869  
 F-PLACE2000317  
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796  
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088  
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299  
 F-PLACE2000347//ESTs, Moderately similar to F18547\_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817  
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645  
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045  
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861  
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032  
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638  
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953  
 F-PLACE2000398  
 F-PLACE2000399  
 F-PLACE2000404  
 45 F-PLACE2000411  
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082  
 55 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241  
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,  
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384  
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128  
 F-PLACE3000029  
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248  
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842  
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.  
 122752:AF026445  
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295  
 10 F-PLACE3000121  
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081  
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603  
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243  
 F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016  
 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871  
 F-PLACE3000148  
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:  
 AB014572  
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023  
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:  
 U79666  
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:  
 AB011147  
 F-PLACE3000160  
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219  
 F-PLACE3000194  
 F-PLACE3000197  
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546  
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975  
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//  
 Hs.77522:X62744  
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216  
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377  
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-  
 35 56:200:85//Hs.133089:AF064019  
 F-PLACE3000226  
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568  
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-  
 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
 40 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and ge-  
 nomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046  
 F-PLACE3000244  
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858  
 F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650  
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944  
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770  
 F-PLACE3000310  
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586  
 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219  
 50 F-PLACE3000331  
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:  
 AB014545  
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741  
 F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis ele-  
 55 gans]//2.9e-59:474:77//Hs.125850:AA885355  
 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194  
 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:  
 234:63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441  
 F-PLACE3000363  
 F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928  
 F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641  
 5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432  
 F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637  
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785  
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270  
 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715  
 10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541  
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:  
 116:78//Hs.77579:AF013263  
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:  
 H61502  
 15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:  
 AB018344  
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161  
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:  
 183:93//Hs.108326:AB006202  
 20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874  
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888  
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:  
 AB018352  
 25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:  
 AC004131  
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533  
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.  
 40993:AF000148  
 30 F-PLACE4000063  
 F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713  
 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819  
 F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058  
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:  
 35 AB007931  
 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751  
 F-PLACE4000129  
 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627  
 F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856  
 40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367  
 F-PLACE4000192  
 F-PLACE4000211  
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594  
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329  
 45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317  
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250  
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609  
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886  
 50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200  
 F-PLACE4000261  
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:  
 100//Hs.118849:AA215645  
 F-PLACE4000270  
 55 F-PLACE4000300  
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966  
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365  
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798



F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292  
 F-PLACE4000367  
 F-PLACE4000369  
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256  
 5 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823  
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540  
 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982  
 10 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200  
 F-PLACE4000445  
 F-PLACE4000450  
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874  
 F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075  
 15 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951  
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289  
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731  
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022  
 20 F-PLACE4000548  
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:AF000986  
 F-PLACE4000581  
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080  
 25 F-PLACE4000593//ESTS, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675  
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074  
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:AB002446  
 30 F-PLACE4000650  
 F-PLACE4000654  
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132  
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299  
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688  
 35 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:AB014554  
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254  
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877  
 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194  
 F-THYRO1000034  
 F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099  
 F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326  
 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345  
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557  
 F-THYRO1000085  
 F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065  
 F-THYRO1000107  
 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503  
 F-THYRO1000121  
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732  
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:AF087142  
 55 F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203  
 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416  
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219  
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590

F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520

35 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

45 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324  
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204  
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871  
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:  
 AF061573  
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481  
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:  
 10 452:58//Hs.11538:AF006084  
 F-THYRO1000787  
 F-THYRO1000793  
 F-THYRO1000796  
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:  
 15 AB002446  
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087  
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339  
 F-THYRO1000843  
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788  
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170  
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:  
 190:75//Hs.133526:N21103  
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531  
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.  
 25 92381:AB007956  
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:  
 839:98//Hs.78106:AF079529  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836  
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263  
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963  
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear  
 gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169  
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907  
 F-THYRO1000983  
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646  
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307  
 F-THYRO1001003  
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369  
 F-THYRO1001033//H.sapiens mRNA for cyclin II//0.0061:287:60//Hs.3232:Z46788  
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830  
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130  
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700  
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416  
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425  
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074  
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788  
 F-THYRO1001173  
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385  
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163  
 F-THYRO1001204  
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219  
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461  
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309  
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:  
 AF027156  
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836  
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872  
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333  
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545  
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207  
 5 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939  
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607  
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993  
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946  
 F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694  
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659  
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788  
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//  
 15 Hs.102877:U41315  
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099  
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215  
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830  
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943  
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904  
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663  
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211  
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046  
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335  
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572  
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655  
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535  
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849  
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071  
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046  
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659  
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463  
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568  
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089  
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238  
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552  
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691  
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560  
 F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229  
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813  
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590  
 45 F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725  
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324  
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295  
 F-THYRO1001828  
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823  
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:M24283  
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198  
 F-VESEN1000122  
 55 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885  
 F-Y79AA1000033  
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.  
9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:  
AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:  
AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:  
AF068706

F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:  
AF091080F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:  
AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:  
98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:  
AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:  
AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:  
D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
- F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
- 10 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
- F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
- 15 F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
- F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
- F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
- F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
- F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
- F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
- F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
- F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
- F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
- F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependant kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
- F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
- 45 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
- F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
- F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
- F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
- 55 F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
- F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
- F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533  
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124  
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332  
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778  
 5 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173  
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720  
 F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382  
 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611  
 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943  
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045  
 F-Y79AA1002093  
 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865  
 F-Y79AA1002115  
 15 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395  
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955  
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538  
 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515  
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:  
 20 96//Hs.111637:AA305890  
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984  
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477  
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045  
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:  
 AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:  
 AB014555  
 30 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:  
 AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 35 cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 40 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302  
 45

#### Homology Search Result Data 5.

**[0310]** The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

**[0311]** Data include

the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0312]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

**[0313]** Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III  
 [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434  
 R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233  
 R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198  
 5 R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087  
 R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340  
 R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329  
 R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788  
 R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.  
 10 55918:AA151667  
 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:  
 AB018340  
 R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:  
 AB014540  
 15 R-HEMBA1000158//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:  
 100//Hs.126925:AA931237  
 R-HEMBA1000158  
 R-HEMBA1000180//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863  
 R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545  
 20 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366  
 R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927  
 R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847  
 R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311  
 R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532  
 25 R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874  
 R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:  
 AB007944  
 R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019  
 30 R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808  
 R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424  
 R-HEMBA1000282//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:  
 AA811920  
 R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485  
 35 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962  
 R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409  
 R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099  
 R-HEMBA1000302//ESTs//7.4e-76:386:97//Hs.22276:AA191323  
 R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024  
 R-HEMBA1000307//ESTs//9.3e-99:472:98//Hs.163512:AA903238  
 R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560  
 40 R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//  
 Hs.73614:U83460  
 R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243  
 R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:  
 K00629  
 R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857  
 50 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938  
 R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960  
 R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//  
 Hs.73614:U83460  
 R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878  
 55 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248  
 R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920  
 R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:  
 AI005282



R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700  
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140  
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189  
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143  
 5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014  
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349  
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316  
 R-HEMBA1000460  
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370  
 10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219  
 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster  
 ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449  
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528  
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087  
 15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571  
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318  
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531  
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885  
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414  
 20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280  
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:  
 U15782  
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.  
 99722:AI422277  
 25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809  
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317  
 R-aaaaaaaaaaaaaa//ESTs//2.3e-66:342:97//Hs.71916:AA219699  
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881  
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:  
 30 W74481  
 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196  
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128  
 R-aaaaaaaaaaaaaa  
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788  
 35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944  
 R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:  
 AJ007509  
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE  
 ITK/TSK//0.024:309:61//Hs.89519:L10717  
 40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041  
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.  
 158334:U86136  
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424  
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438  
 45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:  
 AA643235  
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:  
 AB014590  
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390  
 50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929  
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136  
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922  
 R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:  
 55 AI141736  
 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:  
 AF057280  
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213  
 R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612  
 R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931  
 R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777  
 R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110  
 R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219  
 R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131  
 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219  
 R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612  
 R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795  
 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087  
 R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939  
 R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027  
 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977  
 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258  
 R-HEMBA1000851  
 R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689  
 R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794  
 R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202  
 R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608  
 R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951  
 R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219  
 R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154  
 R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672  
 R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508  
 R-HEMBA1000919  
 R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597  
 R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619  
 R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291  
 R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074  
 R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750  
 R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977  
 R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498  
 R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590  
 R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170  
 R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878  
 R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464  
 R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902  
 R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881  
 R-HEMBA1001007  
 R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764  
 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836  
 R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937  
 R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360  
 R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292  
 R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912  
 R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336  
 R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616  
 R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521  
 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886  
 5 R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813  
 R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420  
 R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961  
 R-HEMBA1001080  
 10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788  
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674  
 R-HEMBA1001094  
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245  
 R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219  
 15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974  
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320  
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530  
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341  
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265  
 20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219  
 R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358  
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961  
 25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896  
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194  
 R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080  
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316  
 30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932  
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728  
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181  
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674  
 35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534  
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324  
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219  
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162  
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214  
 40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019  
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977  
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950  
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838  
 45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259  
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080  
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816  
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837  
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334  
 50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550  
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458  
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482  
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439  
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204  
 55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081  
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714  
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364  
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199  
 R-HEMBA1001415  
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981  
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704  
 5 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263  
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982  
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546  
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077  
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503  
 10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220  
 R-HEMBA1001463  
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008  
 R-HEMBA1001478  
 R-HEMBA1001497  
 15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426  
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503  
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269  
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493  
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723  
 20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270  
 R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348  
 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219  
 R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324  
 R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880  
 25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030  
 R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652  
 R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329  
 R-HEMBA1001589  
 R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874  
 30 R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627  
 R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530  
 R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694  
 35 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158  
 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398  
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554  
 R-HEMBA1001658  
 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343  
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943  
 R-HEMBA1001675  
 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598  
 50 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
 R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452  
 55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219  
 R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105  
 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353  
 R-HEMBA1001744  
 R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
 R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
 5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
 R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
 R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
 R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
 R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
 10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
 R-nnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019  
 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969  
 R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334  
 15 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179  
 R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290  
 R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
 R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
 R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210  
 20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250  
 R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
 R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517  
 25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
 R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:Z48051  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329  
 30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969  
 R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128  
 R-HEMBA1001910  
 R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438  
 35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685  
 R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
 R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145  
 40 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470  
 R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390  
 R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
 45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
 R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
 R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
 R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
 R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825  
 50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178  
 R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
 R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
 55 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353  
 R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801  
 R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
 R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550  
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
 R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312  
 5 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135  
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369  
 10 R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402  
 R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854  
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868  
 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957  
 15 R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734  
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199  
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642  
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337  
 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674  
 20 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915  
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043  
 R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081  
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457  
 25 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622  
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958  
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357  
 30 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503  
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342  
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315  
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151  
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606  
 35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814  
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202  
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426  
 40 R-HEMBA1002257  
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675  
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314  
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595  
 45 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818  
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314  
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822  
 50 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094  
 R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563  
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435  
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237  
 55 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954  
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849  
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267  
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069  
 R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085  
 R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193  
 5 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394  
 R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219  
 R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995  
 R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133  
 R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449  
 10 R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990  
 R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972  
 R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923  
 15 R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700  
 R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804  
 R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881  
 R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012  
 20 R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519  
 R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219  
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587  
 R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904  
 25 R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838  
 R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351  
 30 R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881  
 R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715  
 R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041  
 R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970  
 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696  
 35 R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307  
 R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945  
 R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896  
 40 R-nnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396  
 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282  
 R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477  
 R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315  
 45 R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884  
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521  
 R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168  
 50 R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163  
 R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526  
 R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792  
 R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090  
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126  
 55 R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127  
 R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491  
 R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333  
 R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709  
 R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320  
 5 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:AF071185  
 R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204  
 R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013  
 R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757  
 10 R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514  
 R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830  
 R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827  
 R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670  
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//  
 15 Hs.33787:AF037261  
 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011  
 R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820  
 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087  
 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481  
 20 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165  
 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679  
 R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732  
 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892  
 R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085  
 25 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369  
 R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405  
 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579  
 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219  
 R-nnnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064  
 30 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682  
 R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080  
 R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480  
 R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577  
 35 R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827  
 R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366  
 R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442  
 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182  
 40 R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627  
 R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238  
 R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903  
 R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235  
 45 R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402  
 R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249  
 R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223  
 R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//  
 50 Hs.104800:AA709155  
 R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624  
 R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058  
 R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751  
 55 R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845  
 R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615  
 R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219



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R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670  
R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933  
R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389  
R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000  
5 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804  
R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:  
AB014540  
R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943  
R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265  
10 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR  
[S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817  
R-HEMBA1003227//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:  
W27666  
R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305  
15 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834  
R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.  
152663:AF068864  
R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929  
R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219  
20 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392  
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785  
R-HEMBA1003281  
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:  
AB011109  
25 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266  
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353  
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.  
124224:AB001872  
30 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869  
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119  
R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173  
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:  
AF026029  
35 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357  
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540  
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651  
R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588  
R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247  
40 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-  
11:261:65//Hs.87578:AI125363  
R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847  
R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127  
R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204  
45 R-nnnnnnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309  
R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563  
R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013  
R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696  
R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121  
50 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516  
R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080  
R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688  
R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760  
R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058  
55 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817  
R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673  
R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.  
91619:AA552351

R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734  
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522  
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058  
 5 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440  
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099  
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892  
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065  
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212  
 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087  
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042  
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374  
 R-HEMBA1003615  
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167  
 15 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387  
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888  
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021  
 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438  
 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830  
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010  
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783  
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957  
 25 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049  
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635  
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329  
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083  
 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379  
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916  
 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873  
 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064  
 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777  
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080  
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823  
 40 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847  
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839  
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592  
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040  
 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247  
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089  
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214  
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327  
 50 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600  
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236  
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868  
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295  
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344  
 55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163  
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161  
 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033  
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547  
 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911  
 5 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621  
 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930  
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179  
 R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788  
 10 R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187  
 R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659  
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157  
 R-HEMBA1003939  
 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669  
 15 R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545  
 R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591  
 R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562  
 R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253  
 R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525  
 20 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882  
 R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771  
 R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756  
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682  
 25 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105  
 R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899  
 R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011  
 R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774  
 R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461  
 30 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191  
 R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253  
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804  
 R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469  
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717  
 35 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754  
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080  
 R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988  
 R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652  
 R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251  
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918  
 R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562  
 R-HEMBA1004133  
 R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736  
 R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320  
 45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219  
 R-HEMBA1004150//GRANCALCIN//0.99:357:59//Hs.79381:M81637  
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087  
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855  
 R-HEMBA1004199  
 50 R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701  
 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282  
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518  
 55 R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748  
 R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617  
 R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832

R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353  
 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389  
 R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258  
 5 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus  
 norvegicus]//2.1e-61:221:86//Hs.7089:W37284  
 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962  
 R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-  
 89:465:95//Hs.113660:D20018  
 10 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931  
 R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:  
 AF091081  
 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-  
 92:559:89//Hs.28298:AA203228  
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:  
 15 97//Hs.101766:AF022795  
 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:  
 U13061  
 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7  
 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961  
 20 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426  
 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679  
 R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281  
 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904  
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714  
 25 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561  
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231  
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336  
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240  
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:  
 30 D89667  
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353  
 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:  
 X77494  
 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869  
 35 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057  
 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264  
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084  
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219  
 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717  
 40 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:  
 AA648933  
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.  
 12940:AI123518  
 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503  
 45 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829  
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033  
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172  
 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306  
 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034  
 50 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941  
 R-HEMBA1004507  
 R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-  
 GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271  
 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:  
 55 281:89//Hs.58414:AA196947  
 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972  
 R-HEMBA1004554  
 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913  
 R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243  
 R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769  
 R-nnnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661  
 5 R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970  
 R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915  
 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785  
 10 R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152  
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393  
 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454  
 R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442  
 15 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348  
 R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560  
 R-HEMBA1004672//EST//6.7-e-76:315:97//Hs.20821:R19368  
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252  
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562  
 20 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042  
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881  
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219  
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235  
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317  
 25 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151  
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275  
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828  
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651  
 30 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428  
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081  
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498  
 R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679  
 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504  
 35 R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380  
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705  
 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092  
 R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633  
 40 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476  
 R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167  
 R-nnnnnnnnnnnnn  
 R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732  
 R-HEMBA1004806  
 45 R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676  
 R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002  
 R-HEMBA1004847  
 50 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120  
 R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267  
 R-HEMBA1004864  
 R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362  
 R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409  
 55 R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676  
 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470  
 R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011  
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

- R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388  
 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053  
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
- 5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883  
 R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215  
 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434  
 R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007  
 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
- 10 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040  
 R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035  
 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065  
 R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404  
 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683
- 15 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329  
 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894  
 R-HEMBA1004995  
 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
- 20 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212  
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548  
 R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382
- 25 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067  
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348  
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436  
 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
- 30 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451  
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905  
 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789  
 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077  
 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
- 35 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561  
 R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739  
 R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952  
 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
- 40 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957  
 R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694  
 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
- 45 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914  
 R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766  
 R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239  
 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836
- 50 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284  
 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687  
 R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331  
 R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834  
 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
- 55 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157  
 R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862  
 R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391  
 R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750  
 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219  
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519  
 R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046  
 5 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169  
 R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472  
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606  
 R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467  
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.  
 10 129735:AF010144  
 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350  
 R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653  
 R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305  
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150  
 15 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:  
 92//Hs.43864:AA131568  
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278  
 R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725  
 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059  
 20 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757  
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:  
 453:99//Hs.4854:AF041248  
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960  
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391  
 25 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961  
 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494  
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353  
 R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:  
 K00627  
 30 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445  
 R-HEMBA1005497  
 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788  
 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//  
 Hs.62608:S58544  
 35 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870  
 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:  
 AI219740  
 R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322  
 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045  
 40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981  
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788  
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.  
 17035:AI080471  
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350  
 45 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926  
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627  
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193  
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:  
 182:76//Hs.133526:N21103  
 50 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709  
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497  
 R-HEMBA1005577  
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538  
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392  
 55 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539  
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990  
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905  
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125  
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390  
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422  
 5 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.  
 19400:AA662845  
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377  
 R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081  
 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522  
 10 R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.  
 10458:AF088219  
 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973  
 R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477  
 R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450  
 R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258  
 15 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:  
 U44060  
 R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//  
 1.7e-47:376:84//Hs.26988:U66406  
 R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055  
 20 R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943  
 R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:  
 AJ006470  
 R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815  
 R-nnnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672  
 25 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096  
 R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:  
 U21936  
 R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974  
 R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.  
 30 10458:AF088219  
 R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601  
 R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960  
 R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201  
 R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618  
 35 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911  
 R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917  
 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970  
 R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252  
 R-HEMBA1005894  
 40 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686  
 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363  
 R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632  
 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:  
 AB011098  
 45 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867  
 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418  
 R-HEMBA1005963  
 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.  
 26285:AF082516  
 50 R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199  
 R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618  
 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875  
 R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268  
 55 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951  
 R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508  
 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490  
 R-nnnnnnnnnnnnn



R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612  
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517  
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313  
 5 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//  
 Hs.73614:U83460  
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297  
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293  
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931  
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635  
 10 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:  
 AB007958  
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542  
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212  
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930  
 15 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627  
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906  
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125  
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557  
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//  
 20 Hs.23617:AA928683  
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522  
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:  
 AF083384  
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881  
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.  
 10552:AA524401  
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:  
 92//Hs.104129:AA923278  
 R-nnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770  
 30 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.  
 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821  
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735  
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019  
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037  
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:  
 U33931  
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:  
 AI204587  
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219  
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184  
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204  
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075  
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382  
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008  
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787  
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830  
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:  
 AB011166  
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651  
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:582:84//Hs.23094:M19503  
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923  
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778  
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878  
 55 R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004  
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964  
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380  
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784  
 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895  
 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403  
 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441  
 5 R-HEMBA1006474  
 R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984  
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701  
 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223  
 10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350  
 R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720  
 R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387  
 R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117  
 R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505  
 15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566  
 R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300  
 R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628  
 R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934  
 20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331  
 R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154  
 R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594  
 R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064  
 25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876  
 R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725  
 R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876  
 R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280  
 30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390  
 R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219  
 R-HEMBA1006612  
 R-nnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247  
 R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630  
 35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067  
 R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889  
 R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185  
 40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777  
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282  
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511  
 45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102  
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594  
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842  
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435  
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263  
 50 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695  
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313  
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062  
 55 R-HEMBA1006717  
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002  
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627  
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646  
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763  
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881  
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562  
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936  
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705  
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978  
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333  
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305  
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272  
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556  
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087  
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:  
 15 AB018315  
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453  
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739  
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117  
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400  
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308  
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712  
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382  
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:  
 AJ010841  
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321  
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457  
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827  
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325  
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679  
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440  
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293  
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363  
 R-HEMBA1007045  
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788  
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839  
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140  
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272  
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866  
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-  
 40 40:163:83//Hs.152369:AA504818  
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087  
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025  
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597  
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272  
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438  
 R-HEMBA1007147  
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818  
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674  
 R-nnnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085  
 50 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954  
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987  
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990  
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:  
 55 AB018340  
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864  
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934  
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062  
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207  
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543  
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804  
 5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990  
 R-HEMBA1007301  
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917  
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:AA205569  
 10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629  
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452  
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848  
 15 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684  
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333  
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403  
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090  
 20 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969  
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418  
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332  
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449  
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME  
 25 III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465  
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928  
 R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702  
 R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954  
 30 R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802  
 R-HEMBA1000050//ESTs//0.039:91:74//Hs.163189:AA236903  
 R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107  
 R-HEMBA1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584  
 35 R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939  
 R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997  
 R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353  
 R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193  
 R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540  
 40 R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239  
 R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521  
 R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692  
 R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915  
 45 R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951  
 R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223  
 R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558  
 R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965  
 R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353  
 50 R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364  
 R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019  
 R-HEMBA10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214  
 55 R-HEMBA1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106  
 R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219  
 R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783  
 R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

R-HEMBB1000264  
 R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//  
 Hs.16079:AA083522  
 R-HEMBB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385  
 5 R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:  
 AB011129  
 R-HEMBB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458  
 R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353  
 R-HEMBB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601  
 10 R-HEMBB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034  
 R-HEMBB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219  
 R-HEMBB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576  
 R-HEMBB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480  
 R-HEMBB-1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084  
 15 R-HEMBB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219  
 R-HEMBB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736  
 R-HEMBB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651  
 R-HEMBB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020  
 R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008  
 20 R-HEMBB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590  
 R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.  
 92381:AB007956  
 R-HEMBB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969  
 R-HEMBB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840  
 25 R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642  
 R-HEMBB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173  
 R-HEMBB1000404//ESTs//0.088:298:59//Hs.61607:AA032026  
 R-HEMBB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591  
 R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087  
 30 R-HEMBB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63//  
 Hs.142209:AA873303  
 R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990  
 R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221  
 R-HEMBB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438  
 35 R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396  
 R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390  
 R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506  
 R-HEMBB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219  
 R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080  
 40 R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125  
 R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703  
 R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087  
 R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080  
 R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099  
 45 R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662  
 R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:  
 AF052288  
 R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986  
 R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258  
 50 R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709  
 R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618  
 R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247  
 R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895  
 R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704  
 55 R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391  
 R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199  
 R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125  
 R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152  
 R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531  
 R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522  
 R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582  
 5 R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963  
 R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100  
 R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939  
 R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988  
 R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705  
 10 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293  
 R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454  
 R-nnnnnnnnnnnn/Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723  
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219  
 R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412  
 15 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403  
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306  
 R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881  
 R-HEMBB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272  
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925  
 20 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522  
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445  
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541  
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771  
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091  
 25 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718  
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961  
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219  
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447  
 R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124  
 30 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219  
 R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881  
 R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176  
 R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545  
 R-HEMBB1000840//ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876  
 35 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137  
 R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599  
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942  
 R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141  
 40 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247  
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740  
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258  
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830  
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881  
 45 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066  
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983  
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325  
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742  
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874  
 50 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784  
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881  
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503  
 R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354  
 R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007  
 55 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242  
 R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369  
 R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625  
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112  
 R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:  
 H58762  
 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214  
 5 R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814  
 R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080  
 R-HEM BB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562  
 R-HEM BB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385  
 R-HEM BB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975  
 10 R-HEM BB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107  
 R-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:  
 AB014518  
 R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:  
 AB007944  
 15 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785  
 R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381  
 R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803  
 R-HEM BB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:233:70//Hs.37181:D64108  
 R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353  
 20 R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080  
 R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426  
 R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092  
 R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942  
 R-HEM BB1001126  
 25 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:  
 285:73//Hs.554:M25077  
 R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881  
 R-HEM BB1001151  
 30 R-HEM BB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-  
 65:331:96//Hs.154179:AA579197  
 R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878  
 R-nnnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162  
 R-HEM BB1001177  
 35 R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349  
 R-HEM BB1001199  
 R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183  
 R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549  
 R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573  
 40 R-HEM BB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,  
 antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795  
 R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817  
 R-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//  
 Hs.71873:AA148213  
 45 R-HEM BB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560  
 R-HEM BB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236  
 R-HEM BB1001253//EST//0.0011:84:77//Hs.124579:AA853987  
 R-HEM BB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268  
 R-HEM BB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.  
 50 159897:AB007970  
 R-HEM BB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087  
 R-HEM BB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412  
 R-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III  
 [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021  
 55 R-HEM BB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840  
 R-HEM BB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112  
 R-HEM BB1001302  
 R-HEM BB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEM BB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627  
 R-HEM BB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627  
 R-HEM BB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873  
 5 R-HEM BB1001326//ESTs//0.85:174:62//Hs.133487:AI393754  
 R-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222  
 R-HEM BB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365  
 R-HEM BB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639  
 R-HEM BB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470  
 10 R-HEM BB1001346  
 R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354  
 R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721  
 R-HEM BB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055  
 15 R-HEM BB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087  
 R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617  
 R-HEM BB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219  
 R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205  
 R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699  
 20 R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970  
 R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350  
 R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342  
 R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644  
 R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651  
 25 R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846  
 R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317  
 R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201  
 R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236  
 R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515  
 30 R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293  
 R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881  
 R-HEM BB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468  
 R-HEM BB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481  
 R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515  
 35 R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280  
 R-HEM BB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915  
 R-HEM BB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159  
 40 R-HEM BB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459  
 R-HEM BB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353  
 R-HEM BB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869  
 R-HEM BB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274  
 R-HEM BB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962  
 45 R-HEM BB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521  
 R-HEM BB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329  
 R-HEM BB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944  
 R-HEM BB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219  
 R-HEM BB1001588//EST//8.3e-27:363:69//Hs.141603:N66015  
 50 R-HEM BB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184  
 R-HEM BB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044  
 R-HEM BB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888  
 R-HEM BB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272  
 R-HEM BB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082  
 55 R-HEM BB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633  
 R-HEM BB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813  
 R-HEM BB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438  
 R-HEM BB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577



R-HEM BB1001668//ESTs//0.73:212:62//Hs.8928:N32572  
 R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546  
 R-HEM BB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534  
 5 R-HEM BB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358  
 R-HEM BB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867  
 R-HEM BB1001704//EST//0.96:248:57//Hs.163025:AA703038  
 R-HEM BB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080  
 10 R-HEM BB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569  
 R-HEM BB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645  
 R-HEM BB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113  
 15 R-HEM BB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403  
 R-HEM BB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488  
 R-HEM BB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287  
 R-HEM BB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059  
 R-HEM BB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211  
 20 R-HEM BB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352  
 R-HEM BB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369  
 R-HEM BB1001785//ESTs//0.040:390:58//Hs.116651:AA993406  
 R-HEM BB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253  
 25 R-HEM BB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391  
 R-HEM BB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247  
 R-HEM BB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503  
 R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209  
 30 R-HEM BB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957  
 R-HEM BB1001839  
 R-HEM BB1001850//EST//0.020:119:68//Hs.32767:H38125  
 R-HEM BB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539  
 35 R-HEM BB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106  
 R-HEM BB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397  
 R-HEM BB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434  
 R-HEM BB1001872//EST//0.85:156:64//Hs.119501:AA487980  
 R-HEM BB1001874//EST//0.64:107:70//Hs.147482:AI215572  
 40 R-HEM BB1001875//EST//0.079:199:59//Hs.121810:AA775240  
 R-HEM BB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081  
 R-HEM BB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310  
 R-HEM BB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191  
 R-HEM BB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725  
 45 R-HEM BB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915  
 R-HEM BB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216  
 R-HEM BB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750  
 R-HEM BB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897  
 R-HEM BB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390  
 50 R-HEM BB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251  
 R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325  
 R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875  
 R-HEM BB1001944//EST//0.034:228:57//Hs.93664:N23366  
 55 R-HEM BB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875  
 R-HEM BB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589  
 R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998  
 R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522  
 R-HEMBB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881  
 R-HEMBB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972  
 5 R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147  
 R-HEMBB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531  
 R-HEMBB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475  
 R-HEMBB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572  
 10 R-HEMBB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223  
 R-HEMBB1001996  
 R-HEMBB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798  
 R-HEMBB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627  
 R-HEMBB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334  
 15 R-HEMBB1002009//EST//2.9e-44:245:94//Hs.28788:R66896  
 R-HEMBB1002015//EST//0.0027:198:63//Hs.160868:AI359052  
 R-HEMBB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900  
 R-HEMBB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426  
 R-HEMBB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638  
 20 R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080  
 R-HEMBB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638  
 R-HEMBB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840  
 R-HEMBB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671  
 R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144  
 25 R-HEMBB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193  
 R-HEMBB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881  
 R-HEMBB1002115  
 R-HEMBB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814  
 30 R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006  
 R-HEMBB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553  
 R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073  
 R-HEMBB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185  
 35 R-HEMBB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934  
 R-HEMBB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881  
 R-HEMBB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841  
 R-HEMBB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584  
 R-HEMBB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631  
 40 R-HEMBB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807  
 R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503  
 R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363  
 R-HEMBB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112  
 R-HEMBB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223  
 45 R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892  
 R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637  
 R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228  
 50 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841  
 R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613  
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522  
 R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085  
 55 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467  
 R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055  
 R-HEMBB1002387  
 R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

168:77//Hs.133526:N21103

R-HEM BB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280

R-HEM BB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293

R-HEM BB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353

R-HEM BB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087

R-HEM BB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089

R-HEM BB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083

R-HEM BB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176

R-HEM BB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969

R-HEM BB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017

R-HEM BB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142

R-HEM BB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615

R-HEM BB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278

R-HEM BB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538

R-HEM BB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672

R-HEM BB1002531//EST//0.024:147:61//Hs.148305:AA909605

R-HEM BB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478

R-HEM BB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259

R-HEM BB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813

R-HEM BB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830

R-HEM BB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189

R-HEM BB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045

R-HEM BB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138

R-HEM BB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087

R-HEM BB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424

R-HEM BB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923

R-HEM BB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881

R-HEM BB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896

R-HEM BB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265

R-HEM BB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977

R-HEM BB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150

R-HEM BB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917

R-HEM BB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247

R-HEM BB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219

R-HEM BB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881

R-HEM BB1002677//ESTs//0.65:159:62//Hs.163517:AI419775

R-HEM BB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339

R-HEM BB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646

R-HEM BB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753

R-HEM BB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099

R-HEM BB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487

R-HEM BB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398

R-HEM BB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842

R-HEM BB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547

R-HEM BB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682

R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701

R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219

R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152

R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901

R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165  
 R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350  
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531  
 5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065  
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099  
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241  
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713  
 10 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352  
 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172  
 15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577  
 R-MAMMA1000133  
 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017  
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970  
 20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881  
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263  
 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787  
 R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162  
 25 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069  
 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611  
 R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054  
 30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881  
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103  
 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425  
 R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946  
 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315  
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090  
 R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041  
 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238  
 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814  
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977  
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369  
 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694  
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956  
 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000287  
 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892  
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067  
 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251  
 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434  
 R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491  
 55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998  
 R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881  
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159  
 R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912  
 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087  
 5 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659  
 R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523  
 R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065  
 R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132  
 10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060  
 R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973  
 R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198  
 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958  
 15 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099  
 R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171  
 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081  
 20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067  
 R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390  
 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452  
 R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461  
 25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171  
 R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179  
 R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447  
 R-MAMMA1000458  
 30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176  
 R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361  
 R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959  
 R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886  
 R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759  
 35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219  
 R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390  
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390  
 R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267  
 R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236  
 40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131  
 R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561  
 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211  
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872  
 R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548  
 45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219  
 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042  
 R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267  
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105  
 50 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180  
 R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361  
 R-MAMMA1000623  
 R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002  
 55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203  
 R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162  
 R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065  
 R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476  
 R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212  
 5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343  
 R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644  
 R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333  
 R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569  
 10 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515  
 R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329  
 R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942  
 R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267  
 15 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893  
 R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915  
 R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141  
 R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288  
 20 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205  
 R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503  
 R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627  
 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131  
 25 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256  
 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353  
 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204  
 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439  
 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150  
 30 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163  
 R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73919:X81637  
 R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675  
 R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881  
 R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902  
 35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358  
 R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097  
 R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955  
 R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251  
 40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390  
 R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212  
 R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311  
 R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922  
 R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099  
 45 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399  
 R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875  
 R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243  
 R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128  
 R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166  
 50 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107  
 R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215  
 R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329  
 R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093  
 55 R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634  
 R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989  
 R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335  
 R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727  
 R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281  
 R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428  
 5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053  
 R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178  
 R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795  
 10 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147  
 R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881  
 R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204  
 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304  
 15 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881  
 R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263  
 R-MAMMA1001003//Sialoporphin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075  
 20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313  
 R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333  
 R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814  
 R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536  
 R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461  
 25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390  
 R-nnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650  
 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881  
 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487  
 30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532  
 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748  
 R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353  
 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944  
 R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503  
 35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222  
 R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926  
 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587  
 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686  
 40 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576  
 R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267  
 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750  
 45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029  
 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399  
 R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179  
 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131  
 R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750  
 50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970  
 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251  
 R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959  
 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519  
 R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202  
 55 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348  
 R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637  
 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293  
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202  
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315  
 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701  
 5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619  
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307  
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569  
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149  
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561  
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001  
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643  
 15 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144  
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371  
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876  
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135  
 20 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426  
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984  
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709  
 25 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471  
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426  
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519  
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127  
 30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478  
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322  
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216  
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881  
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831  
 35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275  
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957  
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267  
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168  
 40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618  
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892  
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542  
 R-MAMMA1001465  
 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317  
 45 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394  
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065  
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522  
 R-MAMMA1001510  
 50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242  
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969  
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696  
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140  
 55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305  
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441  
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792



R-MAMMA1001604

R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616

R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272

R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315

R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074

R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377

R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144

R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219

R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248

R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550

R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081

R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957

R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884

R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088

R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:AI082338

R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596

R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923:AI161158

R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651

R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666

R-MAMMA1001744

R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817

R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041

R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413

R-MAMMA1001757//ESTs//1.0e-9:8:488:96//Hs.45184:C14904

R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276

R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847

R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325

R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825

R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481246

R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460

R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238

R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644

R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744

R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313

R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892

R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659

R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979

R-MAMMA1001818

R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881

R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519

R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140

R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394

R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811

R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461

R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219

R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840

R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944

R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:7811Hs/138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3-0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696

R-MAMMA1002236

R-MAMMA1002243

5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080

R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript

KIAA0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452

R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503

R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094

R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280

25 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183

R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084

R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658

R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317

30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897

R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618

R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439

R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127

R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228

35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390

R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367

R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637

R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080

R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475

40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587

R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236

R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542

R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219

45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061

R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845

R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294

R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488

50 R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588

R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477

R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475

R-MAMMA1002434//ESTS, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348

55 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996

R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

89121:AB007954

R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076

R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106

R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496

R-MAMMA10024807//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460

R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293

R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664

R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214

R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147

R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851

R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058

R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681

R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693

R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433

R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371

R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258

R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874

R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737

R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369

R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053

R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389

R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670

R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306

R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081

R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881

R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.93332:AA811920

R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488

R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390

R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421

R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915

R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776

R-MAMMA1002655

R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886

R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087

R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606

R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:D86987

R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385

R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675

R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510

R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986

R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234  
 R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858  
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333  
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571  
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219  
 R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757  
 R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907  
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452  
 10 R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776  
 R-MAMMA1002758  
 R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281  
 R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651  
 15 R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272  
 R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750  
 R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145  
 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812  
 R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198  
 20 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260  
 R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319  
 R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881  
 R-MAMMA1002835  
 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723  
 25 R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395  
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238  
 R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081  
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067  
 R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941  
 30 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592  
 R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194  
 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871  
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219  
 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811  
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783  
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915  
 R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087  
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179  
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002  
 R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881  
 R-MAMMA1002938  
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503  
 R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243  
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353  
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081  
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630  
 R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835  
 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279  
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019  
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179  
 R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857  
 R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617  
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.92023:AI022248  
 R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189  
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315  
R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358  
5 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321  
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160  
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940  
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941  
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862  
10 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348  
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881  
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559  
R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911  
15 R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969  
R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652  
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651  
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283  
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366  
20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788  
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125  
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537  
R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861  
25 R-nnnnnnnnnnnnn  
R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736  
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640  
R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312  
30 R-NT2RM4000027  
R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663  
R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169  
R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379  
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549:97//Hs.95665:AF070639  
35 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817  
R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708  
R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312  
R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:AI246301  
40 R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397  
R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962  
R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160  
R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113  
45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723  
R-NT2RM400019911ESTs//10.020:95:6511Hs.146203:AI254528  
R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876  
R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219  
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255  
50 R-NT2RM4000215  
R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760  
R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602  
55 R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031  
R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974  
R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

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R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128  
R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673  
R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219  
R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637  
5 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881  
R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:A1224479  
R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063  
R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542  
R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140  
10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:  
AA775879  
R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGEN-  
IC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977  
R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285  
15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235:  
AA192359  
R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173  
R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:A1150687  
R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865  
20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:  
492:96//Hs.21090:AA418587  
R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.  
111279:W84558  
R-NT2RM4000496  
25 R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:A1358465  
R-NT2RM4000514//ESTS//1.7e-112:552:96//Hs.6686:AA205496  
R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC  
REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879  
R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731  
30 R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461  
R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777  
R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198  
R-NT2RM4000585//EST//0.28:63:77//Hs.150024:A1291981  
R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437  
35 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891  
R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589  
R-nnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697  
R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:  
519:96//Hs.14779:N64822  
40 R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144  
R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531  
R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510  
R-nnnnnnnnnnnn  
R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128  
45 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
//2.2e-103:519:95//Hs.6823:W18181  
R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311  
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:  
AB018303  
50 R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046  
R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988  
R-NT2RM4000764  
R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174  
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:  
55 AB007920  
R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.  
154069:U06452  
R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:A1417008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891  
 R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:  
 M21868  
 5 R-NT2RM4000813  
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:  
 AI219667  
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031  
 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864  
 10 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597  
 R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343  
 R-nnnnnnnnnnnnn  
 R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-  
 96:450:99//Hs.142076:AA604514  
 15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262  
 R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887  
 R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647  
 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:  
 AA650126  
 20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:  
 AB018272  
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:  
 AB014539  
 R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352  
 25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.  
 32170:AB015132  
 R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300  
 R-nnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798  
 R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324  
 30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962  
 R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276  
 R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311  
 R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848  
 R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085  
 35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-  
 43:273:91//Hs.109005:N31174  
 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942  
 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849  
 R-NT2RM4001203  
 40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307  
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410  
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677  
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184  
 R-NT2RM4001309  
 45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857  
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899  
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352  
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.  
 18442:AI129307  
 50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339  
 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476  
 R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211  
 R-NT2RM4001382  
 R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507  
 55 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790  
 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:  
 94//Hs.15744:AI055859  
 R-NT2RM4001412



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R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895  
R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054  
R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812  
5 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277  
R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739  
R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067  
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585  
10 R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664  
R-NT2RM40015227//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219  
R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072  
R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027  
R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene  
15 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046  
R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009  
R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946  
20 R-nnnnnnnnnnnnn  
R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171  
R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871  
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334  
25 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079  
R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957  
R-NT2RM4001650  
R-NT2RM4001662  
R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938  
30 R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496  
R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440  
R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686  
R-nnnnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465  
35 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887  
R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390  
R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200  
40 R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629  
R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740  
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270  
R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956  
R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567  
45 R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920  
R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839  
R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551  
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070  
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619  
50 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652  
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000  
R-nnnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280  
55 R-NT2RM40018657//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711  
R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252  
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149

R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178  
 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:  
 535:95//Hs.30991:AA994438  
 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143  
 5 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893  
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:  
 AF098162  
 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268  
 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917  
 10 R-ntnnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097  
 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265  
 R-NT2RM4001984  
 R-NT2RM4001987  
 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528  
 15 R-NT2RM4002018  
 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087  
 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435  
 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226  
 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887  
 20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179  
 R-ntnnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:  
 AF071309  
 R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629  
 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//  
 25 Hs.109274:AA193416  
 R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655  
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528  
 R-ntnnnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409  
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620  
 30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712  
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987  
 R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090  
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535  
 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258  
 35 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400  
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343  
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678  
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079  
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 40 //5.1e-112:569:95//Hs.23900:U82984  
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglu-  
 cosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190  
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219  
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864  
 45 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263  
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638  
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461  
 R-NT2RM4002294  
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164  
 50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498  
 R-ntnnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913  
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198  
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:  
 AB014549  
 55 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594  
 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884  
 R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328  
 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

98//Hs.16464:W19606  
 R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677  
 R-NT2RM4002446  
 R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142  
 5 R-NT2RM4002457  
 R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890  
 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.  
 8765:AF083255  
 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:  
 10 AB014591  
 R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884  
 R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029  
 R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//  
 15 Hs.31030:H50467  
 R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788  
 R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057  
 R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312  
 R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE [Bos  
 20 taurus]//2.3e-89:435:97//Hs.15830:AA165698  
 R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569  
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]  
 //9.6e-28:194:87//Hs.59346:AI126802  
 R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096  
 25 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081  
 R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115  
 R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713  
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 30 4.3e-64:309:98//Hs.6216:AF061749  
 R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798  
 R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910  
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:  
 AA775879  
 35 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881  
 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097  
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.  
 54877:AF050078  
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.  
 40 102576:AJ010230  
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338  
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064  
 R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757  
 R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827  
 45 R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419  
 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356  
 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III  
 [C.elegans]//1.9e-19:153:86//Hs.5268:W22670  
 R-nnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099  
 50 R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513  
 R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-  
 89:457:95//Hs.3832:AI208601  
 R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548  
 R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820  
 55 R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190  
 R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741  
 R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373  
 R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897

R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382

R-NT2RP2000232

5 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683

R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379

R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005

R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840

10 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649

R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382

R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635

R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865

15 R-NT2RP2000289

R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249

R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712

R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381

20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398

25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441

R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981

30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010

R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265

35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425

R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045

R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013

R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078

40 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215

R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896

R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348

R-NT2RP2000523

R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144

45 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514

R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222

R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275

R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396

50 R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767

R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347

R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368

R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279

R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965

55 R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642

R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419

R-NT2RP2000809

R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

R-nnnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404  
 R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918  
 R-NT2RP2000819  
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511  
 5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6  
 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165  
 R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552  
 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345  
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:  
 10 AB018284  
 R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267  
 R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266  
 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III  
 [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477  
 15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:  
 AB018298  
 R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021  
 R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481  
 R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
 20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537  
 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521  
 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643  
 R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660  
 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108  
 25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665  
 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068  
 R-NT2RP2001119  
 R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348  
 R-NT2RP2001137  
 30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512  
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145  
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:  
 AB007949  
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287  
 35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510  
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402  
 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358  
 R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//  
 Hs.44014:AA632298  
 40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996  
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353  
 R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229  
 R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775  
 R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665  
 45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205  
 R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//  
 2.3e-43:238:93//Hs.106632:N25679  
 R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138  
 R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178  
 50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028  
 R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038  
 R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.  
 sapiens]//3.9e-74:411:93//Hs.47305:AA195153  
 R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875  
 55 R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:  
 469:97//Hs.20483:AA522505  
 R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030  
 R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

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R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728  
 R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:AI341556  
 R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394  
 R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453  
 5 R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765  
 R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539  
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219  
 R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513  
 R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146  
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:  
 Y14494  
 R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240  
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//  
 1.9e-15:99:95//Hs.99742:AF035586  
 15 R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816  
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.  
 67619:AB007957  
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661  
 R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884  
 20 R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995  
 R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767  
 R-NT2RP2001613  
 R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294  
 R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090  
 25 R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845  
 R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336  
 R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323  
 R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579  
 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538  
 30 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100  
 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840  
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:  
 AF091754  
 R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037  
 35 R-NT2RP2001861  
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941  
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088  
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:  
 AA113849  
 40 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724  
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423  
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268  
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087  
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180  
 45 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594  
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588  
 R-NT2RP2001969  
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745  
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:  
 89//Hs.18760:AA166678  
 50 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233  
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332  
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627  
 R-NT2RP2002041  
 55 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938  
 R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895  
 R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068  
 R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091



R-NT2RP2002672

R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572

R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

5 R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300

R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108

R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

10 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537

R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

15 R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

R-NT2RP2002880

20 R-NT2RP2002891

R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894

R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143

R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096

R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771

25 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480

R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060

R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213

R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291

30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329

R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311

R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642

R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594

35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082

R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081

R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512

R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345

R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355

40 R-NT2RP2003125

R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986

R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506

R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379

R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067

45 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952

R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156

R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816

R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074

R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253

50 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661

R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438

R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937

R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525

55 R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427

R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106

R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087



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R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811  
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838  
R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611  
10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.  
75875:U49278  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//  
Hs.35086:AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:  
15 AB007916  
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347  
R-NT2RP2003984  
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:  
20 AI149968  
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478  
R-NT2RP2004041  
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
R-nnnnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
25 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500  
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241  
30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:  
583:97//Hs.16520:AI224533  
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544  
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974  
R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
35 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
R-NT2RP2004196  
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:  
40 AA483305  
R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.  
54900:AF039687  
R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
45 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:  
50 AF000416  
R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
R-NT2RP2004347  
R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173  
R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310  
55 R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624  
R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192  
R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III  
[Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916



R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161  
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507  
 R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887  
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220  
 5 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757  
 R-NT2RP2005108  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564  
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743  
 10 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383  
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180AI341261  
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744  
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438  
 15 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582  
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648  
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509  
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166  
 20 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258  
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587  
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503  
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596  
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272  
 R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001  
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219  
 30 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590  
 R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261  
 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338  
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701  
 35 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699  
 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445  
 R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544  
 40 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247  
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304  
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697  
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631  
 45 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068  
 R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423  
 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096  
 R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307  
 50 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936  
 R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019  
 R-NT2RP2005476//ESTs//5.1 e-40:205:9811Hs.101577:AI168526  
 R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573  
 R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455  
 55 R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540  
 R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426  
 R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Orctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755  
 R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME  
 I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071  
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:  
 5 570:9411Hs.119023:AF092563  
 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:  
 433:95//Hs.36942:AA524535  
 R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856  
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:  
 10 AJ012449  
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:  
 AB007963  
 R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572  
 R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567  
 15 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169  
 R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240  
 R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733  
 R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060  
 R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788  
 20 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229  
 R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211  
 R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740  
 R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173  
 R-NT2RP2005651//ESTS, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:  
 25 AA868470  
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302  
 R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987  
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//  
 Hs.25664:AF089814  
 30 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229  
 R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236  
 R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643  
 R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs.  
 9095:AA532630  
 35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:  
 AB018342  
 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//  
 Hs.14298:AI417523  
 R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982  
 40 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455  
 R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153  
 R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258  
 R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064  
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//  
 45 Hs.159651:AF068868  
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.  
 26285:AF082516  
 R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163  
 R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463  
 50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-  
 112:559:96//Hs.14214:AI189379  
 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.  
 22151:AI214321  
 R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664  
 55 R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724  
 R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398  
 R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746  
 R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122  
 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403  
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062  
 R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462  
 5 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105  
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133  
 R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315  
 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268  
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:  
 10 94//Hs.16667:T92427  
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170  
 R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419  
 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988  
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080  
 15 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347  
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II  
 [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631  
 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492  
 R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714  
 20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093  
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918  
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//  
 Hs.46440:U21943  
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365  
 25 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522  
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258  
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435  
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:  
 AB014554  
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276  
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398  
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484  
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312  
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253  
 35 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928  
 R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999  
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262  
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015  
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:  
 40 N78664  
 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771  
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412  
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321  
 R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411  
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:  
 77//Hs.1361:M55053  
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.  
 115325:D84488  
 R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092  
 50 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146  
 R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595  
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266  
 R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478  
 R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679  
 55 R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947  
 R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474  
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886  
 R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

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R-nnnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829  
R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112  
R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598  
5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972  
R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219  
R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213  
R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202  
10 R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095  
R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574  
R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029  
R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715  
R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241  
15 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000  
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164  
R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418  
R-NT2RP3000186  
20 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882  
R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091  
R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306  
R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817  
R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819  
25 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239  
R-NT2RP3000251  
R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177  
R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073  
R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446  
30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323  
R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117  
R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438  
R-NT2RP3000324  
35 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267  
R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689  
R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225  
R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177  
R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741  
40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423  
R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303  
R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106  
R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185  
45 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947  
R-NT2RP3000433  
R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340  
R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254  
50 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102  
R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492  
R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408  
R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600  
55 R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141  
R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667  
R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151  
R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.95:85:71//Hs.5184:AA709151  
R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180  
R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:A1198036  
R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071  
R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447  
R-NT2RP3000582//ESTS//2.1 e-25:131:80//Hs.152465:AA563785  
R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:A1241511  
R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817  
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:A1190916  
R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312  
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880  
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049  
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:A1127394  
R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:A1090739  
R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315  
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022  
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084  
R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185  
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185  
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873  
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:A1085578  
R-NT2RP3000736  
R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-  
ESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960  
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:A1310447  
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243  
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:A1378583  
R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810  
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582  
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:A1151081  
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082  
R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022  
R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:A1051657  
R-NT2RP3000850  
R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272  
R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895  
R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741  
R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837  
R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:A1014673  
R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468  
R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217  
R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385  
R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:AA035728  
R-NT2RP3000919  
R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407  
R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178  
R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542  
R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405  
R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:A1088029  
R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044  
R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.145956:AA007349  
R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.0012:447:58//Hs.2133:U18991  
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874  
R-NT2RP3001096//ESTS//1.1e-110:540:96//Hs.42824:AA873182



R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832  
 R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325  
 R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:  
 C06063  
 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575  
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878  
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779  
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180  
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166  
 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188  
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761  
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305  
 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 //9.6e-113:552:97//Hs.23900:U82984  
 15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717  
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266  
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460  
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139  
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963  
 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196  
 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399  
 R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588  
 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:  
 AA524416  
 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631  
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997  
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135  
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857  
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965  
 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651  
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332  
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691  
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571  
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989  
 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:  
 U35234  
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:  
 AB007920  
 R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653  
 40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798  
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090  
 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778  
 R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//  
 Hs.96200:AA218942  
 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375  
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232  
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628  
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186  
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898  
 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817  
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158  
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692  
 R-nnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397  
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374  
 55 R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-  
 101:482:98//Hs.124135:AA910560  
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994  
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658  
 R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280  
 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009  
 R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783  
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395  
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
 6.8e-112:549:9711Hs.28285:AF064801  
 R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047  
 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750  
 10 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463  
 R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:  
 AA524416  
 R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477  
 R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337  
 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194  
 R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328  
 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798  
 R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598  
 R-NT2RP3001629  
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149  
 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989  
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709  
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030  
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189  
 25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648  
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225  
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558  
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390  
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312  
 30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618  
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669  
 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
 //4.1e-80:444:91//Hs.6823:W18181  
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099  
 35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923  
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810  
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440  
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968  
 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:  
 40 N92517  
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725  
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:  
 AB007928  
 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900  
 45 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962  
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292  
 R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117  
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900  
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792  
 50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642  
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180  
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666  
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
 AI123300  
 55 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781  
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737  
 R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]  
 //1.3e-95:483:96//Hs.5771:W74591

R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990  
R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325  
R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889  
R-NT2RP3001989//ESTS, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:AI201540  
R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088  
R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779  
R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729  
R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219  
R-NT2RP3002033  
R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081  
R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426  
R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221  
R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486  
R-NT2RP3002062  
R-nnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657  
R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139  
R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148  
R-NT2RP3002102  
R-NT2RP3002108  
R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385  
R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703  
R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534:96//Hs.59523:AA602837  
R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293  
R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024  
R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713  
R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120  
R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598  
R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446  
R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588  
R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672  
R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743  
R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171  
R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898  
R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500  
R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]//1.8e-19:136:87//Hs.106928:AI041737  
R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667  
R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887  
R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:Y16355  
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:AB014578  
R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486  
R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185  
R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436  
R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246  
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272  
R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673  
R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815  
R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880  
R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850  
R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673  
R-NT2RP3002603  
R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365  
 R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573  
 R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172  
 5 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [*Drosophila melanogaster*]//5.9e-109:537:97//Hs.19348:AA151678  
 R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502  
 R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871  
 R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//5.0e-101:524:95//Hs.32580:AI123601  
 10 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169  
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945  
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159  
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973  
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958  
 15 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377  
 R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240  
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080  
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678  
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641  
 20 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262  
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314  
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286  
 25 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975  
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698  
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961  
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [*Saccharomyces cerevisiae*]//112.0e-56:387:86//Hs.144597:W20143  
 30 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850  
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116  
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553  
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423  
 35 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [*Mus musculus*]//3.0e-100:528:94//Hs.90353:N98551  
 R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355  
 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912  
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [*C.elegans*]//5.9e-83:392:99//Hs.101364:AA534439  
 40 R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809  
 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466  
 R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441  
 R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520  
 R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982  
 45 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [*Mus musculus*]//3.3e-107:535:96//Hs.27437:AA004208  
 R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632  
 R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774  
 R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007  
 50 R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226  
 R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944  
 R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796  
 R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634  
 R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573  
 55 R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107  
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [*Dictyostelium discoideum*]//2.0e-40:229:93//Hs.17377:AI078151  
 R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628  
 R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960  
 R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061  
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983  
 5 R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035  
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055  
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818  
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261  
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931  
 10 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445  
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289  
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993  
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102  
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155  
 15 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567  
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272  
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721  
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095  
 20 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372  
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041  
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023  
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828  
 25 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268  
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:AI057529  
 30 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556  
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)<sub>n</sub>/(GTG)<sub>n</sub> repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952  
 R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430  
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681  
 35 R-NT2RP3003564  
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721  
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944  
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759  
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448  
 40 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957  
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310  
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714  
 R-NT2RP3003672  
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036  
 45 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768  
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923  
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 50 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913  
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446  
 55 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224  
 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611  
 5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170  
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
 10 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221  
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593  
 R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
 15 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
 R-NT2RP3004041  
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
 R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139  
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537  
 20 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092  
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696  
 25 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334  
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093  
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126  
 30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619  
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680  
 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794  
 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252  
 35 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827  
 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628  
 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468:95//Hs.5117:AA831530  
 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623  
 40 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630  
 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264  
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258  
 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223  
 R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044  
 45 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224  
 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934  
 R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985  
 R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621  
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917  
 50 R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616  
 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332  
 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406  
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925  
 55 R-NT2RP3004480  
 R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504  
 R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.47393:AA218858

R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
 R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//  
 1.8e-83:465:92//Hs.137064:AA318257  
 R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
 5 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
 R-nnnnnnnnnnnnn  
 R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
 R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
 R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
 10 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
 R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
 R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
 R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
 R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
 15 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase  
 (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680  
 R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
 R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
 R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
 20 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266  
 R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945  
 R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
 R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
 25 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:  
 AB007952  
 R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
 R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
 R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III  
 30 [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
 R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
 R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569  
 R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:  
 35 AB014600  
 R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
 R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390  
 R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:  
 40 AJ006470  
 R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:  
 AF091092  
 R-NT2RP4000263  
 45 R-nnnnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]  
 //4.7e-104:525:96//Hs.152069:AA548972  
 R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631  
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524  
 R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760  
 50 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390  
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:  
 AB018281  
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-  
 110:527:98//Hs.31323:AF044195  
 55 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130  
 R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498  
 R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376  
 R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:







R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511  
 R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385  
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863  
 R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292  
 5 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium  
 tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:  
 88//Hs.136189:AA133224  
 R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552  
 10 R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285  
 R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437  
 R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251  
 R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906  
 R-NT2RP4001575  
 15 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]  
 //8.7e-112:557:97//Hs.7558:AA526812  
 R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776  
 R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657  
 R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737  
 20 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:  
 AF007151  
 R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361  
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II  
 [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734  
 25 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805  
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.  
 15562:U96629  
 R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-  
 30 CURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922  
 R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692  
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926  
 R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315  
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:  
 35 W28098  
 R-NT2RP4001803  
 R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133  
 R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434  
 R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826  
 40 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087  
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528  
 45 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606  
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099  
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
 R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793  
 50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637  
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:  
 AA775879  
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
 R-NT2RP4002018  
 55 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:  
 90:86//Hs.41127:AA555184  
 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679  
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198  
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507  
 5 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565  
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407  
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592  
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555  
 10 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272  
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090  
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934  
 15 R-OVARC1000004  
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929  
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635  
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273  
 R-OVARC1000017  
 20 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286  
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073  
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041  
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367  
 R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787  
 25 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259  
 R-nnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703  
 R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370  
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942  
 30 R-OVARC1000106  
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250  
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312  
 R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482  
 35 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214  
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090  
 R-OVARC1000151  
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023  
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629  
 40 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258  
 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864  
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874  
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958  
 45 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130  
 R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079  
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476  
 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777  
 50 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449  
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743  
 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682  
 55 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863  
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672  
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423  
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 5 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//  
 Hs.73614:U83460  
 10 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:  
 AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576  
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211  
 15 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 20 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219  
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248  
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021  
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106  
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285  
 25 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587  
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627  
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219  
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053  
 R-OVARC1000605  
 30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.  
 159897:AB007970  
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073  
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:  
 AB011162  
 35 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480  
 R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522  
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875  
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517  
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901  
 40 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461  
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-  
 45 28:430:69//Hs.42457:AA523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066  
 50 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:  
 Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637  
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584  
 55 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096  
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292  
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953  
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401  
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350  
 5 R-OVARC1000912  
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814  
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127  
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696  
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215  
 10 R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794  
 R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971  
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219  
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394  
 R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909  
 15 R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:AA532784  
 R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811  
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874  
 R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448  
 20 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629  
 R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270  
 R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117  
 R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630  
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:  
 25 137:74//Hs.77579:AF013263  
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149  
 R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046  
 R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384  
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962  
 30 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231  
 R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652  
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657  
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844  
 35 R-OVARC1001074  
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029  
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897  
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782  
 40 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984  
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548  
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312  
 45 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226  
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223  
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727  
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200  
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219  
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223  
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:80//Hs.97203:U83171  
 R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343  
 55 R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826  
 R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025  
 R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668  
 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166  
 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929  
 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708  
 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532  
 5 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113  
 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:AB011090  
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637  
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344  
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219  
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356  
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247  
 15 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216  
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657  
 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844  
 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777  
 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415  
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:AB011147  
 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958  
 R-OVARC1001391  
 R-nnnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913  
 25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651  
 R-OVARC1001419  
 R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136  
 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427  
 R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345  
 30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592  
 R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700  
 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694  
 R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089  
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:AF016507  
 35 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219  
 R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539  
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492  
 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388  
 40 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7/4.4e-20:150:89//Hs.155160:AF031166  
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087  
 R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019  
 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965  
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869  
 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659  
 R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854  
 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080  
 R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784  
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:AA046954  
 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276  
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:AF057280  
 55 R-nnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:540:92//Hs.117741:AA903456  
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:  
 AB014575  
 R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127  
 R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604  
 5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978  
 R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333  
 R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688  
 R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831  
 R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110  
 10 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705  
 R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621  
 R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160  
 R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809  
 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence/1.9e-105:571:91//Hs.25300:  
 15 AF070611  
 R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476  
 R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:  
 AB011147  
 R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310  
 20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//  
 1.6e-87:346:90//Hs.6216:AF061749  
 R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435  
 R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855  
 R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842  
 25 R-OVARC1001928  
 R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:  
 253:88//Hs.117741:AA903456  
 R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637  
 R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.  
 30 22744:AI379892  
 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875  
 R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729  
 R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887  
 R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531  
 35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:  
 AB007934  
 R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556  
 R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:  
 AB018315  
 40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860  
 R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130  
 R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME  
 III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691  
 R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825  
 45 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923  
 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631  
 R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160  
 R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478  
 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
 50 7.5e-32:164:99//Hs.144194:AA706337  
 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920  
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557  
 R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223  
 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870  
 55 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440  
 R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503  
 R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612  
 R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

R-PLACE1000066//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk10c10.3 [*C.elegans*]/1.4e-61:331:94//Hs.30026:AI356771  
 R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659  
 R-PLACE1000081  
 5 R-PLACE1000094  
 R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505  
 R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [*H.sapiens*]/5.5e-103:538:94//Hs.9670:AA632135  
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291  
 10 R-PLACE1000185//ESTs, Weakly similar to No definition line found [*C.elegans*]/2.0e-19:114:95//Hs.7036:W22072  
 R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946  
 R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916  
 15 R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077  
 R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545  
 R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912  
 R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940  
 R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424  
 20 R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126  
 R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994  
 R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708  
 R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959  
 R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089  
 25 R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799  
 R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125  
 R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131  
 R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456  
 30 R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [*H.sapiens*]/2.0e-58:410:81//Hs.97579:AA398118  
 R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793  
 R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [*H.sapiens*]/3.2e-109:549:95//Hs.19074:U69566  
 R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [*R.norvegicus*]/3.5e-83:435:94//Hs.26510:AA700425  
 35 R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729  
 R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:AB014540  
 R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION [*Saccharomyces cerevisiae*]/1.9e-26:220:81//Hs.163791:W25348  
 40 R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485  
 R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353  
 R-nnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542  
 R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030  
 45 R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087  
 R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301  
 R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308  
 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265  
 50 R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))/1.4e-102:559:92//Hs.29595:AJ005896  
 R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353  
 R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485  
 55 R-PLACE1000716  
 R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701  
 R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396  
 R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [*C.el-*



egans]/3.9e-40:224:94//Hs.87889:AA262008

R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548

R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482

R-nnnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219

R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189

R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135

R-nnnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588

R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039

R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118:-AI141558

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846

R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697

R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689

R-PLACE1000979

R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725

R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146

R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736

R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762

R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120

R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124

R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580

R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141

R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268

R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610

R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594

R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834

R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527

R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297

R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812

R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464

R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131

R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371

R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780

R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460

R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548

R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601

R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056

R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160

R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077

R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030

R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419

R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:  
 AF091087  
 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
 R-PLACE1001440  
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.  
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547  
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625  
 10 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617  
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
 R-PLACE1001517//Homo sapiens hGAAl mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969  
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153  
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:  
 15 170:85//Hs.155456:AA707265  
 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601  
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
 20 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:  
 AF054174  
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.  
 114547:AA167095  
 25 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526  
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
 R-PLACE10016727//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:  
 141:62//Hs.153060:AA195804  
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-  
 30 113:545:97//Hs.3688:AF069250  
 R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124  
 R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903  
 R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667  
 R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993  
 35 R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171  
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113  
 R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266  
 R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479  
 R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937  
 40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:  
 AF061243  
 R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662  
 R-PLACE1001761  
 R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980  
 45 R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236  
 R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//  
 1.3e-93:463:95//Hs.40820:AF058953  
 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219  
 50 R-PLACE1001845  
 R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868  
 R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009  
 R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098  
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:  
 55 AF099936  
 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:  
 AB014523  
 R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941  
 R-PLACE1002046  
 R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595  
 R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094  
 5 R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619  
 R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552  
 R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632  
 R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311  
 R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293  
 10 R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937  
 R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614  
 R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189  
 R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965  
 15 R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745  
 R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793  
 R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788  
 R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892  
 R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257  
 20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503  
 R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308  
 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271  
 R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291  
 R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381  
 25 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
 R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
 R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804  
 R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
 R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320  
 30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263  
 R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
 R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
 35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869  
 R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256  
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774  
 40 R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
 R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437  
 R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
 R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738  
 45 R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
 R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208  
 R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147  
 R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
 50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180  
 R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
 R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586  
 55 R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865  
 R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099  
 R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955  
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392  
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.  
 61518:AA167094  
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756  
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762  
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332  
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
 R-PLACE1002962  
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
 R-PLACE10029937//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:  
 502:89//Hs.32232:AA604268  
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268  
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499  
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075  
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:  
 U04840  
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777  
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.  
 25 6318:AI131178  
 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359  
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920  
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757  
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467  
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924  
 R-PLACE1003176  
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453  
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017  
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802  
 35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123  
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//  
 Hs.73614:U83460  
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131  
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:  
 40 551:92//Hs.52431:AA625326  
 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986  
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.  
 29147:AA883993  
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:  
 45 97//Hs.155050:AA908765  
 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438  
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701  
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 cds//1.1e-99:469:98//Hs.6564:U92715  
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636  
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234  
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591  
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941  
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909  
 55 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755  
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020  
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840  
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671  
 R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270  
 R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952  
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505  
 5 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980  
 R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461  
 R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209  
 R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321  
 10 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591  
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956  
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178  
 15 R-PLACE1003584  
 R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542  
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106  
 R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875  
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200  
 20 R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299  
 R-nnnnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446  
 R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943  
 R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285  
 R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247  
 25 R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607  
 R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521  
 R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866  
 R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639  
 R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987  
 30 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087  
 R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023  
 R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512  
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965  
 R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798  
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757  
 R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909  
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147  
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092  
 40 R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059  
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058  
 R-nnnnnnnnnnnnn  
 R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871  
 45 R-nnnnnnnnnnnnn  
 R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595  
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915  
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259  
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804  
 50 R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760  
 R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236  
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110  
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567  
 55 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330  
 R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231  
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052  
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244  
 R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714  
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080  
 R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601  
 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//  
 4.7e-78:434:91//Hs.153504:AF044321  
 R-PLACE1004197  
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//  
 1.5e-105:501:98//Hs.24640:AF069493  
 10 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952  
 R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630  
 R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209  
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124  
 R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800  
 15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:  
 121:66//Hs.1938:S82362  
 R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//1.4e-107:581:  
 91//Hs.127007:AF084830  
 R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114  
 20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:  
 279:77//Hs.38687:AA744496  
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.  
 71435:AI253099  
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588  
 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:  
 77//Hs.1361:M55053  
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:  
 379:93//Hs.16232:AF100153  
 R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309  
 30 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556  
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-  
 98:572:90//Hs.14202:N46000  
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467  
 R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665  
 35 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
 R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283  
 R-PLACE1004451  
 R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980  
 40 R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721  
 R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578  
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194  
 R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:  
 278:61//Hs.89663:L13286  
 45 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117  
 R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493  
 R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164  
 R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553  
 R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.  
 50 115325:084488  
 R-PLACE1004550  
 R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742  
 R-PLACE1004629//ESTs, Weakly similar to OS-9 precucosor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181  
 R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903  
 55 R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734  
 R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257  
 R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs.  
 80019:AF035606  
 R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482  
 R-PLACE1004686  
 5 R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552  
 R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374  
 R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:  
 AI279571  
 R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997  
 10 R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391  
 R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619  
 R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195  
 R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374  
 R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367  
 15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548  
 R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619  
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178  
 R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856  
 R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-  
 20 108:358:99//Hs.3688:AF069250  
 R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356  
 R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.  
 73821:M35663  
 R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185  
 25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299  
 R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901  
 R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]  
 //6.5e-71:381:93//Hs.8383:AA013272  
 R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308  
 30 R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete  
 cds//1.8e-37:330:78//Hs.113259:AF023456  
 R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881  
 R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597  
 R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563  
 35 R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948  
 R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.  
 17839:AF099936  
 R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980  
 R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166  
 40 R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013  
 R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106  
 R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789  
 R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776  
 R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335  
 45 R-PLACE1005026  
 R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegi-  
 cus]//0.72:145:66//Hs.11215:N56719  
 R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:  
 AB011147  
 50 R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase  
 [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605  
 R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103  
 R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985  
 R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080  
 55 R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364  
 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531:92//Hs.75437:L40401  
 R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336  
 R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

U91985

R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225  
 R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423  
 R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349  
 5 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013  
 R-nnnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227  
 R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589  
 R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830  
 R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211  
 10 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532  
 R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767  
 R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524  
 R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633  
 R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516  
 15 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322  
 R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937  
 R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797  
 R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614  
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960  
 20 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343  
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975  
 R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901  
 R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394  
 R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978  
 25 R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304  
 R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423  
 R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503  
 R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607  
 R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046  
 30 R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875  
 R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220  
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185  
 R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325  
 35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470  
 R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325  
 R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927  
 40 R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555  
 R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261  
 R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835  
 R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612  
 45 R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023  
 R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927  
 R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857  
 R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964  
 R-PLACE1005630  
 50 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452  
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255  
 R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169  
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587  
 55 R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355  
 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332  
 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259



R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137

R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070

R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087

5 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.109857:AA088385

R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941

R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327

R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693

10 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058

R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870

R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965

R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471

R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305

15 R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842

R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558

R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981

R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501

R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793

20 R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503

R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361

R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142

R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913

R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729

25 R-PLACE1005953

R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:AI097079

R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239

R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897

30 R-PLACE1005990

R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353

R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:AI192946

R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-100:596:88//Hs.24284:AA595596

35 R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276

R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164:AI096332

R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765

R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314

40 R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904

R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002

R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977

45 R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:59//Hs.904:U84010

R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886

R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925

R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128

50 R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239

R-nnnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:AI125280

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433

R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:AI361807

55 R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507

R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114

R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664

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R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555  
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472  
R-nnnnnnnnnnnnn/Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142  
5 R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532:95//Hs.41151:AI301961  
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548  
R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839  
10 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132  
R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265  
R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503  
R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900  
R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168  
15 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044  
R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284  
R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053  
R-PLACE1006382  
R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748  
R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881  
20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258  
R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629  
R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139  
R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961  
R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297  
25 R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418  
R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722  
R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374  
R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717  
R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723  
30 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368  
R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532  
R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214  
R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443  
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
35 9.3e-118:590:95//Hs.155377:U97670  
R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322  
R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615  
R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384  
R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522  
40 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627  
R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736  
R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214  
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172  
R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861  
45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622  
R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658  
R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234  
R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515  
R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335  
50 R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989  
R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847  
R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159  
R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//  
55 1.0e-87:481:92//Hs.141263:H64113  
R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933  
R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA-828359  
R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008  
R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536

R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131  
 R-nnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348  
 R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089  
 R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168  
 5 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514  
 R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078  
 R-nnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956  
 R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520  
 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982  
 10 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636  
 R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257  
 R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366  
 R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971  
 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503  
 15 R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575  
 R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027  
 R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202  
 R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646  
 R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417  
 20 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948  
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794  
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765  
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998  
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619  
 25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495  
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450  
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499  
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909  
 30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071  
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087  
 R-PLACE1007301  
 35 R-PLACE1007317  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594  
 40 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945  
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877  
 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771  
 45 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857  
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171  
 50 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514  
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230  
 R-PLACE1007478  
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975  
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533  
 55 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072  
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657

R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377  
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087  
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612  
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404  
 5 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840  
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179  
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176  
 10 R-PLACE1007632  
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106  
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946  
 R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//  
 9.0e-37:190:97//Hs.23437:AA707331  
 15 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944  
 R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]  
 //3.4e-61:384:89//Hs.92918:AA133274  
 R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.  
 91251:U66685  
 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:  
 AF061243  
 R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:  
 AA476815  
 25 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:  
 AB014585  
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322  
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778  
 30 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903  
 R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
 8.6e-27:143:98//Hs.144194:AA706337  
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503  
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044  
 35 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050  
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839  
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503  
 R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:  
 40 AB018309  
 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178  
 R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832  
 R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060  
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.  
 45 92381:AB007956  
 R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510  
 R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966  
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.  
 50 5671:AF084530  
 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:  
 465:93//Hs.78106:AF079529  
 R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900  
 R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]  
 //3.8e-97:493:95//Hs.6141:U69564  
 55 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835  
 R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612  
 R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]  
 //2.0e-115:575:95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935  
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269  
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469  
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334  
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617  
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266  
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102  
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701  
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
 R-nnnnnnnnnnnnn  
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705  
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276  
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//  
 Hs.146477:AI128445  
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579  
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052  
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-  
 41:448:72//Hs.139007:H74314  
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242  
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:  
 30 536:87//Hs.7570:W31010  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326  
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778  
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387  
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636  
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816  
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
 R-PLACE1008532  
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223  
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064  
 R-PLACE1008621//ESTS, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:  
 AA778649  
 R-nnnnnnnnnnnnn  
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
 R-PLACE1008627//ESTS//1.6e-90:475:93//Hs.102401:AI004972  
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512  
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612  
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353  
 55 R-PLACE10086507//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.  
 147967:AF044333  
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830  
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

76//Hs.1361:M55053

R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600

R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303

R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408

R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313

R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930

R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217

R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905

R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810

R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428

R-nnnnnnnnnnnnnnn

R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502

R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878

R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308

R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018

R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653

R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680

R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573

R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419

R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112

R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520

R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195

R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139

R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008

R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142

R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448

R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546

R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136

R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549

R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983

R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945

R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747

R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920

R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005

R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322

R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948

R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707

R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717

R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396

R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701

R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248

R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680

R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018

R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423

R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279

R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503

R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397

R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782

R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760



R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347  
 R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219  
 R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204  
 R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//  
 7.6e-104:546:94//Hs.8215:AA521150  
 R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905  
 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.  
 10 11183AF065482  
 R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375  
 R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424  
 R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615  
 R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:  
 15 U69567  
 R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015  
 R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103  
 R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270  
 R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130  
 20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359  
 R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897  
 R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313  
 R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466  
 R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037  
 25 R-PLACE1010231  
 R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478  
 R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545  
 R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535  
 R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788  
 30 R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081  
 R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568  
 R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219  
 R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-  
 32:190:77//Hs.152369:AA504818  
 35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327  
 R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594  
 R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:  
 AJ224162  
 R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152  
 40 R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816  
 R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:  
 AF039081  
 R-PLACE1010492  
 R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031  
 45 R-nnnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455  
 R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306  
 R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033  
 R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116  
 R-PLACE1010599  
 50 R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418  
 R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895  
 R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475  
 R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:  
 391:95//Hs.163495:W57637  
 55 R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805  
 R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719  
 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102  
 R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:



91//Hs.22383:R51067

R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659

R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973

R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564

R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189

R-PLACE1010743

R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250

R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024

R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627

R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558

R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:AI091203

R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896

R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472

R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048

R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917

R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182

R-PLACE1010891

R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983

R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023

R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630

R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093

R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126

R-nnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:AF064244

R-PLACE1010944

R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519

R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219

R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437

R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580

R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846

R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867

R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153

R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135

R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219

R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537

R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094

R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478

R-PLACE101111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587

R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:AA875998

R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795

R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333

R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673

R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782

R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

**EP 1 074 617 A2**

R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671  
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299  
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693  
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602  
5 R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772  
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913  
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849  
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807  
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291  
10 R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578  
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337  
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376  
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194  
15 R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337  
R-nnnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102  
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607  
20 R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887  
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255  
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278  
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294  
25 R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576  
R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421  
R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985  
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672  
R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548  
30 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067  
R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965  
R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900  
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535  
R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036  
35 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838  
R-PLACE1011675  
R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025  
R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503  
40 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392  
R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426  
R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:Z48051  
R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627  
45 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179  
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067  
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
50 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497  
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617  
55 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969  
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285  
R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890

R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256  
 R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
 5 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080  
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504  
 10 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868  
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452  
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073  
 15 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622  
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147  
 20 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390  
 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219  
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179  
 R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236  
 25 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941  
 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789  
 R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662  
 R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988  
 30 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558  
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134  
 R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357  
 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219  
 35 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778  
 R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292  
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067  
 R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378  
 R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191  
 40 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717  
 R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600  
 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363  
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:AI004779  
 45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664  
 R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.I18732:AI344055  
 R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380  
 R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058  
 50 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789  
 R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618  
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848  
 R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081  
 55 R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731  
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277  
 R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781  
 R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189  
 R-PLACE2000399  
 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [*Saccharomyces cerevisiae*]//4.2e-109:540:96//Hs.6762:AA088424  
 5 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941  
 R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [*C.elegans*]//1.6e-97:436:95//Hs.24647:W19739  
 R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333  
 R-PLACE2000427//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEESI42F [*C.elegans*]//3.0e-113:543:97//Hs.16933:AA976002  
 10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523  
 R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986  
 R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887  
 R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390  
 R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714  
 15 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638  
 R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228  
 R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642  
 R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838  
 R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:  
 20 AB011147  
 R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763  
 R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979  
 R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830  
 R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727  
 25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739  
 R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792  
 R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369  
 R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142  
 R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815  
 30 R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223  
 R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [*Avian spleen necrosis virus*]//4.8e-36:262:88//  
 Hs.31532:H18272  
 R-PLACE3000157  
 R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219  
 35 R-PLACE3000160  
 R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
 R-PLACE3000194  
 R-PLACE3000197//ESTs//1.4e-3 8:197:98//Hs.146341:AI269930  
 R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [*Sus scrofa*]//0.018:261:61//Hs.  
 40 131370:AA927516  
 R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
 R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084  
 R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964  
 R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
 45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014  
 R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878  
 R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811  
 R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [*Emericella nidulans*]//7.5e-  
 110:549:95//Hs.13692:AA632002  
 50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307  
 R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:  
 82//Hs.97203:U83171  
 R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
 R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-  
 55 plete cds//4.0e-59:456:80//Hs.108966:U48696  
 R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830  
 R-PLACE3000320//Interleuldn 10//9.6e-42:288:85//Hs.2180:M57627  
 R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [*Homo sapiens*]//5.8e-34:190:95//Hs.

114531:N74103

R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315

R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837

R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688

R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377

R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380

R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683

R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888

R-PLACE3000363

R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881

R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430

R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534

R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570

R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528

R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230

R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160

R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108

R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460

R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077

R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219

R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519

R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899

R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980

R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352

R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240

R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031

R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292

R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444

R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547

R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739

R-PLACE4000100

R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931

R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969

R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582

R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147

R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186

R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734

R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949

R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080

R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219

R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216

R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442

R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586

R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782  
 R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131  
 R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454  
 R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460  
 5 R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414  
 R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478  
 R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656  
 R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425  
 10 R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818  
 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649  
 R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502  
 R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780  
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063  
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053  
 R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932  
 20 R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210  
 R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290  
 R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527  
 R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185  
 25 R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532  
 R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524  
 R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249  
 R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889  
 R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651  
 30 R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438  
 R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435  
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353  
 R-THYRO1000107//Interieuldn 10//2.8e-43:292:84//Hs.2180:M57627  
 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359  
 35 R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108  
 R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764  
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142  
 40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217  
 R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426  
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258  
 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946  
 45 R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189  
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219  
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219  
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:AJ005698  
 50 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:AB014552  
 R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063  
 R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349  
 55 R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:AB014588  
 R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075  
 R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925  
 R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674  
 5 R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068  
 R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547  
 R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175  
 R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:AB018333  
 10 R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:U29091  
 R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064  
 R-nnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250  
 R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456  
 15 R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081  
 R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429  
 R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601  
 R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638  
 R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:AI309761  
 20 R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426  
 R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280  
 R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333  
 25 R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360  
 R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005  
 R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965  
 R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511  
 R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193  
 30 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485  
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587  
 R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
 35 R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415  
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
 R-THYRO1000637  
 R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H. sapiens]//4.9e-46:245:95//Hs.97398:AA398634  
 40 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
 R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384  
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063  
 45 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
 R-THYRO1000712  
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
 50 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624  
 R-THYRO1000777  
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
 55 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144  
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381  
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594  
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

R-THYRO1000829  
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627  
 R-THYRO1000852//ESTs//2.3e-20:157:85//Hs.149580:AI281881  
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011  
 5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663  
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871  
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234  
 10 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529  
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182  
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859  
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761  
 15 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440  
 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881  
 R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524  
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777  
 20 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131  
 R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489  
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717  
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070  
 25 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223  
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497  
 R-THYRO1001100  
 R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834  
 30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417  
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399  
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922  
 R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853  
 35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075  
 R-THYRO1001177  
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744  
 R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151  
 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932  
 40 R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629  
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640  
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561  
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269  
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230  
 45 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642  
 R-nnnnnnnnnnnnnn//ESTs//0.16:422:5.9//Hs.23876:AA082935  
 R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250  
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033  
 50 R-THYRO1001365  
 R-THYRO1001374  
 R-THYRO001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:467:75//Hs.37181:D64108  
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627  
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733  
 55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197  
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979  
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977



R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172  
 R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082  
 R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219  
 5 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135  
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110  
 R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094  
 10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936  
 R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594  
 R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413  
 R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958  
 15 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741  
 R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247  
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025  
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886  
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase (DHAPAT)  
 20 mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190  
 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874  
 R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282  
 R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446  
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//  
 25 Hs.118633:AJ225089  
 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957  
 R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726  
 R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691  
 30 R-THYRO1001721  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184  
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172  
 R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323  
 R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474  
 35 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224  
 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788  
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956  
 R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123  
 40 R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314  
 R-VESEN1000122  
 R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289  
 R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321  
 45 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178  
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540  
 R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629  
 R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792  
 50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849  
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991  
 R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103  
 R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812  
 55 R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624  
 R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936  
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363  
 R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635  
 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210  
 R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808  
 5 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//  
 4.4e-66:339:97//Hs.8215:AA521150  
 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-  
 44:279:88//Hs.139007:H74314  
 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018  
 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613  
 10 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758  
 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292  
 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-  
 60:362:88//Hs.6381:AI188509  
 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320  
 15 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881  
 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.  
 41723:U37426  
 R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848  
 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:  
 20 AI125280  
 R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455  
 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:  
 AF060503  
 R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC  
 25 REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818  
 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:  
 95//Hs.83023:AF093670  
 R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III  
 [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330  
 30 R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405  
 R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463  
 R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433  
 R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359  
 R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512  
 35 R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642  
 R-nnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405  
 R-Y79AA1000805  
 R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227  
 R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650  
 40 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.  
 55836:U85647  
 R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079  
 R-Y79AA1000968  
 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181  
 45 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049  
 R-Y79AA1000985  
 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851  
 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067  
 R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407  
 50 R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325  
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:  
 AB011135  
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047  
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260  
 55 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155  
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015  
 R-Y79AA1001167  
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884



R-nnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715  
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.  
 50441:AA747428  
 R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349  
 5 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//  
 6.5e-86:518:90//Hs.25682:AA857843  
 R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274  
 R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977  
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:  
 10 AB014592  
 R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:  
 507:96//Hs.25895:AI341537  
 R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555  
 R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288  
 15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:  
 AB014534  
 R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985  
 R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371  
 R-Y79AA1002361  
 20 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908  
 R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000  
 R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
 R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026  
 R-nnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]  
 25 //4.4e-62:390:88//Hs.143930:AI207821  
 R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
 R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
 R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

# Homology Search Result Data 6

**[0314]** Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
 es. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be  
 compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Ho-  
 35 mology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash  
 mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712  
 C-HEMBA1000030  
 40 C-HEMBA1000046  
 C-HEMBA1000050  
 C-HEMBA1000076  
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 1.9E-12//368aa//24%//P08553  
 45 C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555  
 C-HEMBA1000193  
 C-HEMBA1000227  
 50 C-HEMBA1000288  
 C-HEMBA1000302  
 C-HEMBA1000304  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-  
 49//107aa//91 %//035594  
 55 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//  
 AL049654  
 C-HEMBA1000387  
 C-HEMBA1000392

C-HEMBA1000460  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279  
 C-HEMBA1000501  
 5 C-HEMBA1000508  
 C-HEMBA1000520  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS).//2.6E-12//73aa//41%//P02826  
 C-HEMBA1000534  
 10 C-HEMBA1000555  
 C-HEMBA1000568  
 C-HEMBA1000588  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295  
 C-HEMBA1000636  
 15 C-HEMBA1000682  
 C-HEMBA1000686  
 C-HEMBA1000719  
 C-HEMBA1000727  
 C-HEMBA1000752  
 20 C-HEMBA1000817  
 C-HEMBA1000851  
 C-HEMBA1000867  
 C-HEMBA1000869  
 C-HEMBA1000872  
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//  
 1.6E-30//127aa//40%//P43366  
 C-HEMBA1000918  
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-  
 MOSOME X.//1E-10//288aa//23%//Q19124  
 30 C-HEMBA1000946  
 C-HEMBA1000968  
 C-HEMBA1000971  
 C-HEMBA1000975  
 C-HEMBA1001009  
 35 C-HEMBA1001022  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//  
 1.4E-12//131aa//38%//Q01485  
 C-HEMBA1001052  
 C-HEMBA1001080  
 40 C-HEMBA1001085  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//  
 176aa//57%//P48059  
 C-HEMBA1001109  
 C-HEMBA1001122  
 45 C-HEMBA1001133  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)  
 (FRAGMENT).//1.5E-116//197aa//58%//Q06730  
 C-HEMBA1001140  
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646  
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//  
 AB020678  
 C-HEMBA1001235  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733  
 C-HEMBA1001281  
 55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//  
 29%//Q60401  
 C-HEMBA1001303  
 C-HEMBA1001310

C-HEMBA1001326  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081  
 5 C-HEMBA1001388  
 C-HEMBA1001398  
 C-HEMBA1001405  
 C-HEMBA1001407  
 C-HEMBA1001413  
 10 C-HEMBA1001415  
 C-HEMBA1001446  
 C-HEMBA1001450  
 C-HEMBA1001455  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850  
 15 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166  
 C-HEMBA1001533  
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657  
 C-HEMBA1001581  
 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450  
 25 C-HEMBA1001702  
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386  
 C-HEMBA1001731  
 C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009  
 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675  
 C-HEMBA1001815  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676  
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230  
 C-HEMBA1001864  
 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342  
 C-HEMBA1001987  
 C-HEMBA1002018  
 40 C-HEMBA1002049  
 C-HEMBA1002084  
 C-HEMBA1002125  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293  
 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694  
 C-HEMBA1002191  
 C-HEMBA1002199  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161  
 50 C-HEMBA1002237  
 C-HEMBA1002265  
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537  
 C-HEMBA1002349  
 55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563  
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793  
 C-HEMBA1002430

C-HEMBA1002439  
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994  
 C-HEMBA1002460  
 C-HEMBA1002462  
 5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175  
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%//P17437  
 C-HEMBA1002477  
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732  
 10 C-HEMBA1002515  
 C-HEMBA1002542  
 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%//AF075587  
 C-HEMBA1002583  
 15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169  
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351  
 C-HEMBA1002688  
 C-HEMBA1002696  
 C-HEMBA1002750  
 20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414  
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636  
 C-HEMBA1002777  
 C-HEMBA1002794  
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185  
 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1002850  
 C-HEMBA1002863  
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%//Q09297  
 30 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148  
 C-HEMBA1002937  
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//P16157  
 35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710  
 C-HEMBA1002954  
 C-HEMBA1002971  
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646  
 40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%//Q02224  
 C-HEMBA1003033  
 C-HEMBA1003035  
 C-HEMBA1003041  
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439  
 45 C-HEMBA1003067  
 C-HEMBA1003096  
 C-HEMBA1003117  
 C-HEMBA1003129  
 50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940  
 C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%//AL079278  
 55 C-HEMBA1003175  
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551  
 C-HEMBA1003199

C-HEMBA1003222  
 C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%//Q02088  
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%//Q06548  
 C-HEMBA1003257  
 5 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%//P32506  
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%//AB024436  
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%//AB011109  
 C-HEMBA1003322  
 10 C-HEMBA1003327  
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.00000002//248aa//23%//Q02224  
 C-HEMBA1003370  
 C-HEMBA1003380  
 C-HEMBA1003395  
 15 C-HEMBA1003402  
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%//AB020712  
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6E-312//1414bp//99%//AL050287  
 C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709  
 20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139  
 C-HEMBA1003447  
 C-HEMBA1003461  
 C-HEMBA1003463  
 C-HEMBA1003528  
 25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%//P50480  
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//P53384  
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%//P16874  
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%//P19474  
 30 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%//Q13330  
 C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039  
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//35%//P19682  
 35 C-HEMBA1003615  
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%//AB015344  
 C-HEMBA1003621  
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q13207  
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973  
 40 C-HEMBA1003711  
 C-HEMBA1003807  
 C-HEMBA1003864  
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%//P16372  
 45 C-HEMBA1003959  
 C-HEMBA1003989  
 C-HEMBA1004074  
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%//AF091234  
 50 C-HEMBA1004146  
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%//AB023145  
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748  
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%//AF095927  
 55 C-HEMBA1004246  
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//99%//AF092094  
 C-HEMBA1004289



C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955  
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//  
 AF089841  
 C-HEMBA1004596  
 5 C-HEMBA1004693  
 C-HEMBA1004736  
 C-HEMBA1004753  
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082  
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//  
 10 L39060  
 C-HEMBA1004763  
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547  
 C-HEMBA1004771  
 C-HEMBA1004776  
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851  
 C-HEMBA1004806  
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//  
 Q00004  
 C-HEMBA1004850  
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//  
 100%//AL080114  
 C-HEMBA1004923  
 C-HEMBA1004929  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401  
 25 C-HEMBA1004933  
 C-HEMBA1004954  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
 0.00000096//286aa//23%//P12036  
 C-HEMBA1005475  
 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270  
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//  
 151aa//37%//P16372  
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-  
 225//1189bp//88%//AF076183  
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043  
 C-HEMBA1006377  
 C-HEMBA1006467  
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552  
 C-HEMBA1006530  
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 0.000000043//111aa//40%//Q01485  
 C-HEMBA1006795  
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258  
 C-HEMBA1006936  
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//  
 AP078849  
 C-HEMBA1007342  
 C-HEMBA1000008  
 C-HEMBA1000018  
 50 C-HEMBA1000024  
 C-HEMBA1000025  
 C-HEMBA1000036  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//  
 1582bp//80%//AF084928  
 55 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799  
 C-HEMBA1000103  
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEM BB1000136  
 C-HEM BB1000215  
 C-HEM BB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5//  
 2.7E-12//112aa//47%//Q09530  
 5 C-HEM BB1000244  
 C-HEM BB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-  
 MOSOME V.//6.1E-09//242aa//26%//Q23256  
 C-HEM BB1000338  
 C-HEM BB1000339  
 10 C-HEM BB1000391  
 C-HEM BB1000438  
 C-HEM BB1000449  
 C-HEM BB1000589  
 C-HEM BB1000591  
 15 C-HEM BB1000623  
 C-HEM BB1000630  
 C-HEM BB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//  
 232aa//28%//P78970  
 C-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671  
 20 C-HEM BB1000671  
 C-HEM BB1000673  
 C-HEM BB1000705  
 C-HEM BB1000706  
 C-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//  
 25 U53475  
 C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847  
 C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//  
 1.2E-126//613bp//97%//AF111105  
 C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-  
 30 54//232aa//43%//P39956  
 C-HEM BB1000807  
 C-HEM BB1000810  
 C-HEM BB1000848  
 C-HEM BB1000852  
 35 C-HEM BB1000870  
 C-HEM BB1000887  
 C-HEM BB1000908  
 C-HEM BB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102  
 C-HEM BB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//  
 40 99%//AF116910  
 C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974  
 C-HEM BB1000975  
 C-HEM BB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-  
 18//178aa//30%//P28575  
 45 C-HEM BB1000991  
 C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//  
 P51523  
 C-HEM BB1001014  
 C-HEM BB1001024  
 50 C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087  
 C-HEM BB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//  
 80%//AF010144  
 C-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803  
 55 C-HEM BB1001096  
 C-HEM BB1001105  
 C-HEM BB1001117  
 C-HEM BB1001126

C-HEM BB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
 C-HEM BB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267  
 C-HEM BB1001153  
 5 C-HEM BB1001169  
 C-HEM BB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357  
 C-HEM BB1001182  
 C-HEM BB1001199  
 C-HEM BB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187  
 10 C-HEM BB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897  
 C-HEM BB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966  
 C-HEM BB1001289  
 C-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081  
 15 C-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703  
 C-HEM BB1001331  
 C-HEM BB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175  
 C-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441  
 20 C-HEM BB1001369  
 C-HEM BB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEM BB1001387  
 C-MAMMA1002317  
 25 C-MAMMA1002319  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926  
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190  
 C-NT2RM1000242  
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028  
 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942  
 C-NT2RM1000669  
 C-NT2RM1000781  
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138  
 35 C-NT2RM1001008  
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360  
 C-NT2RM1001074  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//  
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence.//0//1740bp//99%//AL031291  
 40 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167  
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703  
 45 C-NT2RM2000032  
 C-NT2RM2000042  
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102  
 50 C-NT2RM2000093  
 C-NT2RM2000101  
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223  
 C-NT2RM2000192  
 55 C-NT2RM2000239  
 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2E-314//1416bp//100%//AL080069  
 C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//  
 P14918  
 C-NT2RM2000287  
 C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//  
 5 AB020666  
 C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132  
 C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274  
 C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//  
 U48251  
 10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-  
 OTIDE//1.7E-68//419aa//36%//P50849  
 C-NT2RM2000374  
 C-NT2RM2000395  
 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-  
 15 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT).//1.6E-54//344aa//33%//P32802  
 C-NT2RM2000407  
 C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//  
 Q08469  
 20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//  
 157aa//28%//P36113  
 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%//  
 P22211  
 C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823  
 25 C-NT2RM2000502  
 C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243  
 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//  
 32%//P17437  
 C-NT2RM2000540  
 30 C-NT2RM2000567  
 C-NT2RM2000569  
 C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
 1.7E-187//741aa//46%//P73505  
 C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987  
 35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973  
 C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//  
 0//2712bp//99%//AF156487  
 C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//  
 AF179221  
 40 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//4.4E-32//319aa//35%//Q08170  
 C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272  
 C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558  
 C-NT2RM2000639  
 45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576  
 C-NT2RM2000669  
 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391  
 C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//  
 36%//Q15404  
 50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342  
 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//  
 P41877  
 C-NT2RM2000795  
 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//  
 55 98%//P23514  
 C-NT2RM2000837  
 C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//  
 AB015046

C-NT2RM2000952  
 C-NT2RM2000984  
 C-NT2RM2001004  
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809  
 5 C-NT2RM2001065  
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//  
 26%//P46577  
 C-NT2RM2001131  
 C-NT2RM2001141  
 10 C-NT2RM2001152  
 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//  
 1335bp//99%//AL080109  
 C-NT2RM2001194  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143  
 15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//  
 32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 20 DOHYDROLASE).//1.3E-180//328aa//99%//P13264  
 C-NT2RM2001243  
 C-NT2RM2001247  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//  
 P53995  
 25 C-NT2RM2001291  
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//  
 AL080063  
 C-NT2RM2001312  
 C-NT2RM2001319  
 30 C-NT2RM2001324//ZYGXIN.//6.8E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808  
 C-NT2RM2001370  
 C-NT2RM2001393  
 C-NT2RM2001420  
 35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//  
 100%//AL050146  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//  
 437aa//57%//P52569  
 C-NT2RM2001504  
 40 C-NT2RM2001524  
 C-NT2RM2001544  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//  
 90aa//42%//P38660  
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-  
 45 61//312aa//44%//P19474  
 C-NT2RM2001582  
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610  
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692  
 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931  
 50 C-NT2RM2001930  
 C-NT2RM2001935  
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320  
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//  
 212aa//23%//P38250  
 55 C-NT2RM2001982  
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//  
 P37838  
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%//Q12730  
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%//Q09782  
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.000000029//83aa//44%//P40796  
 5 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%//P46837  
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789  
 10 C-NT2RM2002049  
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878  
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%//Q61990  
 15 C-NT2RM2002091  
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840  
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435  
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%//P49695  
 20 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%//P47805  
 C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%//AL117402  
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167  
 25 C-NT2RM4000061  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101  
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%//P25386  
 30 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%//P16381  
 C-NT2RM4000197  
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255  
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%//L20303  
 35 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%//M99438  
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637  
 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371  
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412  
 C-NT2RM4000395  
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769  
 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//24%//Q10297  
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280  
 50 C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%//P39955  
 C-NT2RM4000511  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%//P16884  
 C-NT2RM4000520  
 55 C-NT2RM4000585  
 C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%//AF186273  
 C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000040  
 C-NT2RP1000063  
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834  
 5 C-NT2RP1000101  
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471  
 C-NT2RP1000112  
 C-NT2RP1000124  
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859  
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165  
 C-NT2RP1000170  
 C-NT2RP1000191  
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357  
 C-NT2RP1000243  
 15 C-NT2RP1000259  
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730  
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551  
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447  
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343  
 C-NT2RP1000357  
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187  
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159  
 C-NT2RP1000416  
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423  
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257  
 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580  
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653  
 C-NT2RP1000481  
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686  
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020  
 C-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367  
 40 C-NT2RP1000581  
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233  
 C-NT2RP1000688  
 C-NT2RP1000695  
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379  
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434  
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566  
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960  
 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223  
 C-NT2RP1000846  
 C-NT2RP1000851  
 55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566  
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823  
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-

105//504bp//99<%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338

C-NT2RP1000980

C-NT2RP1000988

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//1529bp//61%//L01790

C-NT2RP1001014

C-NT2RP1001395

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917

C-NT2RP1001424

C-NT2RP1001449

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%//AJ005257

C-NT2RP1001466

C-NT2RP1001475

C-NT2RP1001482

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//O35566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%//P47758

C-NT2RP1001616

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%//O34136

C-NT2RP2000007

C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//P51523

C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//34%//Q01730

C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749

C-NT2RP2000054

C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON).//9.4E-16//45aa//100%//P49446

C-NT2RP2000067

C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//383aa//32%//P33450

C-NT2RP2000079

C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338

C-NT2RP2000091

C-NT2RP2000097

C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356

C-NT2RP2000120

C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//P41877

C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206

C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585

C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891

C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329



C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//  
 AB023225  
 C-NT2RP2000173  
 C-NT2RP2000175  
 5 C-NT2RP2000195  
 C-NT2RP2000205  
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568  
 C-NT2RP2000232  
 10 C-NT2RP2000233  
 C-NT2RP2000239  
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558  
 C-NT2RP2000270  
 15 C-NT2RP2000274  
 C-NT2RP2000283  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//  
 25%//Q10297  
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676  
 20 C-NT2RP2000298  
 C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//  
 1193bp//99%//U82381  
 C-NT2RP2000328  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 25 226aa//92%//P08760  
 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//  
 674aa//46%//P17564  
 C-NT2RP2000369  
 C-NT2RP2000412  
 30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//  
 100%//P52597  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//  
 99%//AF102265  
 C-NT2RP2000438  
 35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844  
 C-NT2RP2000503  
 C-NT2RP2000510  
 C-NT2RP2000516  
 C-NT2RP2000603  
 40 C-NT2RP2000617  
 C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514  
 C-NT2RP2000656  
 C-NT2RP2000658  
 C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 45 C-NT2RP2000704  
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.7E-100//  
 488aa//44%//O32038  
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623  
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680  
 50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//  
 29%//Q99104  
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//  
 P13466  
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174  
 55 C-NT2RP2000819  
 C-NT2RP2000841  
 C-NT2RP2000845  
 C-NT2RP2000863

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C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/060841  
 C-NT2RP2000892  
 C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244  
 5 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%/AL050390  
 C-NT2RP2000938  
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%/AB018298  
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704  
 C-NT2RP2000985  
 10 C-NT2RP2001036  
 C-NT2RP2001044  
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%/AB007957  
 C-NT2RP2001065  
 15 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.8E-46//222aa//45%/Q20939  
 C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232  
 C-NT2RP2001094  
 C-NT2RP2001119  
 20 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440  
 C-NT2RP2001218  
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.2E-10//366aa//28%/P14105  
 C-NT2RP2001381  
 25 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp//100%/AL080146  
 C-NT2RP2001427  
 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%/AB018340  
 C-NT2RP2001675  
 30 C-NT2RP2001721  
 C-NT2RP2001907  
 C-NT2RP2001969  
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378  
 35 C-NT2RP2002046  
 C-NT2RP2002154  
 C-NT2RP2002208  
 C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%/P42568  
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521  
 40 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%/AB015594  
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958  
 C-NT2RP2002426  
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289  
 45 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073  
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815  
 50 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345  
 C-NT2RP2002621  
 C-NT2RP2002672  
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%/O14345  
 55 C-NT2RP2002769  
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392  
 C-NT2RP2002954  
 5 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669  
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129  
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190  
 C-NT2RP2003108  
 10 C-NT2RP2003117  
 C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//AF079765  
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652  
 C-NT2RP2003177  
 15 C-NT2RP2003194  
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811  
 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572  
 C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337  
 20 C-NT2RP2003367  
 C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378  
 C-NT2RP2003446  
 C-NT2RP2003533  
 25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261  
 C-NT2RP2003596  
 C-NT2RP2003629  
 C-NT2RP2003687  
 30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481  
 C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669  
 C-NT2RP2003793  
 35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175  
 C-NT2RP2003986  
 C-NT2RP2004042  
 C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820  
 40 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120  
 C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044  
 C-NT2RP2004463  
 45 C-NT2RP2004602  
 C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139  
 C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291  
 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%//Q92355  
 50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490  
 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588  
 C-NT2RP2004802  
 55 C-NT2RP2004841  
 C-NT2RP2004936  
 C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692  
 C-NT2RP2004999

C-NT2RP2005000

C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515

C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779

C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447

5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743

C-NT2RP2005140

C-NT2RP2005147

C-NT2RP2005159

10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025

C-NT2RP2005270

C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053

C-NT2RP2005293

C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576

15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247

C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823

C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170

20 C-NT2RP2005441

C-NT2RP2005453

C-NT2RP2005464

C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127

C-NT2RP2005472

25 C-NT2RP2005495

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563

30 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526

C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366

35 C-NT2RP2005555

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085

40 C-NT2RP2005622

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623

C-NT2RP2005637

C-NT2RP2005640

45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101

C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814

C-NT2RP2005683

50 C-NT2RP2005690

C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.000000003//169aa//28%//P38074

C-NT2RP2005748

55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943  
 C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849  
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//  
 2.7E-180//656bp//99%//AF151351  
 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-  
 CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-  
 BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038  
 C-NT2RP2005781  
 C-NT2RP2005804  
 10 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223  
 C-NT2RP2005853  
 C-NT2RP2005868  
 C-NT2RP2005886  
 C-NT2RP2005890  
 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188  
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837  
 C-NT2RP2006038  
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//1.5E-13//185aa//38%//Q08170  
 20 C-NT2RP2006052  
 C-NT2RP2006069  
 C-NT2RP2006071  
 C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//  
 99%//AL049970  
 25 C-NT2RP2006106  
 C-NT2RP2006141  
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554  
 C-NT2RP2006196  
 C-NT2RP2006200  
 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484  
 C-NT2RP2006237  
 C-NT2RP2006238  
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//  
 388aa//32%//P46821  
 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262  
 C-NT2RP2006333  
 C-NT2RP2006365  
 C-NT2RP2006393  
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//  
 0.00000034//50aa//50%//Q61658  
 40 C-NT2RP2006456  
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266  
 C-NT2RP2006467  
 C-NT2RP2006472  
 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710  
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP1IG1) (P450-NMB) (OLFACTIVE).//4.2E-134//  
 486aa//50%//P24461  
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//  
 169aa//25%//P09543  
 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708  
 C-NT2RP3000072  
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164  
 C-NT2RP3000220  
 C-NT2RP3000251  
 55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334  
 C-NT2RP3000312  
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor  
 Sp1.//0//1544bp//100%//AJ242978

C-NT2RP3000333  
 C-NT2RP3000348  
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN  
 HP0303.//0.000000028//185aa//31%//O25074  
 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 226aa//92%//P08760  
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1  
 and Prp6.//0//2072bp//98%//AB019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293  
 10 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//  
 1.7E-139//679aa//41%//O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
 C-NT2RP3000484  
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160  
 15 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//  
 P15151  
 C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283  
 C-NT2RP3000599  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523  
 20 C-NT2RP3000644  
 C-NT2RP3000661  
 C-NT2RP3000665  
 C-NT2RP3000690  
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650  
 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//Q61982  
 C-NT2RP3000836  
 C-NT2RP3000841  
 C-NT2RP3000850  
 C-NT2RP3000852  
 30 C-NT2RP3000859  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds.//6.9E-69//1611bp//61%//U53445  
 C-NT2RP3000869  
 C-NT2RP3000901  
 35 C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%//AF064257  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 2.7E-185//585bp//88%//AF015264  
 C-NT2RP3000980  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN  
 40 STAUFEN.//0.00000006//78aa//48%//P25159  
 C-NT2RP3001004  
 C-NT2RP3001081  
 C-NT2RP3001084  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433  
 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201  
 C-NT2RP3001109  
 C-NT2RP3001116  
 C-NT2RP3001119  
 C-NT2RP3001133  
 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//  
 196aa//27%//P53154  
 C-NT2RP3001214  
 55 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//  
 P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-  
 BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

C-NT2RP3001236  
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%//P14873  
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718  
 5 C-NT2RP3001307  
 C-NT2RP3001325  
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905  
 C-NT2RP3001392  
 10 C-NT2RP3001396  
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P49711  
 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009  
 C-NT2RP3001420  
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//O33529  
 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//O09053  
 C-NT2RP3001457  
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//P11632  
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395  
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801  
 20 C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%//P20964  
 C-NT2RP3001621  
 C-NT2RP3001629  
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q92609  
 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468  
 C-NT2RP3001676  
 C-NT2RP3001679  
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%//Q04652  
 30 C-NT2RP3001896  
 C-NT2RP3001915  
 C-NT2RP3001929  
 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742  
 C-NT2RP3004466  
 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%//P34110  
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532  
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126  
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.000000038//150aa//28%//Q01484  
 40 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445  
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946  
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266  
 45 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084  
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097  
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//45%//P54352  
 50 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P35526  
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa//37%//Q64375  
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657  
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538  
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568  
 55 C-NT2RP4000129  
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150  
 C-NT2RP4000151  
 C-NT2RP4000159  
 C-NT2RP4000185  
 5 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600  
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//P15287  
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470  
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173  
 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968  
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115  
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631  
 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372  
 C-NT2RP4000355  
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281  
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195  
 20 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570  
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
 C-NT2RP4000381  
 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738  
 C-NT2RP4000415  
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701  
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078  
 30 C-NT2RP4000449  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%//P50101  
 35 C-NT2RP4000480  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484  
 40 C-NT2RP4000500  
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818  
 C-NT2RP4000524  
 C-NT2RP4000541  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319  
 45 C-NT2RP4000560  
 C-NT2RP4000588  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730  
 C-NT2RP4000638  
 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625  
 C-NT2RP4000704  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//Q11073  
 55 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267  
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148  
 C-NT2RP4000737



C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 0.000000032//67aa//31%//P53915  
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939  
 5 C-NT2RP4000833  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265  
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-  
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175  
 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314  
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//  
 227aa//36%//Q06828  
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//1.5E-76//346aa//43%//Q61068  
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900  
 20 C-NT2RP4000955  
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//  
 90aa//42%//P38660  
 C-NT2RP4000975  
 C-NT2RP4000979  
 25 C-NT2RP4000984  
 C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579  
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA  
 POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968  
 30 C-NT2RP4001006  
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181  
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.5E-  
 92//443aa//44%//Q09996  
 C-NT2RP4001057  
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375  
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA<sup>2+</sup>-ATPASE).//1.3E-123//  
 563aa//46%//P13586  
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967  
 C-NT2RP4001086  
 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-  
 INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400  
 C-NT2RP4001100  
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//  
 P38378  
 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736  
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283  
 C-NT2RP4001138  
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAISE (EC 3.5.1.18) (SDAP).//0.00000021//  
 93aa//33%//P44514  
 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750  
 C-NT2RP4001149  
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
 3.4E-29//385aa//29%//P35331  
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
 55 4.7E-29//227aa//35%//P52178  
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//  
 65 %//U95760  
 C-NT2RP4001207

C-NT2RP4001210  
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//  
 90aa//42%//P38660  
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652  
 5 C-NT2RP4001235  
 C-NT2RP4001256  
 C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682  
 C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082  
 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32-%//Q07283  
 10 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-  
 CASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391  
 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%//  
 AJ001119  
 C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014  
 15 C-NT2RP4001343  
 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//  
 1400bp//100%//AB017494  
 C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete  
 cds.//1.4E-58//2425bp//59%//U53445  
 20 C-NT2RP4001353  
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-  
 19//222aa//30%//Q08180  
 C-NT2RP4001373  
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 25 TEIN KINASE 1).//9.2E-17//146aa//35%//P18160  
 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%//  
 Q10085  
 C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140  
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141  
 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q99676  
 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//  
 AF129131  
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-  
 PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218  
 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010  
 C-NT2RP4001502  
 C-NT2RP4001507  
 C-NT2RP4001524  
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-  
 40 54//242aa//3 8%//P25656  
 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//3202bp//99%//AF152961  
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902  
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26,%//Q02453  
 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197  
 C-NT2RP4001571  
 C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756  
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830  
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//  
 50 1.7E-141//373aa//47%//P73505  
 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676  
 C-NT2RP4001614  
 C-NT2RP4001634  
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469  
 55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323  
 C-NT2RP4001677  
 C-NT2RP4001679  
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

100 KD SUBUNIT).//4E-10//243aa//25%//Q10568

C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//Q10282

C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%//Q09332

C-NT2RP4001739

C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//P51523

C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174

C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232

C-NT2RP4001803

C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//Q35566

C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083

C-NT2RP4001828

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%//AF155595

C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709

C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%//AL050390

C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aa//25%//Q00808

C-NT2RP4001901

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024

C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA- ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO- ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816

C-NT2RP4001953

C-NT2RP4001966

C-NT2RP4001975

C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652

C-NT2RP4002052

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1E-137//679aa//40%//Q43143

C-NT2RP4002071

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//39%//Q05481

C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655

C-NT2RP4002298

C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938

C-NT2RP4002791

C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F1 72 (from clone DKFZp434F172).//0//2557bp//99%//AL080202

C-NT2RP4002905

C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552

C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808

C-NT2RP5003492

C-NT2RP5003500

C-NT2RP5003506

C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//P37116

C-NT2RP5003524

C-NT2RP5003534

C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262

C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

O14727

C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922

C-OVARC1000035

C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//

5 0.00000032//60aa//45 %//P80022

C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874

C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//

8.4E-14//259aa//30%//P51610

C-OVARC1000113

10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955

C-OVARC1000148

C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//

2.5E-95//461bp//98%//AJ242975

C-OVARC1000168

15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//AF068332

C-OVARC1000212

C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)

(MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665

20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//30%//P14904

C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249

C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363

25 C-OVARC1000321

C-OVARC1000326

C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//

200aa//27%//P40004

C-OVARC1000347

30 C-OVARC1000384

C-OVARC1000411

C-OVARC1000420

C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205

C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//

35 99%//AL080126

C-OVARC1000461

C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075

C-OVARC1000466

C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-

40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452

C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636

C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850

C-OVARC1000564

C-OVARC1000576

45 C-OVARC1000588

C-OVARC1000605

C-OVARC1000640

C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772

50 C-OVARC1000661

C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886

C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//01//1172bp//97%//AJ130978

55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946

C-OVARC1001162

C-OVARC1001243

C-OVARC1001296

C-OVARC1001360  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//99%//AJ224819  
 C-OVARC1001425  
 5 C-PLACE1000005  
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//134aa//43%//P52046  
 10 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%//AB020639  
 C-PLACE1000185  
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194  
 C-PLACE1000347  
 C-PLACE1000374  
 15 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660  
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246  
 20 C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//0.0000028//134aa//29%//P53368  
 C-PLACE1000435  
 C-PLACE1000444  
 C-PLACE1000562  
 25 C-PLACE1000564  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455  
 C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//AF044201  
 30 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891  
 C-PLACE1000716  
 C-PLACE1000748  
 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449  
 35 C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548  
 C-PLACE1000798  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.5E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010  
 40 C-PLACE1000948  
 C-PLACE1000972  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070  
 C-PLACE1001000  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
 45 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652  
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIREMENT).//3E-33//138aa//42%//Q61103  
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%//Q12929  
 50 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0//2118bp//99%//AC005412  
 C-PLACE1001412  
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%//AL031660  
 55 C-PLACE1001503  
 C-PLACE1001570  
 C-PLACE1001610  
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

(THIOESTERASE n).//4E-81//263aa//56%//P08635  
 C-PLACE1001729  
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381  
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//  
 5 Q57290  
 C-PLACE1001810  
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//  
 0//1995bp//99%//AF058953  
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524  
 10 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737  
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935  
 C-PLACE1001928  
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091  
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211  
 15 C-PLACE1002072  
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
 SE).//0.00000053//188aa//29%//P49606  
 C-PLACE1002140  
 C-PLACE1002163  
 20 C-PLACE1002170  
 C-PLACE1002433  
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105  
 C-PLACE1002465  
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256  
 25 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//  
 1750bp//99%//AF068180  
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391  
 C-PLACE1002794  
 C-PLACE1002815  
 30 C-PLACE1002839  
 C-PLACE1002851  
 C-PLACE1002941  
 C-PLACE1002996  
 C-PLACE1003045  
 35 C-PLACE1003092  
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268  
 C-PLACE1003108  
 C-PLACE1003145  
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 40 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743  
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750  
 C-PLACE1003200  
 C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//  
 99%//AL080133  
 45 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//  
 P51522  
 C-PLACE1003334  
 C-PLACE1003342  
 C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete  
 50 cds.//0//2435bp//99%//U92715  
 C-PLACE1003369  
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200  
 C-PLACE1003611  
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824  
 55 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//8E-19//209aa//34%//Q08170  
 C-PLACE1003711  
 C-PLACE1003723

C-PLACE1003762  
 C-PLACE1003771  
 C-PLACE1003784  
 C-PLACE1003923  
 5 C-PLACE1003936  
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 2.4E-124//326aa//73%//P80385  
 C-PLACE1004104  
 C-PLACE1004114  
 10 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//6.1E-181//340aa//96%//P29387  
 C-PLACE1004149  
 C-PLACE1004156  
 C-PLACE1004161  
 15 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q62556  
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//  
 0//1882bp//99%//AF069493  
 C-PLACE1004258  
 20 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%//O15393  
 C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//  
 AF084830  
 C-PLACE1004289  
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750  
 25 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588  
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//  
 2512bp//99%//AF100153  
 C-PLACE1004376  
 C-PLACE1004388  
 30 C-PLACE1004405  
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%//Q63448  
 C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283  
 C-PLACE1004451  
 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823  
 C-PLACE1004473  
 C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//  
 99%//AF026445  
 C-PLACE1004516  
 40 C-PLACE1004548  
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100  
 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568  
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438  
 C-PLACE1004645  
 45 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%//  
 X66277  
 C-PLACE1004664  
 C-PLACE1004672  
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//  
 50 96%//P12815  
 C-PLACE1004691  
 C-PLACE1004722  
 C-PLACE1004736  
 C-PLACE1004740  
 55 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPO-  
 NENT) (N- RECOGNIN).//4.4E-35//578aa//27%//O60152  
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224//  
 790bp//98%//AB022918

- C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337
- C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.7E-65//695aa//29%//Q01631
- 5 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170
- C-PLACE1004824
- C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891
- C-PLACE1004885
- 10 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//O42643
- C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//P06151
- C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%//AF099936
- 15 C-PLACE1004934
- C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794
- C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073
- C-PLACE1004982
- 20 C-PLACE1005026
- C-PLACE1005027
- C-PLACE1005046
- C-PLACE1005077
- C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401
- 25 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652
- C-PLACE1005111
- C-PLACE1005181
- C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636
- C-PLACE1005206
- 30 C-PLACE1005232
- C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
- C-PLACE1005261
- C-PLACE1005266
- C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182
- 35 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352
- C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760
- C-PLACE1005308
- C-PLACE1005313
- 40 C-PLACE1005327
- C-PLACE1005335
- C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//O33335
- 45 C-PLACE1005374
- C-PLACE1005480
- C-PLACE1005481
- C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276
- 50 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251
- C-PLACE1005550
- C-PLACE1005554
- C-PLACE1005623
- 55 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
- C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350



C-PLACE1005730  
 C-PLACE1005755  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)  
 (THIOESTERASE II).//2.5E-79//209aa//53%//P08635  
 5 C-PLACE1005803  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//  
 AF027156  
 C-PLACE1005851  
 C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120  
 10 C-PLACE1005923  
 C-PLACE1005925  
 C-PLACE1005934  
 C-PLACE1005936  
 C-PLACE1005951  
 15 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-  
 54//455aa//32%//P14904  
 C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//  
 25 254aa//25%//P38129  
 C-PLACE1005990  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876  
 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//  
 AF039023  
 25 C-PLACE1006139  
 C-PLACE1006159  
 C-PLACE1006167  
 C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706  
 C-PLACE1006195  
 30 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747  
 C-PLACE1006225  
 C-PLACE1006236  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//  
 P28675  
 35 C-PLACE1006246  
 C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//  
 1271-bp//99%//AL080066  
 C-PLACE1006335  
 C-PLACE1006357  
 40 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085  
 C-PLACE1006412  
 C-PLACE1006414  
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910  
 C-PLACE1006445  
 45 C-PLACE1006470  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595  
 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//  
 Q00004  
 C-PLACE1006492  
 50 C-PLACE1006531  
 C-PLACE1006552  
 C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
 2182bp//99%//AC007383  
 C-PLACE1006615  
 55 C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145  
 C-PLACE1006673  
 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//  
 734bp//62%//AB015630

- C-PLACE1006704  
C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263  
C-PLACE1006782
- 5 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%//P08547  
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123  
C-PLACE1006883
- 10 C-PLACE1006901  
C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181  
C-PLACE1006932  
C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000
- 15 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998  
C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421  
C-PLACE1006961  
C-PLACE1006962
- 20 C-PLACE1006966  
C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542  
C-PLACE1007021  
C-PLACE1007105
- 25 C-PLACE1007178  
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%//P54304  
C-PLACE1007238  
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%//D50495
- 30 C-PLACE1007242  
C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579  
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908  
C-PLACE1007274
- 35 C-PLACE1007282  
C-PLACE1007301  
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649  
C-PLACE1007342
- 40 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870  
C-PLACE1007367  
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715
- 45 C-PLACE1007386  
C-PLACE1007402  
C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320  
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487
- 50 C-PLACE1007450  
C-PLACE1007452  
C-PLACE1007460  
C-PLACE1007484
- 55 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734  
C-PLACE1007507  
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728

C-PLACE1007524  
 C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//  
 1485bp//98%//AF159164  
 C-PLACE1007544  
 5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//  
 P34537  
 C-PLACE1007583  
 C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676  
 C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194  
 10 C-PLACE1007621  
 C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506  
 C-PLACE1007645  
 C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194  
 C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//  
 15 8.7E-09//279aa//28%//Q26457  
 C-PLACE1007690  
 C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535  
 C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243  
 C-PLACE1007725  
 20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265  
 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//  
 AB014585  
 C-PLACE1007746  
 C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602  
 25 C-PLACE1007810  
 C-PLACE1007843  
 C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//  
 99%//AP000010  
 C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309  
 30 C-PLACE1007897  
 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//  
 25%//Q99323  
 C-PLACE1007954  
 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//  
 35 AF084530  
 C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//  
 99%//AF079529  
 C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//  
 48%//P52272  
 40 C-PLACE1007990  
 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-  
 SITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622  
 C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//  
 1833bp//99%//AC005628  
 45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
 CLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590  
 C-PLACE1008095  
 C-PLACE1008122  
 C-PLACE1008129  
 50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//  
 31%//Q09531  
 C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709  
 C-PLACE1008209  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//  
 55 671aa//77%//P53620  
 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689  
 C-PLACE1008280  
 C-PLACE1008309

- C-PLACE1008329  
 C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432  
 C-PLACE1008401
- 5 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527  
 C-PLACE1008457  
 C-PLACE1008465
- 10 C-PLACE1008488  
 C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%//AL031778  
 C-PLACE1008531  
 C-PLACE1008532
- 15 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620  
 C-PLACE1008568  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199  
 C-PLACE1008621  
 C-PLACE1008626  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
 C-PLACE1008629
- 25 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333  
 C-PLACE1008693  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406
- 30 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974  
 C-PLACE1008813  
 C-PLACE1008854  
 C-PLACE1008867  
 C-PLACE1008887  
 C-PLACE1008902  
 C-PLACE1008925
- 40 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623  
 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
 C-PLACE1009045  
 C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582  
 C-PLACE1009090
- 45 C-PLACE1009091  
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432  
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814  
 C-PLACE1009110  
 C-PLACE1009111
- 50 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086  
 C-PLACE1009158  
 C-PLACE1009166
- 55 C-PLACE1009174  
 C-PLACE1009186  
 C-PLACE1009190  
 C-PLACE1009230

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295

C-PLACE1009328

C-PLACE1009335

5 C-PLACE1009338

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067

C-PLACE1009375

C-PLACE1009388

10 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047//165aa//33%//Q09820

C-PLACE1009434

C-PLACE1009443

C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356

15 C-PLACE1009459

C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319

C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40//179aa//37%//P34580

20 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418

C-PLACE1009542

C-PLACE1009571

C-PLACE1009581

25 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808

C-PLACE1009607

C-PLACE1009621

C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159

C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%//P55161

30 C-PLACE1009665

C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534

C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876

C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200

35 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120

C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp//100%//AB012190

C-PLACE1009794

C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712

40 C-PLACE1009886

C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%//P53145

C-PLACE1009971

45 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%//P28175

C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%//AL080122

C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//736bp//73%//U48288

50 C-PLACE1010023

C-PLACE1010031

C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692

C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482

C-PLACE1010076

55 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671

C-PLACE1010102

C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//O04652

C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

99%//AL049385

C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082

C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662

C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130

C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722

C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%//AL080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%//P52178

C-PLACE1010324

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.000000002//126aa//29%//P34024

C-PLACE1010364

C-PLACE1010383

C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643

C-PLACE1010491

C-PLACE1010492

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%//AB022718

C-PLACE1010529

C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//P253 86

C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546

C-PLACE1010616

C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642

C-PLACE1010629

C-PLACE1010630

C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755

C-PLACE1010714

C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%//AB019987

C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//AF020267

C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061

C-PLACE1010786

C-PLACE1010800

C-PLACE1010811

C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%//Q05481

C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182

C-PLACE1010900

C-PLACE2000050

C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-//2.4E-191//828aa//48%//P21783

C-PLACE4000590

C-PLACE4000638

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aa//34%//P49816

C-Y79AA1001647

## Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-  
PLE 16).

[0316] Data include

the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)//0.13//52//38//P25860  
F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
64E)//2.2e-28//104//59//Q24574  
F-HEMBA1003854//VERPROLIN//0.012//138//31//P37370  
F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT)//0.93//39//  
33//Q37131  
F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2)//0.90//20//50//P38524  
F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16)//7.6e-46//141//58//Q15973  
F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT)//0.0033//32//46//P70560  
F-HEMBA1006092//VERPROLIN//1.0//62//35//P37370  
F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10)//0.30//41//36//P12350  
F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR//0.089//21//52//Q02593  
F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY)//0.38//156//30//P28697  
F-HEMBB1000672  
F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65)//1.0//30//36//P16012  
F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1)//3.7e-54//  
241//47//P47853  
F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3)//0.59//48//39//Q51483  
F-MAMMA1002094  
F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.26//58//27//P06333  
F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)//8.9e-20//83//48//P10895  
F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT)//1.0//42//40//P19326  
F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
PRECURSOR (ALS)//6.0e-23//207//32//Q02833  
F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3)//0.012//156//28//Q90267  
F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//0.0012//81//37//P13816  
F-NT2RP2000198//CREB-BINDING PROTEIN//0.29//98//37//Q92793  
F-NT2RP2000551//PROTEIN Q300//0.00017//23//60//Q02722  
F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401//1.0//41//29//Q57844  
F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC//0.27//13//61//Q01644  
F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-)//0.089//99//29//Q99014  
F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)-//4.0e-13//177//  
28//P16372  
F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//0.37//12//75//P53820  
F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)//0.99//61//32//Q42616  
F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2//3.3e-10//90//35//Q06666  
F-NT2RP2002843//CYTOCHROME B//0.78//103//26//P48884  
F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG//0.40//28//46//P37209  
F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1//0.80//55//32//P81303  
F-NT2RP2004095  
F-NT2RP2004732  
F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.18//18//55//Q48251  
F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003  
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323  
 F-NT2RP2005882  
 5 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217  
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276  
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204  
 10 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).//0.064//110//34//P39881  
 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95//29//P15583  
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29//P17437  
 15 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162  
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124//31//P28284  
 F-OVARC1001029  
 20 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377  
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845  
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).//3.2e-08//205//24//P53046  
 25 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

## Homology Search Result Data 8.

30 **[0318]** The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

**[0319]** Data include

the name of clone,  
 35 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0320]** Data are not shown for the clones in which the P-value was higher than 1.

40 F-HEMBA1000497  
 F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710  
 F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces.//1.7e-05//412//61//AC005081  
 45 F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386  
 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953  
 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641  
 50 F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851  
 F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738  
 F-HEMBA1006406//HS\_2268\_B2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566  
 55 F-HEMBA1006650//H.sapiens CpG island DNA genomic MseI fragment, clone 5h5, forward read cpg5h5.f1a.//9.4e-24//143//96//Z55730  
 F-HEMBA1006812//X.laevis xUBFalpha mRNA for upstream binding factor 2.//0.96//234//64//X59863



F-HEM BB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158

F-HEM BB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760

5 F-HEM BB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127

F-MAMMA1001252

F-MAMMA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993

10 F-NT2RM4000634//Chionocetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136

F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108

F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199

15 F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961

F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411

F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670

20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827

F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812

F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622

F-NT2RP2001214

25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189

F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589

F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094

30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097

F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22//377//69//AP000018

35 F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050

F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476

F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233

40 F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698

F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035

F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970

45 F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410

F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770

F-NT2RP2005806//Mus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652

50 F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242

F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775

F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cpg13g5.rt1a.//2.2e-18//163//85//Z56771

55 F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.3e-76//351//86//AC005180

F-NT2RP3003155

F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

F-OVARC1000008///0.0040//674//57//M82836

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461

F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427

F-PLACE1003030

F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//3.1e-39//214//98//AL031660

#### Homology Search Result Data 9.

**[0321]** The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

**[0322]** Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

**[0323]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

**[0324]** Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567

R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785

R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281

R-HEMBA1004193//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567

R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598

R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//AC004678

R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282

R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.8e-55//430//81//Z82207

R-HEMBA100672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//AC006166

R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593

R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 unordered pieces.//0.00097//410//59//AC004688

R-MAMMA1001252//Homo sapiens clone 201104, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 unordered pieces.//2.9e-13//364//64//AC004529

R-MAMMA1002094//HS\_3163\_A1\_A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1-6e-21//283//73//  
 AC005258  
 R-NT2RM4000657  
 R-NT2RM4000783  
 5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey se-  
 quence.//4.0e-07//62//98//AQ203073  
 R-NT2RM4001178  
 R-NT2RM4002420  
 10 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence,  
 complete sequence.//0.58//108//67//AC002307  
 R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//  
 D30043  
 R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.0058//166//  
 69//AC005324  
 15 R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence,  
 and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822  
 R-NT2RP2001460  
 R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey se-  
 quence.//3.4e-91//507//92//AQ114228  
 20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181  
 R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey se-  
 quence.//3.1e-29//178//94//AQ062168  
 R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chro-  
 25 mosome X \*.//5.3e-39//449//72//Z81014  
 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0.0097//498//  
 59//AC005412  
 R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey se-  
 quence.//1.2e-32//344//75//AQ196754  
 30 R-NT2RP2003799///3.6e-05//408//60//AL010237  
 R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in  
 unordered pieces.//2.1e-10//455//61//AL034557  
 R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a  
 novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287  
 35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//  
 315//61//AC005219  
 R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome  
 6 HindDIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63//  
 Z86062  
 40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//  
 AC005232  
 R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//  
 66//U37368  
 R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348  
 45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560  
 R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466  
 R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.8e-44//307//86//  
 AC005180  
 R-NT2RP3003155  
 50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//  
 95//65//B21351  
 R-OVARC1000008  
 R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//  
 AC005161  
 55 R-OVARC1000751//HS\_2222\_A2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143  
 R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC  
 RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.1e-88//497//91//AL031660

#### Homology Search Result Data 10.

**[0325]** The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

**[0326]** Data include

the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

**[0327]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element;, mRNA sequence.//3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element;, mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN ; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element ; mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997  
 F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA se-  
 quence.//5.0e-07//116//71//AA017066  
 F-NT2RP2000660//qx01g11.x1 NCI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA se-  
 5 quence.//0.027//120//65//AI225283  
 F-NT2RP2001214  
 F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA se-  
 quence.//0.0013//89//78//AI651878  
 F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'  
 10 similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//2.3e-18//120//93//AA427992  
 F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains  
 Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687  
 F-NT2RP2002677  
 F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491  
 15 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//1.9e-19//229//76//AA705059  
 F-NT2RP2002843//wt88dl2.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR:  
 P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//314//67//  
 AI964055  
 F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA se-  
 20 quence.//0.38//106//68//AI763133  
 F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//  
 91//AL049979  
 F-NT2RP2004095  
 F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691  
 25 F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR:  
 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ; mRNA sequence.//0.0020//220//61//AI969546  
 F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194  
 F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770  
 F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mR-  
 30 NA sequence.//2.0e-05//385//62//Z78328  
 F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362  
 F-NT2RP3001282  
 F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to con-  
 tains MSR1.t1 TAR1 TAR1 repetitive element ; mRNA sequence.//2.6e-07//245//66//AW008782  
 35 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA se-  
 quence.//0.58//164//64//R46086  
 F-NT2RP3003155  
 F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997  
 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565  
 40 F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541  
 F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802  
 F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to con-  
 tains element L1 repetitive element ; mRNA sequence.//0.0012//145//68//AI252422  
 F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA se-  
 45 quence.//7.1e-31//275//76//AA868469  
 F-PLACE1003030  
 F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//  
 1.2e-57//737//67//AJ010046  
 F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3',  
 50 mRNA sequence.//2.2e-21//216//76//H52716

## Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones  
 55 selected in EXAMPLE 16.).

[0329] Data include

the name of clone,

title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

- 5 **[0330]** Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.  
**[0331]** Data are not shown for the clones in which the P-value was higher than 1.

10 R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains  
Alu repetitive element;contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83//  
AA614254

R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
278971 3', mRNA sequence.//0.004511193//63//N63303

R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//  
80//AL049263

15 R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-  
tains Alu repetitive element;contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81//  
AI914747

R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA  
sequence.//0.017//118//69//AI218308

20 R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-  
quence.//4.6e-111//522//99//AI861830

R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5',  
mRNA sequence.//1.2e-22//295//72//AL041450

R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE: 1949489  
25 3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963

R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-//76//AB018295

R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630

R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087

30 R-HEMBA100672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//  
74//AL096734

R-HEMBA1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar  
to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788

R-HEMBA1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321

35 R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-  
tains Alu repetitive element;contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91//  
AA504355

R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mR-  
NA sequence.//2.5e-68//328//99//AI936520

40 R-NT2RM4000634//DKFZp434F2016\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3',  
mRNA sequence.//8.2e-20//185//81//AL041146

R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992

R-NT2RM4000783

R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136

45 R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA se-  
quence.//0.77//96//62//AI457506

R-NT2RM4002420//wl58b04.x1 NCI\_CGAP\_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA se-  
quence.//2.4e-85//438//94//AI857508

R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA se-  
50 quence.//1.9e-45//270//91//AA738352

R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA se-  
quence.//3.3e-53//311//85//AI417680

R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA se-  
quence.//4.3e-26//142//97//AA805691

55 R-NT2RP2001214//tw65g08.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains  
element MSR1 repetitive element ; mRNA sequence.//1.5e-57//289//97//AI680174

R-NT2RP2001460

R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'

similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//6.0e-13//85//96//AA427992  
R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA  
sequence.//0.0016//208//65//R22302  
R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096  
5 R-NT2RP2002755//qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3',  
mRNA sequence.//1.5e-26//419//66//AI190698  
R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to  
contains L1.t1 L1 repetitive element;; mRNA sequence.//1.8e-45//463//74//AI749673  
R-NT2RP2003101//ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA se-  
10 quence.//7.5e-73//347//99//AI758824  
R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294  
R-NT2RP2004095//zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to con-  
tains element MER32 repetitive element ; mRNA sequence.//9.6e-07//188//66//AA436455  
R-NT2RP2004732//tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to con-  
15 tains Alu repetitive element;contains element L1 repetitive element ; mRNA sequence.//4.3e-25//414//68//  
AI678956  
R-NT2RP2004920//wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA se-  
quence.//6.8e-91//483//93//AI694022  
R-NT2RP2005454//yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
20 279616 3', mRNA sequence.//0.0070//325//59//N48302  
R-NT2RP2005776//qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1939307 3',  
mRNA sequence.//7.5e-08//89//82//AI338419  
R-NT2RP2005806//wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to con-  
tains MER2.b3 MER2 repetitive element ; mRNA sequence.//3.2e-16//235//71//AI671398  
25 R-NT2RP2005882//wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA se-  
quence.//0.00095//352//59//AI925528  
R-NT2RP3001282//wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199  
R-NT2RP3001723//wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA se-  
30 quence.//4.2e-98//471//98//AI926617  
R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mR-  
NA sequence.//9.2e-50//329//87//AL037910  
R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668  
3' mRNA sequence.//1.4e-30//159//99//AA173172  
35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594  
R-OVARC1000008//wa69e12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA  
sequence.//1.0e-77//376//98//AI699393  
R-OVARC1000724//tf94b10.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA se-  
quence.//0.71//27//100//AI380236  
40 R-OVARC1000751//og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA se-  
quence.//3.5e-13//274//63//AA863306  
R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar  
to contains Alu repetitive element;contains element PTR5 repetitive element ; mRNA sequence.//3.5e-13//175//74//  
N99464  
45 R-PLACE1000814//tg49a08.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar  
to contains LI.t2 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//AI424789  
R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
cds.//4.0e-34//225//90//AF032387  
R-PLACE1005549//tm26b11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA  
50 sequence.//0.91//127//66//AI480253  
R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5'  
similar to contains Alu repetitive element;contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87//  
R92256

55 Homology Search Result Data 12.

[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996

5 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344

C-HEMBA1000129//HYTOTHEICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884

C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738

10 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221

C-HEMBA1000231

C-HEMBA1000264

C-HEMBA1000280

C-HEMBA1000282

15 C-HEMBA1000303//&quot;Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.&quot;//7.1E-254//1440bp//87%//AF030131

C-HEMBA1000333//&quot;Homo sapiens mRNA for KIAA0874 protein, partial cds.&quot;//4.8E-253//1148bp//99%//AB020681

C-HEMBA1000351

20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//815bp//98%//AL050274

C-HEMBA1000396

C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357

C-HEMBA1000442

25 C-HEMBA1000456

C-HEMBA1000504

C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490

C-HEMBA1000519

C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755

30 C-HEMBA1000542//&quot;Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.&quot;//2.2E-194//663bp//83%//D89340

C-HEMBA1000545

C-HEMBA1000557

C-HEMBA1000592//&quot;Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.&quot;//0//1465bp//99%//AF121856

35 C-HEMBA1000594

C-HEMBA1000604

C-HEMBA1000622

C-HEMBA1000637

40 C-HEMBA1000655

C-HEMBA1000657//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.&quot;//7.2E-156//1366bp//76%//U35776

C-HEMBA1000749

C-HEMBA1000769

45 C-HEMBA1000773

C-HEMBA1000774

C-HEMBA1000822

C-HEMBA1000843

C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689

50 C-HEMBA1000870

C-HEMBA1000908

C-HEMBA1000934

C-HEMBA1000972

C-HEMBA1000986

55 C-HEMBA1000991

C-HEMBA1001008

C-HEMBA1001059//&quot;Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.&quot;//4.8E-169//786bp//99%//U06088



C-HEMBA1001094  
 C-HEMBA1001302//&quot;Homo sapiens calcium binding protein precursor, mRNA, complete cds.&quot;//9.6E-258//682bp//94%//AF153686  
 C-HEMBA1001330  
 5 C-HEMBA1001497  
 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%//P19065  
 C-HEMBA1001570  
 10 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803  
 C-HEMBA1001640  
 C-HEMBA1001655  
 C-HEMBA1001672//&quot;Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.&quot;//0//1707bp//98%//AF072247  
 15 C-HEMBA1001711  
 C-HEMBA1001723//&quot;Rattus norvegicus G beta-like protein GBL mRNA, complete cds.&quot;//4.7E-172//1240bp//81%//AF051155  
 C-HEMBA1001746//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.&quot;//7.6E-59//998bp//64%//AF098066  
 20 C-HEMBA1001781  
 C-HEMBA1001804//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.&quot;//0//1637bp//99%//AF125158  
 C-HEMBA1001822//&quot;Mus musculus Ese2L protein mRNA, complete cds.&quot;//1.9E-235//1329bp//89%//AF132479  
 25 C-HEMBA1001824  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332  
 C-HEMBA1001910  
 C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535  
 30 C-HEMBA1001921//&quot;Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.&quot;//0//1850bp//99%//AF000145  
 C-HEMBA1001939  
 C-HEMBA1001950//&quot;Homo sapiens mRNA for KIAA0971 protein, complete cds.&quot;//0//1974bp//99%//AB023188  
 35 C-HEMBA1001967//&quot;Homo sapiens NY-REN-57 antigen mRNA, partial cds.&quot;//0//1721bp//99%//AF155114  
 C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089  
 C-HEMBA1002092//&quot;Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.&quot;//1.3E-271//1583bp//88%//U92703  
 40 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357  
 C-HEMBA1002150  
 C-HEMBA1002151//&quot;Rattus norvegicus p34 mRNA, complete cds.&quot;//1.1E-153//1059bp//82%//AF178669  
 45 C-HEMBA1002189  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226  
 C-HEMBA1002229  
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087  
 50 C-HEMBA1002341//&quot;Homo sapiens mRNA for KIAA0771 protein, partial cds.&quot;//0//1514bp//99%//AB018314  
 C-HEMBA1002417//&quot;Homo sapiens chromosome 19, cosmid R28784, complete sequence.&quot;//1.4E-299//294bp//100%//AC005954  
 C-HEMBA1002547//&quot;Homo sapiens agrin precursor mRNA, partial cds.&quot;//0//1605bp//97%//AF016903  
 55 C-HEMBA1002703  
 C-HEMBA1002779  
 C-HEMBA1002816  
 C-HEMBA1002970

C-HEMBA1002999//&quot;Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.

&quot;//1.4E-171//1552bp//75%//U20286

C-HEMBA1003021

C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014

5 C-HEMBA1003079

C-HEMBA1003273

C-HEMBA1003304

C-HEMBA1003309

C-HEMBA1003376

10 C-HEMBA1003384

C-HEMBA1003531

C-HEMBA1003548

C-HEMBA1003556

C-HEMBA1003571

15 C-HEMBA1003579

C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105

C-HEMBA1003692

C-HEMBA1003720

C-HEMBA1003725

20 C-HEMBA1003729

C-HEMBA1003758

C-HEMBA1003773//&quot;Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.

&quot;//5.8E-81//511bp//86%//U17343

C-HEMBA1003783//&quot;Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.&quot;//

25 1.1E-190//1204bp//84%//AF084259

C-HEMBA1003799

C-HEMBA1003804

C-HEMBA1003805//&quot;Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.&quot;//

0//988bp//95%//AF090402

30 C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484

C-HEMBA1003856

C-HEMBA1003866//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//1.2E-105//1192bp//70%//

AF030430

C-HEMBA1003879

35 C-HEMBA1003880

C-HEMBA1003893

C-HEMBA1003908

C-HEMBA1003937

C-HEMBA1003942

40 C-HEMBA1003958

C-HEMBA1003976

C-HEMBA1003978//&quot;Homo sapiens mRNA for KIAA0840 protein, partial cds.&quot;//0//1530bp//100%//

AB020647

C-HEMBA1003985

45 C-HEMBA1004011

C-HEMBA1004024

C-HEMBA1004038

C-HEMBA1004045

C-HEMBA1004048

50 C-HEMBA1004111//&quot;Homo sapiens mRNA for KIAA1276 protein, partial cds.&quot;//1.00E-163//751bp//99%//AB033102

C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141

C-HEMBA1004138

C-HEMBA1004143

55 C-HEMBA1004150

C-HEMBA1004168//&quot;Homo sapiens geminin mRNA, complete cds.&quot;//3.9E-208//951 bp//99%//

AF067855

C-HEMBA1004200

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153  
 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991  
 C-HEMBA1004238  
 5 C-HEMBA1004248//&quot;Homo sapiens insulin induced protein 2 mRNA, complete cds.&quot;//8.20E-175//  
 552bp//97%//AF125392  
 C-HEMBA1004272  
 C-HEMBA1004274  
 C-HEMBA1004275//&quot;Homo sapiens mRNA for KIAA1111 protein, partial cds.&quot;//0//1341bp//99%//  
 AB029034  
 10 C-HEMBA1004286//&quot;Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.&quot;//  
 0//1982bp//99%//AF022795  
 C-HEMBA1004312  
 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%//Q99676  
 C-HEMBA1004323  
 15 C-HEMBA1004327  
 C-HEMBA1004330  
 C-HEMBA1004341  
 C-HEMBA1004366  
 C-HEMBA1004372  
 20 C-HEMBA1004389//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.  
 &quot;//0//1437bp//99%//AF125158  
 C-HEMBA1004394  
 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-  
 CLOPHILIN-10).//3.2E-32//148aa//52%//P52017  
 25 C-HEMBA1004429  
 C-HEMBA1004460  
 C-HEMBA1004461  
 C-HEMBA1004502  
 C-HEMBA1004554  
 30 C-HEMBA1004560  
 C-HEMBA1004610  
 C-HEMBA1004629  
 C-HEMBA1004632  
 C-HEMBA1004637  
 35 C-HEMBA1004670  
 C-HEMBA1004672  
 C-HEMBA1004697  
 C-HEMBA1004711  
 C-HEMBA1004725  
 40 C-HEMBA1004730  
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743  
 C-HEMBA1004751  
 C-HEMBA1004752  
 45 C-HEMBA1004889//&quot;Human C3f mRNA, complete cds.&quot;//6.70E-24//341aa//26%//U72515  
 C-HEMBA1004934  
 C-HEMBA1004944  
 C-HEMBA1004973  
 C-HEMBA1004977  
 50 C-HEMBA1005009//&quot;Homo sapiens BAF53a (BAF53a) mRNA, complete cds.&quot;//0//1813bp//99%//  
 AF041474  
 C-HEMBA1005083  
 C-HEMBA1005113  
 C-HEMBA1005133  
 55 C-HEMBA1005185  
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929  
 C-HEMBA1005252//&quot;Homo sapiens mRNA for KIAA0585 protein, partial cds.&quot;//1.2E-268//1215bp//  
 99%//AB011157

C-HEMBA1005296  
 C-HEMBA1005314  
 C-HEMBA1005331  
 C-HEMBA1005394  
 5 C-HEMBA1005403  
 C-HEMBA1005423//&quot;Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.  
 &quot;//2E-213//537bp//99%//AF041248  
 C-HEMBA1005468  
 C-HEMBA1005469  
 10 C-HEMBA1005474  
 C-HEMBA1005517  
 C-HEMBA1005518  
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809  
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929  
 15 C-HEMBA1005576//&quot;Homo sapiens mRNA for KIAA0463 protein, partial cds.&quot;//1.1E-181//835bp//  
 99%//AB007932  
 C-HEMBA1005582//&quot;TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL  
 TROPOMYOSIN).&quot;//0.00000009//213aa//27%//P09492  
 C-HEMBA1005583  
 20 C-HEMBA1005595//&quot;DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).&quot;//2.3E-54//562aa//29%//P34036  
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//  
 1448bp//99%//AL050012  
 C-HEMBA1005621//&quot;Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds.&quot;//2.9E-224//  
 1031bp//99%//AF139365  
 25 C-HEMBA1005666  
 C-HEMBA1005680  
 C-HEMBA1005685  
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//  
 4.4E-17//167aa//34%//P25296  
 30 C-HEMBA1005746  
 C-HEMBA1005755  
 C-HEMBA1005813  
 C-HEMBA1005822  
 C-HEMBA1005834  
 35 C-HEMBA1005884  
 C-HEMBA1005891  
 C-HEMBA1005909  
 C-HEMBA1005911  
 C-HEMBA1005931  
 40 C-HEMBA1005963  
 C-HEMBA1005991  
 C-HEMBA1006005  
 C-HEMBA1006031//&quot;Homo sapiens mRNA for putative phospholipase, complete cds.&quot;//0//1413bp//  
 99%//AB019435  
 45 C-HEMBA1006067  
 C-HEMBA1006081  
 C-HEMBA1006091  
 C-HEMBA1006100  
 C-HEMBA1006108//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//4.8E-245//764bp//  
 50 99%//AB023160  
 C-HEMBA1006121  
 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794  
 C-HEMBA1006155  
 C-HEMBA1006158//&quot;Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.&quot;/  
 55 //0//1551bp//99%//AF048693  
 C-HEMBA1006182  
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142  
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//  
 62aa//53%//P42698  
 C-HEMBA1006259  
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%//P10265  
 5 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-  
 FERASE).//1E-210//490aa//77%//P25500  
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//  
 30%//P32505  
 C-HEMBA1006284  
 10 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.2E-12//215aa//23%//P70473  
 C-HEMBA1006293  
 C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.4E-48//  
 248aa//43%//P38821  
 C-HEMBA1006349  
 15 C-HEMBA1006364  
 C-HEMBA1006381  
 C-HEMBA1006398//&quot;Human L1 element L1.6 putative p150 gene, complete cds.&quot;//2E-277//1729bp//  
 85%//U93563  
 C-HEMBA1006445//&quot;Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.&quot;//1.4E-  
 20 270//1224bp//100%//U96750  
 C-HEMBA1006483  
 C-HEMBA1006492  
 C-HEMBA1006497  
 C-HEMBA1006502  
 25 C-HEMBA1006507//&quot;Homo sapiens mRNA for KIAA0666 protein, partial cds.&quot;//0//2334bp//99%//  
 AB014566  
 C-HEMBA1006535  
 C-HEMBA1006559//&quot;Mus musculus PRAJA1 (Praj1) mRNA, complete cds.&quot;//2.8E-206//1107bp//83  
 %//U06944  
 30 C-HEMBA1006566  
 C-HEMBA1006579  
 C-HEMBA1006583  
 C-HEMBA1006612  
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//  
 35 38%//Q58323  
 C-HEMBA1006643  
 C-HEMBA1006674  
 C-HEMBA1006682  
 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
 40 INTERGENIC REGION.//3.3E-22//241aa//31%//P53196  
 C-HEMBA1006717  
 C-HEMBA1006744  
 C-HEMBA1006754  
 C-HEMBA1006767  
 45 C-HEMBA1006789  
 C-HEMBA1006832  
 C-HEMBA1006885//&quot;Homo sapiens gene for Proline synthetase associated, complete cds.&quot;//0//  
 1467bp//96%//AB018566  
 C-HEMBA1006900  
 50 C-HEMBA1006926  
 C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%//  
 AJ010841  
 C-HEMBA1006973//&quot;Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.&quot;//5.6E-143//  
 740bp//94%//AF004828  
 55 C-HEMBA1006993  
 C-HEMBA1007002  
 C-HEMBA1007062  
 C-HEMBA1007080

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626

C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450

C-HEMBA1007194//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.&quot;//0//1588bp//99%//AF139658

C-HEMBA1007206

C-HEMBA1007256

C-HEMBA1007267

C-HEMBA1007281

C-HEMBA1007300//&quot;Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.&quot;//0//1519bp//99%//AF127479

C-HEMBA1007301

C-HEMBA1007319

C-HEMBA1007320

C-HEMBA1007327

C-HEMBA1007347

C-HEMBB1000005

C-HEMBB1000030

C-HEMBB1000048

C-HEMBB1000099

C-HEMBB1000141

C-HEMBB1000198

C-HEMBB1000217//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.&quot;//0//1038bp//99%//AF090385

C-HEMBB1000218

C-HEMBB1000274

C-HEMBB1000312

C-HEMBB1000402

C-HEMBB1000420

C-HEMBB1000480

C-HEMBB1000530

C-HEMBB1000550

C-HEMBB1000556//&quot;Homo sapiens mRNA for KIAA0750 protein, complete cds.&quot;//6.3E-74//1213bp//64%//AB018293

C-HEMBB1000586

C-HEMBB1000592

C-HEMBB1000593//&quot;Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.&quot;//1.3E-107//503bp//99%//AF067864

C-HEMBB1000649

C-HEMBB1000693//&quot;Homo sapiens neuroan1 mRNA, complete cds.&quot;//0//2952bp//94%//AF040723

C-HEMBB1000822

C-HEMBB1000826

C-HEMBB1000890

C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122

C-HEMBB1001008

C-HEMBB1001020//&quot;Homo sapiens mRNA for KIAA0889 protein, complete cds.&quot;//0//1812bp//98%//AB020696

C-HEMBB1001051

C-HEMBB1001112//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//6E-145//961bp//83%//AF077032

C-HEMBB1001221

C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938

C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//P16157

C-HEMBB1001302

C-HEMBB1001335

C-HEMBB1001337

C-HEMBB1001356  
 C-HEMBB1001364  
 C-HEMBB1001366  
 C-HEMBB1001367  
 5 C-HEMBB1001527  
 C-HEMBB1001537  
 C-HEMBB1002359  
 C-HEMBB1002415  
 C-HEMBB1002457  
 10 C-HEMBB1002492  
 C-HEMBB1002495  
 C-HEMBB1002502  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%/P27544  
 C-HEMBB1002600//&quot;Homo sapiens tetraspan NET-5 mRNA, complete cds.&quot;//0//1417bp//99%/AF089749  
 15 C-HEMBB1002607//&quot;Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.  
 &quot;//2E-136//660bp//98%/AF105421  
 C-HEMBB1002684  
 C-HEMBB1002692  
 20 C-HEMBB1002697  
 C-HEMBB1002705//&quot;Homo sapiens CGI-27 protein mRNA, complete cds.&quot;//7.80E-285//841bp//96%/AF132961  
 C-MAMMA1000019  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%/Z47553  
 25 C-MAMMA1000025  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%/P47226  
 C-MAMMA1000069  
 C-MAMMA1000084  
 30 C-MAMMA1000139  
 C-MAMMA1000163  
 C-MAMMA1000171  
 C-MAMMA1000173//&quot;Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete  
 cds.&quot;//2.6E-164//1044bp//87%/AF197060  
 35 C-MAMMA1000277  
 C-MAMMA1000278  
 C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%/X99836  
 C-MAMMA1000309  
 C-MAMMA1000312  
 40 C-MAMMA1000313  
 C-MAMMA1000361  
 C-MAMMA1000388//&quot;Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.&quot;//0//1466bp//99%/AB015132  
 C-MAMMA1000395  
 45 C-MAMMA1000410  
 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%/Q09232  
 C-MAMMA1000421  
 C-MAMMA1000422  
 50 C-MAMMA1000468  
 C-MAMMA1000472  
 C-MAMMA1000490  
 C-MAMMA1000524  
 C-MAMMA1000567  
 55 C-MAMMA1000612//&quot;Rattus norvegicus G beta-like protein GBL mRNA, complete cds.&quot;//1E-95//1115bp//72%/AF051155  
 C-MAMMA1000623  
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%/P48365

C-MAMMA1000664  
 C-MAMMA1000670  
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//4.4E-33//250aa//  
 33%//P42660  
 5 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16)//7.70E-17//246aa//29%//P94524  
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1E-77//395aa//45%//  
 014646  
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein//0//1587bp//99%//AJ011779  
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I//9E-299//1033aa//  
 10 55%//P87115  
 C-MAMMA1000746  
 C-MAMMA1000775  
 C-MAMMA1000824//ACTIN//6.2E-20//284aa//28%//P53500  
 C-MAMMA1000831  
 15 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//7.8E-40//101aa//54%//027540  
 C-MAMMA1000842  
 C-MAMMA1000843  
 C-MAMMA1000856  
 C-MAMMA1000865  
 20 C-MAMMA1000875  
 C-MAMMA1000906  
 C-MAMMA1000908  
 C-MAMMA1000914  
 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8//0//1767bp//99%//AJ250711  
 25 C-MAMMA1000968  
 C-MAMMA1000979  
 C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//  
 1263bp//99%//AF117892  
 C-MAMMA1001021  
 30 C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN)  
 (FODRIN BETA CHAIN) (SPTBN1)."//1.6E-16//113aa//41%//Q01082  
 C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5//0//1440bp//99%//AJ237946  
 C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//  
 AF151830  
 35 C-MAMMA1001078  
 C-MAMMA1001091  
 C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN)//4E-49//125aa//68%//P51521  
 C-MAMMA1001110  
 C-MAMMA1001126  
 40 C-MAMMA1001139//SRE-2 PROTEIN//5.80E-35//239aa//38%//Q09273  
 C-MAMMA1001143  
 C-MAMMA1001154  
 C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR//1.30E-07//81aa//45%//Q92338  
 C-MAMMA1001215  
 45 C-MAMMA1001244  
 C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//  
 89%//AF184275  
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III//2.1E-52//630aa//  
 30%//P34537  
 50 C-MAMMA1001343  
 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823)//0//2131bp//  
 99%//AL080121  
 C-MAMMA1001419  
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT)//  
 55 6.5E-129//260aa//92%//P52623  
 C-MAMMA1001510  
 C-MAMMA1001522  
 C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//



M61764

C-MAMMA1001604

C-MAMMA1001620

C-MAMMA1001635

5 C-MAMMA1001649

C-MAMMA1001686

C-MAMMA1001692

C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%//  
P2157310 C-MAMMA1001754//&quot;Homo sapiens CGI-11 protein mRNA, complete cds.&quot;//0//1837bp//98%//  
AF132945

C-MAMMA1001757

C-MAMMA1001764

C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556

15 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991

C-MAMMA1001790

C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230

C-MAMMA1001858

C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793

20 C-MAMMA1001970

C-MAMMA1002042

C-MAMMA1002068

C-MAMMA1002153

C-MAMMA1002156

25 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880

C-MAMMA1002174

C-MAMMA1002209

C-MAMMA1002219//&quot;Homo sapiens mRNA for KIAA1067 protein, partial cds.&quot;//1.1E-181//861bp//  
98%//AB02899030 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-  
CHANGE FACTOR).//8.8E-217//310aa//86%//P70541

C-MAMMA1002243

C-MAMMA1002268//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//1E-190//  
1624bp//76%//AF068748

35 C-MAMMA1002269

C-MAMMA1002292

C-MAMMA1002294

C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//  
AJ011679

40 C-MAMMA1002312

C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991

C-MAMMA1002333

C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882

C-MAMMA1002353

45 C-MAMMA1002355

C-MAMMA1002356

C-MAMMA1002362

C-MAMMA1002380

C-MAMMA1002384

50 C-MAMMA1002427

C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//  
P47623C-MAMMA1002485//&quot;Homo sapiens stanniocalcin-related protein mRNA, complete cds.&quot;//0//1822bp//  
99%//AF098462

55 C-MAMMA1002494

C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//  
337aa//31%//P43571

C-MAMMA1002530//&amp;quot;Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

cds.&quot;0//1910bp//99%//AF065214  
 C-MAMMA1002554  
 C-MAMMA1002585//&quot;Homo sapiens mRNA for KIAA0860 protein, complete cds.&quot;0//1405bp//99%//  
 5 AB020667  
 C-MAMMA1002598  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//9.5E-16//159aa//37%//Q09931  
 10 C-MAMMA1002655//&quot;Homo sapiens mRNA for ganglioside sialidase, complete cds.&quot;0//1515bp//  
 99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.1E-45//618aa//26%//P27550  
 C-MAMMA1002673  
 C-MAMMA1002684//&quot;Homo sapiens mRNA for KIAA0214 protein, complete cds.&quot;0//3174bp//99%//  
 15 D86987  
 C-MAMMA1002711  
 C-MAMMA1002769//&quot;Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete  
 cds.&quot;2.2E-25//330bp//77%//AF011794  
 C-MAMMA1002775  
 20 C-MAMMA1002782  
 C-MAMMA1002796  
 C-MAMMA1002807  
 C-MAMMA1002838  
 C-MAMMA1002842//&quot;Mus musculus c-Cb1 associated protein CAP mRNA, complete cds.&quot;2.6E-58//  
 25 373bp//81%//U58883  
 C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.4E-160//  
 305aa//85%//P48059  
 C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.7E-30//214aa//  
 35 35%//P48060  
 C-MAMMA1002886  
 C-MAMMA1002890  
 C-MAMMA1002938//&quot;Homo sapiens mRNA for KIAA0698 protein, complete cds.&quot;8.4E-252//1139bp//  
 100%//AB014598  
 C-MAMMA1002964  
 40 C-MAMMA1003011//HESTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874  
 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//P06746  
 C-MAMMA1003015  
 C-MAMMA1003019  
 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-  
 DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//33%//P23851  
 C-MAMMA1003039  
 C-MAMMA1003044  
 C-MAMMA1003049  
 C-MAMMA1003056  
 45 C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%//Q60584  
 C-MAMMA1003066  
 C-MAMMA1003099  
 C-MAMMA1003104  
 C-MAMMA1003113//&quot;Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.&quot;1.1E-234//1178bp//86%//AF071316  
 50 C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%//P46735  
 C-MAMMA1003135  
 C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.3E-218//996bp//99%//Y15062  
 C-MAMMA1003150//&quot;Homo sapiens mRNA for KIAA1096 protein, partial cds.&quot;0//1342bp//99%//  
 55 AB029019  
 C-MAMMA1003166//&quot;Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.&quot;3.10E-158//592bp//97%//AF123052  
 C-NT2RM1000032

C-NT2RM1000035//&quot;Human mRNA for KIAA0199 gene, partial cds.&quot;//0//2948bp//99%//D83782  
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)  
 (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596  
 C-NT2RM1000055//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//3111bp//99%//  
 5 AB020636  
 C-NT2RM1000059  
 C-NT2RM1000062  
 C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 10 C-NT2RM1000119  
 C-NT2RM1000127  
 C-NT2RM1000131//&quot;Homo sapiens mRNA for KIAA0792 protein, complete cds.&quot;//0//2980bp//99%//  
 AB018335  
 C-NT2RM1000132//&quot;Homo sapiens NADH:ubiquinone oxidoreductas NDUFS6 subunit mRNA, nuclear gene  
 15 encoding mitochondrial protein, complete cds.&quot;//7.8E-110//516bp//99%//AF044959  
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902  
 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 20 SPAC10F6.02C.//1.1E-10//94aa//47%//042643  
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//  
 AJ245820  
 C-NT2RM1000244//&quot;Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.&quot;//2E-126//592bp//  
 99%//U81002  
 25 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882  
 C-NT2RM1000256//&quot;Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete  
 cds.&quot;//0//3012bp//99%//AB016789  
 C-NT2RM1000260//&quot;Human mRNA for KIAA0130 gene, complete cds.&quot;//0//3139bp//98%//D50920  
 C-NT2RM1000271  
 30 C-NT2RM1000300  
 C-NT2RM1000314//&quot;Human mRNA for KIAA0159 gene, complete cds.&quot;//0//4349bp//99%//D63880  
 C-NT2RM1000354//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//7.4E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//&quot;Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.&quot;//0//  
 35 1599bp//99%//AF152462  
 C-NT2RM1000365  
 C-NT2RM1000377//&quot;Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.&quot;/  
 //3.2E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 40 0.000000019//67aa//31%//P53915  
 C-NT2RM1000399  
 C-NT2RM1000430//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 1.4E-185//1486bp//81%//AF084928  
 C-NT2RM1000555//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
 45 AB020692  
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//  
 30%//Q08372  
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636  
 C-NT2RM1000661//&quot;Homo sapiens translation initiation factor 4e mRNA, complete cds.&quot;//4.3E-210//  
 50 960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989  
 C-NT2RM1000672  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440  
 C-NT2RM1000699  
 55 C-NT2RM1000741//&quot;Homo sapiens mRNA for KIAA0567 protein, partial cds.&quot;//1.1E-295//1338bp//  
 99%//AB011139  
 C-NT2RM1000742//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
 AF027208

- C-NT2RM1000746//&quot;Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.&quot;//6.70E-227//1043bp//99%//AF141310
- C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202
- 5 C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808
- C-NT2RM1000780
- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.1E-98//571bp//89%//Z97207
- C-NT2RM1000802
- C-NT2RM1000811//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//AF027208
- 10 C-NT2RM1000826//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//AB020692
- C-NT2RM1000829
- C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//P16157
- 15 C-NT2RM1000852//&quot;Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.&quot;//0//2206bp//99%//AF077033
- C-NT2RM1000857//&quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;//0//3716bp//99%//AB023179
- C-NT2RM1000874//&quot;Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.&quot;//1.4E-244//1113bp//99%//AF043733
- 20 C-NT2RM1000882//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;//4.30E-122//1394bp//69%//AF126799
- C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//30%//P34537
- 25 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
- C-NT2RM1000898//&quot;ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).&quot;//8.9E-26//229aa//29%//P02583
- C-NT2RM1000905//&quot;Homo sapiens HSPC021 mRNA, complete cds.&quot;//0//1480bp//99%//AF077207
- 30 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%//P46577
- C-NT2RM1000927
- C-NT2RM1000962
- C-NT2RM1000978
- 35 C-NT2RM1001003//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//2230bp//99%//AF030233
- C-NT2RM1001043
- C-NT2RM1001066
- C-NT2RM1001072//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).&quot;//8.3E-47//259aa//35%//P08487
- 40 C-NT2RM1001085//&quot;Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.&quot;//3.7E-32//460bp//64%//AF053768
- C-NT2RM1001102//&quot;Human HEM45 mRNA, complete cds.&quot;//2.3E-27//482bp//63%//U88964
- 45 C-NT2RM1001105
- C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//99%//AL049943
- C-NT2RM2000420
- C-NT2RM2000566//&quot;Homo sapiens integrin alpha-7 mRNA, complete cds.&quot;//0//2519bp//96%//AF032108
- 50 C-NT2RM2000609
- C-NT2RM2000612//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.&quot;//2.6E-106//1069bp//74%//U35776
- C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160
- 55 C-NT2RM2001588
- C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
- C-NT2RM2001613//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2601bp//99%//AF084458

C-NT2RM2001632//KES 1 PROTEIN.//1.40E-31//342aa//34%//P35844  
 C-NT2RM2001648//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2421bp//99%//  
 AF084458  
 C-NT2RM2001652//&quot;Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.&quot;//0//  
 5 2608bp//99%//AF111162  
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P20107  
 C-NT2RM2001664//&quot;Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete  
 cds.&quot;//0//2471bp//99%//AF044195  
 C-NT2RM2001668//&quot;Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product  
 10 ending in intron 11, complete cds.&quot;//6.2E-16//464bp//62%//AF083391  
 C-NT2RM2001671//&quot;Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.  
 &quot;//0//1843bp//94%//U21155  
 C-NT2RM2001675  
 C-NT2RM2001681  
 15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//  
 30%//Q09674  
 C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF103804  
 C-NT2RM2001696  
 C-NT2RM2001698//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//6.2E-  
 20 253//1170bp//99%//AB028600  
 C-NT2RM2001700//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-  
 CAD) (FRAGMENT).&quot;//5.7E-130//536aa//49%//P50544  
 C-NT2RM2001716  
 C-NT2RM2001723  
 25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//7.2E-16//381aa//27%//Q09931  
 C-NT2RM2001743//&quot;Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.&quot;//  
 0//1498bp//99%//AF011792  
 30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609  
 C-NT2RM2001760//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2379bp//99%//  
 AF084458  
 C-NT2RM2001768  
 C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742  
 35 C-NT2RM2001782//&quot;Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.  
 &quot;//0//1470bp//99%//AF135422  
 C-NT2RM2001784  
 C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//  
 99%//AL050118  
 40 C-NT2RM2001813  
 C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657  
 C-NT2RM2001839//&quot;Homo sapiens calumein (Calu) mRNA, complete cds.&quot;//0//2415bp//97%//  
 AF013759  
 C-NT2RM2001840  
 45 C-NT2RM2001855  
 C-NT2RM2001867//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//967bp//99%//  
 AB023160  
 C-NT2RM2001879  
 C-NT2RM2001983//&quot;Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.&quot;//0//  
 50 1658bp//98%//AF089816  
 C-NT2RM2002145//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 8.5E-191//1524bp//81%//AF084928  
 C-NT2RM4000027  
 C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146  
 55 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003  
 C-NT2RM4000155//&quot;THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--  
 TRNA LIGASE) (THRRS).&quot;//1.2E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBR11-7 gene.//3.6E-21//785bp//60%//X67336

C-NT2RM4000167//&quot;Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.&quot;//0//  
 1946bp//99%//AF071592  
 C-NT2RM4000199  
 C-NT2RM4000200  
 5 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%//Q16600  
 C-NT2RM4000233//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//3.4E-231//1395bp//86%//  
 AF030430  
 C-NT2RM4000244  
 C-NT2RM4000251  
 10 C-NT2RM4000265  
 C-NT2RM4000324  
 C-NT2RM4000327  
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292  
 C-NT2RM4000425  
 15 C-NT2RM4000433//&quot;Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.&quot;//  
 4.1E-271//2085bp//77%//AF062476  
 C-NT2RM4000514  
 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//007230  
 C-NT2RM4000532  
 20 C-NT2RM4000534  
 C-NT2RM4000603  
 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808  
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//2.7E-146//420aa//60%//P27550  
 25 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168  
 C-NT2RM4000689  
 C-NT2RM4000698  
 C-NT2RM4000700  
 C-NT2RM4000712//&quot;Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.&quot;//1E-  
 30 136//1104bp//77%//AF022789  
 C-NT2RM4000717  
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154  
 C-NT2RM4000734//&quot;Homo sapiens mRNA for KIAA0760 protein, partial cds.&quot;//0//2273bp//99%//  
 AB018303  
 35 C-NT2RM4000741//&quot;Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.&quot;//0//2184bp//99%//  
 D88208  
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676  
 C-NT2RM4000764  
 C-NT2RM4000778  
 40 C-NT2RM4000787  
 C-NT2RM4000790  
 C-NT2RM4000795//&quot;Homo sapiens mRNA for KIAA0951 protein, complete cds.&quot;//0//1847bp//96%//  
 AB023168  
 C-NT2RM4000796  
 45 C-NT2RM4000798//&quot;Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA,  
 complete cds.&quot;//0//2603bp//99%//AF084521  
 C-NT2RM4000813  
 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE  
 AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682  
 50 C-NT2RM4000833  
 C-NT2RM4000848  
 C-NT2RM4000852  
 C-NT2RM4000855  
 C-NT2RM4000887  
 55 C-NT2RM4000895  
 C-NT2RM4000950  
 C-NT2RM4000979  
 C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//

100%//AL050092  
 C-NT2RM4001032  
 C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%//Q06138  
 C-NT2RM4001054//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//3.1E-190//1315bp//81%//  
 5 AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//  
 165aa//33%//Q09820  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.9E-86//292aa//  
 48%//Q09417  
 10 C-NT2RM4001140//HOMEODOMAIN PROTEIN MSH-D.//1E-11//103aa//38%//Q01704  
 C-NT2RM4001151  
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q27969  
 C-NT2RM4001160  
 C-NT2RM4001187  
 15 C-NT2RM4001191//&quot;Homo sapiens clone 24963 mRNA sequence, complete cds.&quot;//0//1950bp//99%//  
 AF131737  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742  
 C-NT2RM4001203//&quot;Homo sapiens mRNA for KIAA0839 protein, partial cds.&quot;//0//3047bp//99%//  
 AB020646  
 20 C-NT2RM4001204//&quot;Homo sapiens mRNA for KIAA1089 protein, partial cds.&quot;//0//2349bp//99%//  
 AB029012  
 C-NT2RM4001217//&quot;Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds.&quot;//  
 7.3E-148//1409bp//72%//AF059611  
 C-NT2RM4001256//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//4.30E-55//  
 25 289bp//77%//AF129131  
 C-NT2RM4001258  
 C-NT2RM4001309  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676  
 30 C-NT2RM4001316//&quot;ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.3) (MCAD).&quot;//2.3E-31//334aa//30%//P08503  
 C-NT2RM4001320//&quot;Homo sapiens mRNA for Neuroblastoma, complete cds.&quot;//1.8E-39//728bp//64%//  
 D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626  
 35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.1E-  
 30//265aa//33%//P53742  
 C-NT2RM4001347//&quot;Homo sapiens NY-REN-25 antigen mRNA, partial cds.&quot;//0//2300bp//99%//  
 AF155103  
 C-NT2RM4001371//&quot;Homo sapiens IDN3 mRNA, partial cds.&quot;//0//2524bp//99%//AB019494  
 40 C-NT2RM4001382//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//2.2E-237//1079bp//  
 99%//AF098799  
 C-NT2RM4001384  
 C-NT2RM4001410  
 C-NT2RM4001411//&quot;Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA,  
 45 complete cds.&quot;//0//1962bp//87%//AF020526  
 C-NT2RM4001412//&quot;Homo sapiens nGAP mRNA, complete cds.&quot;//0//1918bp//99%//AF047711  
 C-NT2RM4001414  
 C-NT2RM4001437  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
 50 1.4E-118//444aa//46%//P73505  
 C-NT2RM4001454  
 C-NT2RM4001455  
 C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737  
 C-NT2RM4001489//&quot;Homo sapiens mRNA for KIAA0685 protein, complete cds.&quot;//0//1810bp//99%//  
 55 AB014585  
 C-NT2RM4001522  
 C-NT2RM4001557//&quot;Homo sapiens mRNA for KIAA1040 protein, partial cds.&quot;//0//1547bp//97%//  
 AB028963

C-NT2RM4001565  
 C-NT2RM4001566//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;//0//1900bp//99%//  
 AB029037  
 5 C-NT2RM4001582//&quot;Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.&quot;//  
 1.5E-284//1082bp//90%//AF071317  
 C-NT2RM4001592//&quot;Homo sapiens mRNA for KIAA1122 protein, partial cds.&quot;//0//2170bp//99%//  
 AB032948  
 C-NT2RM4001594  
 10 C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750  
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600  
 C-NT2RM4001629//&quot;MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG  
 3).&quot;//1.5E-93//278aa//38%//Q13368  
 C-NT2RM4001650  
 C-NT2RM4001662  
 15 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//  
 410aa//42%//P37339  
 C-NT2RM4001682  
 C-NT2RM4001710  
 20 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141  
 C-NT2RM4001715  
 C-NT2RM4001731//&quot;Homo sapiens mRNA for KIAA1004 protein, partial cds.&quot;//0//1922bp//100%//  
 AB023221  
 C-NT2RM4001746  
 C-NT2RM4001754  
 25 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//  
 58%//Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164  
 C-NT2RM4001810//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//2377bp//99%//  
 AB020670  
 30 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346  
 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//325aa//37%//P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%//  
 P51523  
 C-NT2RM4001836  
 35 C-NT2RM4001841//&quot;Homo sapiens mRNA for KIAA0920 protein, complete cds.&quot;//0//1861bp//98%//  
 AB023137  
 C-NT2RM4001842  
 C-NT2RM4001856  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779  
 40 C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711  
 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//  
 36%//Q15404  
 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486  
 C-NT2RM4001922//&quot;Homo-sapiens mRNA for KIAA0957 protein, complete cds.&quot;//0//2165bp//99%//  
 45 AB023174  
 C-NT2RM4001930//&quot;Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6)  
 mRNA, complete cds.&quot;//0//1930bp//99%//AF102851  
 C-NT2RM4001940//&quot;Homo sapiens timeless homolog mRNA, complete cds.&quot;//0//2087bp//99%//  
 AF098162  
 50 C-NT2RM4001953  
 C-NT2RM4001965  
 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330  
 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//  
 P51523  
 55 C-NT2RM4001984  
 C-NT2RM4001987//&quot;NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM  
 180) [CONTAINS: N-CAM 140].&quot;//3.2E-17//281aa//30%//P16170  
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1



INTERGENIC REGION.//6.9E-94//589aa//35%//P42935

C-NT2RM4002018

C-NT2RM4002034//&quot;Homo sapiens hiwi mRNA, partial cds.&quot;//1.9E-53//1585bp//60%//AF104260

C-NT2RM4002044

C-NT2RM4002054

C-NT2RM4002063//&quot;Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.&quot;//0//1865bp//99%//U82267

C-NT2RM4002066//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.&quot;//1.50E-211//1123bp//71%//AF117755

C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%//Q04652

C-NT2RM4002128

C-NT2RM4002140

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014

C-NT2RM4002161//&quot;Homo sapiens laforin (EPM2A) mRNA, complete cds.&quot;//0//2671bp//99%//AF084535

C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%//P21590

C-NT2RM4002189//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//6.2E-33//688aa//27%//P08640

C-NT2RM4002205//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//3E-37//122aa//72%//Q07803

C-NT2RM4002213//&quot;Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.&quot;//0//2452bp//100%//AF157028

C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%//P40809

C-NT2RM4002251//&quot;ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI).&quot;//2.2E-36//320aa//38%//P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %//P48778

C-NT2RM4002339

C-NT2RM4002344

C-NT2RM4002373//&quot;Homo sapiens mRNA for KIAA0649 protein, complete cds.&quot;//0//2666bp//99%//AB014549

C-NT2RM4002374

C-NT2RM4002383

C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.3E-29//275aa//30%//P27095

C-NT2RM4002438//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//1.1E-49//611bp//70%//AF129131

C-NT2RM4002446

C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//&quot;ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].&quot;//0.0000016//226aa//24%//P51515

C-NT2RM4002493

C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137

C-NT2RM4002558//&quot;Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.&quot;//0//1797bp//99%//AF055899

C-NT2RM4002567

C-NT2RM4002593

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%//032038

C-NT2RP1000324  
 C-NT2RP1000363//&quot;Homo sapiens mRNA for KIAA0638 protein, partial cds.&quot;//0//1345bp//99%//  
 AB014538  
 C-NT2RP1000418  
 5 C-NT2RP1000513//&quot;Human NifU-like protein (hNifU) mRNA, partial cds.&quot;//6.50E-171//516bp//99%//  
 U47101  
 C-NT2RP1000721  
 C-NT2RP1000730  
 C-NT2RP1000767  
 10 C-NT2RP1000836  
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//  
 33%//Q09531  
 C-NT2RP1000943  
 C-NT2RP1001033//&quot;Homo sapiens delta-tubulin mRNA, complete cds.&quot;//2.10E-285//1290bp//100%//  
 15 AF201333  
 C-NT2RP1001073//&quot;Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.  
 &quot;//8.1E-107//504bp//99%//AF182291  
 C-NT2RP1001199  
 C-NT2RP1001248  
 20 C-NT2RP1001253//&quot;Homo sapiens oscillin (hLn) mRNA, complete cds.&quot;//0//2020bp//99%//AF029914  
 C-NT2RP1001286  
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024  
 C-NT2RP1001310//&quot;Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear  
 25 gene for mitochondrial product.&quot;//0//1732bp//99%//AF176006  
 C-NT2RP1001361//&quot;Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA,  
 complete cds.&quot;//6.5E-116//541bp//100%//AF070652  
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22//  
 284aa//25%//P40074  
 30 C-NT2RP1001432  
 C-NT2RP2000040//&quot;Homo sapiens mRNA for KIAA0747 protein, partial cds.&quot;//0//2648bp//99%//  
 AB013290  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%//  
 AJ242730  
 35 C-NT2RP2000098  
 C-NT2RP2000108  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD  
 SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//  
 40 7.1E-12//213aa//23%//P35251  
 C-NT2RP2000289  
 C-NT2RP2000327  
 C-NT2RP2000337  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910  
 45 C-NT2RP2000459  
 C-NT2RP2000498  
 C-NT2RP2000758  
 C-NT2RP2001137  
 C-NT2RP2001149  
 50 C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370  
 C-NT2RP2001173//&quot;Homo sapiens mRNA for KIAA0480 protein, complete cds.&quot;//0//1780bp//99%//  
 AB007949  
 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLGCF46.1 (FRAGMENT).//6E-10//88aa//38%//  
 P18722  
 55 C-NT2RP2001196  
 C-NT2RP2001226  
 C-NT2RP2001268//&quot;Homo sapiens mRNA for KIAA0810 protein, partial cds.&quot;//0//3301bp//98%//  
 AB018353

C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG)  
 (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%/P28663  
 C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%/P20107  
 C-NT2RP2001312  
 5 C-NT2RP2001327//&quot;TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12  
 PROTEIN).&quot;//5.5E-116//311aa//71%/Q13829  
 C-NT2RP2001328  
 C-NT2RP2001366  
 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%/Q02817  
 10 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//  
 581aa//54%/P93647  
 C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y18004  
 C-NT2RP2001420//&quot;Mus musculus nuclear protein NIP45 mRNA, complete cds.&quot;//9E-112//742bp//  
 82%/U76759  
 15 C-NT2RP2001450  
 C-NT2RP2001467  
 C-NT2RP2001506  
 C-NT2RP2001511//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//3.2E-  
 297//2206bp//75 %//AF093097  
 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%/Y14494  
 C-NT2RP2001536//&quot;Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete  
 cds.&quot;//0//2326bp//99%/AF035586  
 C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%/Q60992  
 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.2E-29//294aa//  
 25 31%/Q09837  
 C-NT2RP2001581  
 C-NT2RP2001597//&quot;RYANODINE RECEPTOR, CARDIAC MUSCLE.&quot;//0.000000036//127aa//36%/P30957  
 C-NT2RP2001628  
 30 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-  
 GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%/P42897  
 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-  
 PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANS-  
 FERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%/P14324  
 35 C-NT2RP2001813  
 C-NT2RP2001883//&quot;Homo sapiens CGI-01 protein mRNA, complete cds.&quot;//0//2306bp//99%/AF132936  
 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%/P53946  
 C-NT2RP2001947  
 40 C-NT2RP2001985//&quot;Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein  
 E6TP1 alpha mRNA, complete cds.&quot;//2.00E-38//435bp//67%/AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%/Q08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//  
 45 1.7E-47//247aa//52%/P35331  
 C-NT2RP2002058//&quot;Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.&quot;//0//  
 2510bp//99%/AF083217  
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7//1.5E-294//1334bp//99%/AF052183  
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%/P18490  
 50 C-NT2RP2002079//&quot;HISTONE H1, GONADAL.&quot;//4.4E-11//214aa//34%/P02256  
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%/AJ007509  
 C-NT2RP2002185//&quot;Homo sapiens ubiquilin mRNA, complete cds.&quot;//0//1789bp//99%/AF176069  
 C-NT2RP2002193//&quot;Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.  
 &quot;//0//2809bp//99%/AB021868  
 55 C-NT2RP2002231  
 C-NT2RP2002235  
 C-NT2RP2002252//&quot;Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.&quot;//0//3118bp//  
 91%/L38621

C-NT2RP2002292  
 C-NT2RP2002408  
 C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037  
 5 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171aa//27%//P30620  
 C-NT2RP2002498  
 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386  
 C-NT2RP2002520//&quot;Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.&quot;//3.70E-34//668bp//61%//AF105427  
 C-NT2RP2002549  
 10 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
 C-NT2RP2002706  
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194  
 C-NT2RP2002800  
 15 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922  
 C-NT2RP2002891  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%//Q18964  
 C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737  
 20 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
 C-NT2RP2003034  
 C-NT2RP2003099  
 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117  
 25 C-NT2RP2003157//&quot;Homo sapiens CGI-74 protein mRNA, complete cds.&quot;//0//2037bp//99%//AF151832  
 C-NT2RP2003158//&quot;Homo sapiens mRNA for proteasome subunit p58, complete cds.&quot;//0//2091bp//99%//D67025  
 C-NT2RP2003165  
 30 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
 C-NT2RP2003277//&quot;Homo sapiens mRNA for KIAA0625 protein, partial cds.&quot;//0//3788bp//99%//AB014525  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400  
 35 C-NT2RP2003297  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886  
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754  
 40 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769  
 C-NT2RP2003393  
 C-NT2RP2003445  
 C-NT2RP2003466//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;7//0//2194bp//99%//AF126799  
 45 C-NT2RP2003480//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.&quot;//0//3012bp//99%//AF125158  
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%//P04175  
 50 C-NT2RP2003511  
 C-NT2RP2003513//&quot;Human mRNA for KIAA0270 gene, partial cds.&quot;//0//2137bp//97%//D87460  
 C-NT2RP2003567//&quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&quot;//0//2343bp//99%//AB007931  
 C-NT2RP2003604//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//2442bp//99%//AF030233  
 55 C-NT2RP2003691  
 C-NT2RP2003713//&quot;Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.&quot;//0//2018bp//99%//AF073344

C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//  
 80%//P53620  
 C-NT2RP2003764  
 C-NT2RP2003769  
 5 C-NT2RP2003777  
 C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%//  
 Q11076  
 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//  
 0.00000016//117aa//29%//Q91955  
 10 C-NT2RP2003981//&quot;Homo sapiens mRNA for KIAA0804 protein, partial cds.&quot;//0//3046bp//99%//  
 AB018347  
 C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//  
 99%//AL050367  
 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599  
 15 C-NT2RP2004066//&quot;Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete  
 sequence.&quot;//0//2410bp//99%//AL034555  
 C-NT2RP2004081  
 C-NT2RP2004124  
 C-NT2RP2004152  
 20 C-NT2RP2004165  
 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-  
 31//424aa//28%//007231  
 C-NT2RP2004239//&quot;Homo sapiens lok mRNA for protein kinase, complete cds.&quot;//0//3044bp//99%//  
 AB015718  
 25 C-NT2RP2004245  
 C-NT2RP2004364  
 C-NT2RP2004365  
 C-NT2RP2004366//&quot;Homo sapiens mRNA for KIAA0986 protein, partial cds.&quot;//0//2790bp//97%//  
 AB023203  
 30 C-NT2RP2004373  
 C-NT2RP2004476//&quot;Homo sapiens cyclin L ania-6a mRNA, complete cds.&quot;//0//2075bp//99%//  
 AF180920  
 C-NT2RP2004551  
 C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903  
 35 C-NT2RP2004600  
 C-NT2RP2004664//&quot;Homo sapiens mRNA for KIAA0460 protein, partial cds.&quot;//0//2368bp//99%//  
 AB007929  
 C-NT2RP2004743  
 C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//  
 40 190aa//41-%//P38692  
 C-NT2RP2004816//&quot;Homo sapiens H beta 58 homolog mRNA, complete cds.&quot;//0//2144bp//96%//  
 AF054179  
 C-NT2RP2004861  
 C-NT2RP2004897  
 45 C-NT2RP2004933//&quot;Homo sapiens mRNA for ZIP-kinase, complete cds.&quot;//0//2103bp//99%//AB007144  
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386  
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)  
 (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%//  
 Q92089  
 50 C-NT2RP2005162//&quot;Homo sapiens aspartyl aminopeptidase mRNA, complete cds.&quot;//0//1615bp//99%//  
 AF005050  
 C-NT2RP2005204//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.  
 &quot;//0//1262bp//99%//AF090385  
 C-NT2RP2005227  
 55 C-NT2RP2005287  
 C-NT2RP2005288//&quot;Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.&quot;//0//  
 2992bp//99%//AF060219  
 C-NT2RP2005490//&quot;Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.&quot;//1.8E-175//1102bp//

83%//AF053628

C-NT2RP2005539//&amp;quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&amp;quot;//0//1560bp//99%//AB020657

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYC-  
OSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053

C-NT2RP2005722//&amp;quot;Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.&amp;quot;//0//2545bp//99%//AB011414

C-NT2RP2005732

C-NT2RP2005784//&quot;Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete  
cds.&quot;//0//2191bp//92%//AF155120C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//  
318aa//31%//P40004C-NT2RP2005859//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//1649bp//99%//  
AB020670

C-NT2RP2006023

C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//  
AL080155

C-NT2RP2006441

C-NT2RP3000002

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//  
53%//Q05481

C-NT2RP3000055

C-NT2RP3000068

C-NT2RP3000080

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN  
CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//  
P46401

C-NT2RP3000092

C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692

C-NT2RP3000134

C-NT2RP3000149

C-NT2RP3000197

C-NT2RP3000207//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLU-  
COSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//2.9E-11//721aa//23%//P08640C-NT2RP3000233//&quot;Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a  
novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of  
proteins. Contains ESTs and GSSs, complete sequence.&quot;//0//1462bp//99%//AL035424

C-NT2RP3000235

C-NT2RP3000247

C-NT2RP3000267

C-NT2RP3000299//&quot;Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.&quot;//0//  
2730bp//82%//D29766

C-NT2RP3000324

C-NT2RP3000341//&quot;Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA,  
nuclear gene encoding mitochondrial protein, complete cds.&quot;//1.5E-246//1124bp//99%//AF106622C-NT2RP3000393//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//  
5.8E-266//1373bp//86%//AF061817C-NT2RP3000441//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA,  
complete cds.&quot;//3.40E-42//645bp//67%//AF098066

C-NT2RP3000449

C-NT2RP3000451

C-NT2RP3000456

C-NT2RP3000542

C-NT2RP3000561

C-NT2RP3000562//&quot;Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.&quot;//0//  
2165bp//99%//AF093097

C-NT2RP3000578//HES1 PROTEIN.//1.3E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

C-NT2RP3000592  
 C-NT2RP3000622  
 C-NT2RP3000624  
 C-NT2RP3000685  
 5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//014153  
 C-NT2RP3000742//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA  
 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).&quot;//4.1E-165//  
 371aa//49%//P10895  
 C-NT2RP3000753  
 10 C-NT2RP3000826  
 C-NT2RP3000865  
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426  
 C-NT2RP3001007  
 C-NT2RP3001055  
 15 C-NT2RP300111//&quot;Homo sapiens TRF-proximal protein mRNA, complete cds.&quot;//1.50E-149//731bp//  
 97%//AF097725  
 C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737  
 C-NT2RP3001126  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154  
 20 C-NT2RP3001232  
 C-NT2RP3001268//&quot;Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.&quot;//0//  
 3606bp//99%//AF198358  
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//  
 1.3E-99//669bp//83%//Y18101  
 25 C-NT2RP3001274//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;//0//2254bp//99%//  
 AB028960  
 C-NT2RP3001281  
 C-NT2RP3001297  
 C-NT2RP3001318  
 30 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508  
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089  
 C-NT2RP3001374  
 C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270  
 35 C-NT2RP3001432  
 C-NT2RP3001447  
 C-NT2RP3001449//&quot;Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the  
 alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A,  
 -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA,  
 40 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal  
 Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)  
 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G  
 protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 complete sequence.&quot;//0//1827bp//99%//AL031282  
 45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-  
 ER 2).//3.2E-90//157aa//59%//P36371  
 C-NT2RP3001459  
 C-NT2RP3001527//&quot;Human Spl40 protein (Spl40) mRNA, complete cds.&quot;//4.3E-290//793bp//93%//  
 U63420  
 50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II.//9.10E-10//158aa//  
 31%//Q10022  
 C-NT2RP3001580//&quot;Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.&quot;//  
 0//1730bp//85%//AF163665  
 C-NT2RP3001587//&quot;Human anthracycline-associated resistance ARX mRNA, complete cds.&quot;//0//  
 55 2617bp//99%//U35832  
 C-NT2RP3001589  
 C-NT2RP3001607  
 C-NT2RP3001608

C-NT2RP3001671//&quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&quot;//0//2310bp//99%//  
 AB020657  
 C-NT2RP3001672//&quot;Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete  
 cds.&quot;//0//2836bp//99%//AF149046  
 5 C-NT2RP3001678  
 C-NT2RP3001688//&quot;Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA,  
 complete cds.&quot;//0//1695bp//99%//AF099013  
 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//  
 P25386  
 10 C-NT2RP3001698  
 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%//P54356  
 C-NT2RP3001716  
 C-NT2RP3001752  
 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//  
 15 55%//P52272  
 C-NT2RP3001844  
 C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//  
 99%//AL050011  
 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.1E-125//302aa//  
 20 60%//P55347  
 C-NT2RP3001898//&quot;Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-  
 1,4-N-acetylglucosaminyltransferase IV, complete cds.&quot;//0//1587bp//100%//AB000624  
 C-NT2RP3001931  
 C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709  
 25 C-NT2RP3002002  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-19211475bp//94%//X86779  
 C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//  
 48%//Q09232  
 30 C-NT2RP3002045//&quot;Homo sapiens mRNA for KIAA0899 protein, partial cds.&quot;//0//33 85bp//99%//  
 AB020706  
 C-NT2RP3002056//&quot;Homo sapiens Rb binding protein homolog mRNA, partial cds.&quot;//0//2374bp//99%//  
 AF083249  
 C-NT2RP3002062//&quot;Homo sapiens mRNA for KIAA0873 protein, partial cds.&quot;//0//3764bp//99%//  
 35 AB020680  
 C-NT2RP3002081//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//4.1E-233//1896bp//69%//AF111423  
 C-NT2RP3002097  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387  
 40 C-NT2RP3002142  
 C-NT2RP3002146  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN  
 GST1-HS).//2.8E-253//474aa//93%//P15170  
 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7//1.9E-151//223aa//91%//Q02614  
 45 C-NT2RP3002166  
 C-NT2RP3002181  
 C-NT2RP3002244  
 C-NT2RP3002248  
 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978  
 50 C-NT2RP3002276  
 C-NT2RP3002304  
 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//  
 3.70E-43//318aa//37%//P05792  
 C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%//AJ133421  
 55 C-NT2RP3002566  
 C-NT2RP3002587  
 C-NT2RP3002590  
 C-NT2RP3002631



C-NT2RP3002650//&quot;Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.&quot;//0//2109bp//87%//AF165163  
 C-NT2RP3002663//&quot;Homo sapiens putative glycolipid transfer protein mRNA, complete cds.&quot;//8.10E-263//1243bp//97%//AF103731  
 5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060  
 C-NT2RP3002763  
 C-NT2RP3002861  
 C-NT2RP3002911  
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%//Q04652  
 10 C-NT2RP3002953//&quot;Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.&quot;//0//2388bp//99%//AF152498  
 C-NT2RP3002988//&quot;Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.&quot;//1.8E-292//1325bp//99%//AF080158  
 C-NT2RP3003008  
 15 C-NT2RP3003101//&quot;Mouse mRNA for tetracycline transporter-like protein, complete cds.&quot;//3.6E-83//807bp//72%//D88315  
 C-NT2RP3003204  
 C-NT2RP3003278  
 C-NT2RP3003282//&quot;Homo sapiens dynamin (DNM) mRNA, complete cds.&quot;//0//2596bp//98%//L36983  
 20 C-NT2RP3003290//&quot;Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.&quot;//1.5e-310//1468bp//82%//AB033922  
 C-NT2RP3003302  
 C-NT2RP3003313//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.&quot;//0//2476bp//99%//AF117657  
 25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//1.3E-35//178aa//44%//Q62191  
 C-NT2RP3003344  
 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084  
 30 C-NT2RP3003377  
 C-NT2RP3003385//&quot;Mus musculus SKD3 mRNA, complete cds.&quot;//0//2133bp//85%//U09874  
 C-NT2RP3003433  
 C-NT2RP3003490//&quot;Homo sapiens mRNA for KIAA0725 protein, partial cds.&quot;//0//2437bp//99%//AB018268  
 35 C-NT2RP3003491//&quot;Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.&quot;//5.6E-36//842bp//62%//AF091624  
 C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886  
 C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820  
 40 C-NT2RP3004209//&quot;Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.&quot;//0//2320bp//99%//AF126736  
 C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%//P52734  
 C-NT2RP3004246  
 45 C-NT2RP3004258//&quot;Homo sapiens ZIS1 mRNA, complete cds.&quot;//0//1861bp//99%//AF065391  
 C-NT2RP3004262//&quot;Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.&quot;//2.4E-248//1126bp//100%//AF088982  
 C-NT2RP3004341  
 C-NT2RP3004378  
 50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798  
 C-NT2RP3004428  
 C-NT2RP3004451  
 C-NT2RP3004454//&quot;Homo sapiens mRNA for KIAA0448 protein, complete cds.&quot;//0//2875bp//99%//AB007917  
 55 C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820  
 C-NT2RP3004498//&quot;Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.&quot;//2E-249//1777bp//80%//U83176  
 C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%//P40484  
 C-NT2RP3004534//&quot;Mouse oncogene (ect2) mRNA, complete cds.&quot;//0//2075bp//87%//L11316  
 C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%//P33755  
 5 C-NT2RP4000907//&quot;Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.&quot;//0//  
 2127bp//86%//D45913  
 C-NT2RP4001029//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//0//1711bp//  
 90%//U20086  
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//  
 186aa//29%//O24076  
 10 C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%//P35844  
 C-NT2RP4001442  
 C-NT2RP4001529//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//1.70E-255//  
 1148bp//90%//U20086  
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//  
 15 P12868  
 C-OVARC1000106//&quot;TROPOMYOSIN 1, FUSION PROTEIN 33.&quot;//0.000032//165aa//27%//P49455  
 C-OVARC1000198  
 C-OVARC1000682//&quot;PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSI-  
 DASE 1B).&quot;//1.1E-209//293aa//95%//P39098  
 20 C-OVARC1000703  
 C-OVARC1000722//&quot;Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, com-  
 plete cds.&quot;//0//759bp//98%//AF038661  
 C-OVARC1000730  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159  
 25 C-OVARC1000781  
 C-OVARC1000787  
 C-OVARC10008347//Homo sapiens mRNA for atopy related autoantigen CALCJ/2.8E-258//1183bp//99%//Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199  
 C-OVARC1000850//&quot;Homo sapiens PB39 mRNA, complete cds.&quot;//0//2095bp//99%//AF045584  
 30 C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P40484  
 C-OVARC1000883  
 C-OVARC1000886  
 C-OVARC1000912  
 35 C-OVARC1000915//&quot;Homo sapiens histone deacetylase 5 mRNA, complete cds.&quot;//1.60E-121//591bp//  
 97%//AF132608  
 C-OVARC1000924  
 C-OVARC1000964  
 C-OVARC1000984  
 40 C-OVARC1001004  
 C-OVARC1001010  
 C-OVARC1001011  
 C-OVARC1001032  
 C-OVARC1001044  
 45 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%//P43490  
 C-OVARC1001068//&quot;Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.&quot;//0//1819bp//  
 99%//AF082657  
 C-OVARC1001074  
 C-OVARC1001092//&quot;Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,  
 50 LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).&quot;//2E-214//769bp//97%//  
 AJ005897  
 C-OVARC1001107//&quot;Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.&quot;//6.1E-  
 276//594bp//98%//AF167572  
 C-OVARC1001154//&quot;Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.&quot;//2.3E-296//  
 55 1561bp//93%//AF055008  
 C-OVARC1001161  
 C-OVARC1001167  
 C-OVARC1001170

C-OVARC1001171//&quot;Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.&quot;  
 //5.7E-151//436bp//92%//U94855  
 C-OVARC1001173  
 C-OVARC1001176  
 5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510  
 C-OVARC1001188  
 C-OVARC1001232//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
 (CPSF 100 KD SUBUNIT).&quot;//5.10E-22//83aa//37%//Q10568  
 C-OVARC1001270  
 10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//  
 0.0000014//224aa//26%//P25976  
 C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444  
 C-OVARC1001344  
 C-OVARC1001369  
 15 C-OVARC1001372//&quot;Homo sapiens mRNA for KIAA0897 protein, partial cds.&quot;//0//840bp//97%//  
 AB020704  
 C-OVARC1001391  
 C-OVARC1001399  
 C-OVARC1001417//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component  
 20 TRAP170 mRNA, complete cds.&quot;//0//1715bp//99%//AF135802  
 C-OVARC1001419//&quot;Homo sapiens GOK (STIM1) mRNA, complete cds.&quot;//4.9E-48//586bp//69%//  
 U52426  
 C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111  
 C-OVARC1001453  
 25 C-OVARC1001476//&quot;Mus musculus YGR163w mRNA homologue, complete cds.&quot;//1.80E-187//  
 510bp//89%//AB017616  
 C-OVARC1001480  
 C-OVARC1001489  
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
 30 PROTEIN 1).//0//777aa//91%//P98161  
 C-OVARC1001525  
 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081  
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//  
 AF031165  
 35 C-OVARC1001600  
 C-OVARC1001610//&quot;Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete  
 cds.&quot;//0//1870bp//99%//AF068302  
 C-OVARC1001702  
 C-OVARC1001703//&quot;Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.&quot;//3.5E-  
 40 16//399bp//61%//AF133670  
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//  
 38%//Q62267  
 C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
 AZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106  
 45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796  
 C-OVARC1001731//&quot;TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.&quot;//4E-122//  
 282aa//85%//P08942  
 C-OVARC1001745  
 C-OVARC1001762//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
 50 AMINO, ACETYLTRANSFERASE 1).&quot;//6.4E-85//514aa//34%//P12945  
 C-OVARC1001766//&quot;Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete  
 cds.&quot;//0//963bp//99%//U97670  
 C-OVARC1001767//&quot;Homo sapiens mRNA for KIAA0675 protein, complete cds.&quot;//0//2083bp//99%//  
 AB014575  
 55 C-OVARC1001768  
 C-OVARC1001791  
 C-OVARC1001795  
 C-OVARC1001802

C-OVARC1001809//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//2.7E-190//  
 1624bp//76%//AF068748  
 C-OVARC1001828  
 C-OVARC1001846  
 5 C-OVARC1001861  
 C-OVARC1001879  
 C-OVARC1001880  
 C-OVARC1001883  
 C-OVARC1001916  
 10 C-OVARC1001928  
 C-OVARC1001942//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
 AMINO, ACETYLTRANSFERASE 1).&quot;//3.1E-81//497aa//35%//P12945  
 C-OVARC1001943//&quot;Mus musculus DEBT-91 mRNA, complete cds.&quot;//0//2035bp//87%//AF143859  
 C-OVARC1001950  
 15 C-OVARC1001987//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//  
 2.3E-220//652bp//84%//AF061817  
 C-OVARC1002050//&quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&quot;//0//  
 1019bp//99%//AB029290  
 C-OVARC1002082  
 20 C-OVARC1002107  
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
 ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//  
 035913  
 C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955  
 25 C-OVARC1002156  
 C-OVARC1002158  
 C-PLACE1000004//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//0//2365bp//99%//AB019602  
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643  
 C-PLACE1000048  
 30 C-PLACE1000050  
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154  
 C-PLACE1000081//&quot;Human SEC7 homolog Tic (TIC) mRNA, complete cds.&quot;//0//2077bp//99%//  
 U63127  
 C-PLACE1000094  
 35 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.8E-62//158aa//81%//P20290  
 C-PLACE1000214  
 C-PLACE1000236  
 C-PLACE1000246  
 40 C-PLACE1000292  
 C-PLACE1000308  
 C-PLACE1000332  
 C-PLACE1000453  
 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//  
 45 P51522  
 C-PLACE1000599  
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918  
 C-PLACE1000653//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//  
 0//1992bp//99%//AF180371  
 50 C-PLACE1000656//&quot;Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and  
 LLNLc110F1857Q7 (RZPD Berlin)).&quot;//2.1E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//&quot;Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.&quot;//  
 0//1366bp//99%//AF119043  
 C-PLACE1000712  
 55 C-PLACE1000749  
 C-PLACE1000769//&quot;Homo sapiens CGI-18 protein mRNA, complete cds.&quot;//0//1985bp//98%//  
 AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734

C-PLACE1000849

C-PLACE1000856//&quot;Homo sapiens mRNA for KIAA0974 protein, partial cds.&quot;//0//1310bp//100%//AB023191

C-PLACE1000931

C-PLACE1000987//&quot;Homo sapiens mRNA for KIAA0724 protein, complete cds.&quot;//0//1749bp//99%//AB018267

C-PLACE1001010

C-PLACE1001015

C-PLACE1001024

C-PLACE1001062//&quot;Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence.&quot;//2.7E-32//470bp//71%//AC006020

C-PLACE1001104

C-PLACE1001168

C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496

C-PLACE1001185//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//1668bp//99%//AB023160

C-PLACE1001238//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//2E-202//1333bp//80%//D14336

C-PLACE1001280

C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X71642

C-PLACE1001304//&quot;Homo sapiens zinc finger protein dp mRNA, complete cds.&quot;//0//2421bp//99%//AF153201

C-PLACE1001311

C-PLACE1001323

C-PLACE1001351

C-PLACE1001414

C-PLACE1001440

C-PLACE1001456

C-PLACE1001517//&quot;Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.&quot;//4.60E-112//392bp//87%//AB002137

C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809

C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//P51523

C-PLACE1001634

C-PLACE1001640

C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408

C-PLACE1001705

C-PLACE1001716

C-PLACE1001720

C-PLACE1001745

C-PLACE1001748//&quot;Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.&quot;//0//2602bp//99%//AF061243

C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein

TRP6.//0//2900bp//99%//AJ006276

C-PLACE1001799

C-PLACE1001845//&quot;Mus musculus cyclin ania-6a mRNA, complete cds.&quot;//3.30E-31//925bp//62%//AF159159

C-PLACE1001897

C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//076094

C-PLACE1002157

C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591

C-PLACE1002227

C-PLACE1002259

C-PLACE1002319

C-PLACE1002395//&quot;Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.&quot;//7.9E-

100//966bp//75%//AB030505  
 C-PLACE1002477  
 C-PLACE1002493//"Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.  
 "//1.7E-113//545bp//98%//AF042273  
 5 C-PLACE1002500  
 C-PLACE1002514  
 C-PLACE1002532//HOMEBOX PROTEIN DLX-5//1.2E-152//289aa//96%//P70396  
 C-PLACE1002537  
 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E//5E-99//386aa//48%//P45890  
 10 C-PLACE10025 83//"GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE  
 RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT)."//5.6E-34//  
 76aa//98%//P39087  
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-)//5.5E-17//76aa//56%//P45340  
 C-PLACE1002625  
 15 C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC)//2.5E-278//543aa//92%//Q28046  
 C-PLACE1002768  
 C-PLACE1002782//"Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds."//3.8E-43//  
 385bp//77%//U50927  
 C-PLACE1002816//HISTONE DEACETYLASE HDA1//2.20E-48//217aa//46%//P53973  
 20 C-PLACE1002853  
 C-PLACE1002908//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//0//  
 1654bp//99%//AB028600  
 C-PLACE1002962  
 C-PLACE1002968  
 25 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4)//1.4E-78//496aa//37%//Q49091  
 C-PLACE1003025  
 C-PLACE1003027//"Homo sapiens mRNA for KIAA0516 protein, partial cds."//2.1e-314//1417bp//  
 100%//AB011088  
 C-PLACE1003044//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//1382bp//96%//  
 30 AB020636  
 C-PLACE1003176  
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001//4.9E-76//309aa//47%//  
 Q15391  
 C-PLACE1003256  
 35 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN//7.9E-22//70aa//47%//P21541  
 C-PLACE1003343  
 C-PLACE1003361  
 C-PLACE1003366//"Homo sapiens otoferlin (OTOF) mRNA, complete cds."//1.4E-78//542bp//67%//  
 AF107403  
 40 C-PLACE1003373  
 C-PLACE1003375  
 C-PLACE1003394//"Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds."//2.30E-150//  
 774bp//94%//M83680  
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//1.3E-40//278aa//36%//P40556  
 45 C-PLACE1003454  
 C-PLACE1003478  
 C-PLACE1003516  
 C-PLACE1003519//H.sapiens hnRNP-E2 mRNA//5.1E-218//905bp//99%//X78136  
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//0.0000011//101aa//32%//  
 50 Q09475  
 C-PLACE1003528  
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-  
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
 NENT)//7.7E-68//404aa//33%//P32802  
 55 C-PLACE1003566  
 C-PLACE1003584  
 C-PLACE1003593  
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL

ACTIVATOR.//0.00000023//82aa//35%//Q02516  
C-PLACE1003618  
C-PLACE1003638  
C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742  
5 C-PLACE1003760//&quot;Homo sapiens tetraspanin TM4-A mRNA, complete cds.&quot;//5.2E-289//1313bp//  
97%//AF133423  
C-PLACE1003768  
C-PLACE1003795  
C-PLACE1003886  
10 C-PLACE1003888//&quot;Homo sapiens mRNA for KIAA1092 protein, partial cds.&quot;//0//2057bp//99%//  
AB029015  
C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//  
584aa//74%//P17812  
C-PLACE1003915//&quot;PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (AR-  
15 GININE- -TRNA LIGASE) (ARGRS).&quot;//2.4E-108//581aa//40%//Q05506  
C-PLACE1004118  
C-PLACE1004256//&quot;Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.&quot;//  
2E-93//960bp//76%//AF115778  
C-PLACE1004274  
20 C-PLACE1004284  
C-PLACE1005331  
C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//  
99%//AL050267  
C-PLACE1005828  
25 C-PLACE1005876//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
(CPSF 100 KD SUBUNIT).&quot;//0//730aa//99%//Q10568  
C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069  
C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
30 (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//  
30%//P98110  
C-PLACE1007053  
C-PLACE1007068  
C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652  
C-PLACE1009921  
35 C-PLACE1010401  
C-PLACE1010856  
C-PLACE1010857  
C-PLACE1010917  
C-PLACE1010925  
40 C-PLACE1010926//&quot;Homo sapiens mRNA for KIAA0554 protein, partial cds.&quot;//0//1160bp//100%//  
AB011126  
C-PLACE1010942//&quot;Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.&quot;//0//1440bp//  
99%//AF114487  
C-PLACE1010944  
45 C-PLACE1010954  
C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890  
C-PLACE1011026  
C-PLACE1011046//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1  
50 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).&quot;//0//646aa//97%//P10894  
C-PLACE1011054  
C-PLACE1011057  
C-PLACE1011109//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//1.50E-  
22//63aa//88%//Q07803  
C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532  
55 C-PLACE1011133  
C-PLACE1011143  
C-PLACE1011165  
C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.-)//3.2E-12//212aa//29%//Q03326  
 C-PLACE1011221  
 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp564O043)//0//2487bp//  
 99%//AL050390  
 5 C-PLACE1011325  
 C-PLACE1011332//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//  
 7.2E-151//697bp//99%//AF102265  
 C-PLACE1011340//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//1.20E-74//380bp//97%//  
 AB019602  
 10 C-PLACE1011399//&quot;Homo sapiens CGI-72 protein mRNA, complete cds.&quot;//3.2E-90//427bp//99%//  
 AF151830  
 C-PLACE1011433//&quot;Homo sapiens mRNA for KIAA0530 protein, partial cds.&quot;//0//1946bp//99%//  
 AB011102  
 C-PLACE1011452  
 15 C-PLACE1011465  
 C-PLACE1011472//&quot;Homo sapiens mRNA for KIAA0712 protein, complete cds.&quot;//0//2022bp//99%//  
 AB018255  
 C-PLACE1011477//&quot;Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.&quot;//0//2040bp//99%//  
 AF065482  
 20 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//  
 4.90E-11//147aa//32%//P52178  
 C-PLACE1011520  
 C-PLACE1011563  
 C-PLACE1011567  
 25 C-PLACE1011576//&quot;Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.&quot;//0//  
 1791bp//82%//L11672  
 C-PLACE1011586  
 C-PLACE1011643  
 C-PLACE1011649  
 30 C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%//P17886  
 C-PLACE1011682  
 C-PLACE1011719  
 C-PLACE1011729  
 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//  
 35 99%//AL050287  
 C-PLACE1011874  
 C-PLACE1011875//&quot;Homo sapiens mRNA for KIAA0580 protein, partial cds.&quot;//4.1E-112//524bp//  
 100%//AB011152  
 C-PLACE1011923//&quot;Homo sapiens serum-inducible kinase mRNA, complete cds.&quot;//0//2782bp//99%//  
 40 AF059617  
 C-PLACE1011982  
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%//  
 Q09475  
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 45 EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%//P42566  
 C-PLACE2000017  
 C-PLACE2000021//&quot;Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, com-  
 plete cds.&quot;//2.7E-107//981bp//74%//AF082556  
 C-PLACE2000047  
 50 C-PLACE2000062//&quot;Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type  
 lectin, complete cds, clone:HP01347.&quot;//6.3E-166//656bp//94%//AB015629  
 C-PLACE2000100  
 C-PLACE2000111  
 C-PLACE2000172  
 55 C-PLACE2000187  
 C-PLACE2000216//&quot;Dog nonerythroid beta-spectrin mRNA, 3' end.&quot;//3.2E-253//1799bp//83%//L02897  
 C-PLACE2000246//&quot;Homo sapiens mRNA for KIAA0795 protein, partial cds.&quot;//4.60E-172//796bp//  
 99%//AB018338



C-PLACE2000317  
 C-PLACE2000341//&quot;Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete  
 cds.&quot;//0//1554bp//99%//AF069307  
 C-PLACE2000366  
 5 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446  
 C-PLACE2000394  
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//  
 90aa//98%//P10586  
 C-PLACE2000411//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;//0//2515bp//99%//  
 10 AB028960  
 C-PLACE2000425  
 C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333  
 C-PLACE2000433  
 C-PLACE2000438//&quot;POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-  
 15 TEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALAC-  
 TOSAMINYLTRANSFERASE)(GALNAC-T1).&quot;//2.1E-86//348aa//41%//Q10472  
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25//  
 165aa//40%//P33450  
 C-PLACE2000477//&quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&quot;//6.7E-  
 20 127//671bp//94%//AF072733  
 C-PLACE3000009  
 C-PLACE3000020//&quot;Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.&quot;//0//  
 2253bp//99%//AF033861  
 C-PLACE3000103  
 25 C-PLACE3000142  
 C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205  
 C-PLACE3000156  
 C-PLACE3000157  
 C-PLACE3000197  
 30 C-PLACE3000208  
 C-PLACE3000226//&quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;//0//4805bp//99%//  
 AB023179  
 C-PLACE3000242//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;//0//2786bp//96%//  
 AB029037  
 35 C-PLACE3000363  
 C-PLACE3000405  
 C-PLACE3000416//&quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&quot;//1.80E-  
 141//565bp//98%//AB029290  
 C-PLACE3000477  
 40 C-PLACE4000106//&quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&quot;//0//6702bp//99%//  
 AB007931  
 C-PLACE4000323  
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT  
 SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771  
 45 C-PLACE4000369//&quot;Homo sapiens mRNA for KIAA1025 protein, partial cds.&quot;//0//4830bp//99%//  
 AB028948  
 C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//  
 99%//AL080196  
 C-PLACE4000558//&quot;Homo sapiens mRNA for KIAA0729 protein, partial cds.&quot;//0//1051bp//97%//  
 50 AB018272  
 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1)  
 (UEGF-1).//9.3E-70//226aa//52%//P10079  
 C-PLACE4000593  
 C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 55 (EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414  
 C-PLACE4000670  
 C-THYRO1000026  
 C-THYRO1000085//&quot;PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.&quot;//2E-72//155aa//92%//

Q06710

C-THYRO1000107

C-THYRO1000111

C-THYRO1000132//&quot;Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.&quot;//1.1E-159//824bp//95%//U97018

C-THYRO1000156

C-THYRO1000173//&quot;Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.&quot;//0//1713bp//99%//AF020797

C-THYRO1000186

C-THYRO1000187

C-THYRO1000241

C-THYRO1000279

C-THYRO1000327//&quot;Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.&quot;//0//1567bp//99%//AF124145

C-THYRO1000452

C-THYRO1000471

C-THYRO1000484

C-THYRO1000502

C-THYRO1000505

C-THYRO1000585//&quot;Homo sapiens protein associated with Myc mRNA, complete cds.&quot;//0//1901bp//99%//AF075587

C-THYRO1000596

C-THYRO1000662//&quot;Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.&quot;//0//2341 bp//99%//AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889

C-THYRO1000715

C-THYRO1000734

C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171

C-THYRO1000756//&quot;ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).&quot;//1.8E-55//243aa//42%//Q64686

C-THYRO1000777

C-THYRO1000783//&quot;Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.&quot;//2.4E-157//1656bp//70%//U37373

C-THYRO1000787

C-THYRO1000793

C-THYRO1000796

C-THYRO1000843

C-THYRO1000852//&quot;Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds.&quot;//3.3E-147//790bp//93%//U68418

C-THYRO1000865

C-THYRO1000895

C-THYRO1000926//&quot;Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.&quot;//0//2387bp//99%//AF079529

C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550

C-THYRO1000952

C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132

C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491

C-THYRO1001031

C-THYRO1001062

C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168

C-THYRO1001133

C-THYRO1001134//&quot;Homo sapiens CGI-78 protein mRNA, complete cds.&quot;//0//1898bp//99%//AF151835

C-THYRO1001173

C-THYRO1001213  
 C-THYRO1001321  
 C-THYRO1001322  
 C-THYRO1001365  
 5 C-THYRO1001401  
 C-THYRO1001411  
 C-THYRO1001434  
 C-THYRO1001534  
 C-THYRO1001541  
 10 C-THYRO1001559  
 C-THYRO1001570  
 C-THYRO1001595  
 C-THYRO1001605  
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//  
 15 99%//AJ002190  
 C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-  
 273//1947bp//82%//AF175968  
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//  
 AJ225089  
 20 C-THYRO1001673  
 C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672  
 C-THYRO1001706  
 C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584  
 C-THYRO1001745  
 25 C-THYRO1001793  
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128  
 C-THYRO1001895  
 C-THYRO1001907  
 C-VESEN1000122  
 30 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916  
 C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//  
 1040bp//65%//U78521  
 C-Y79AA1000065  
 C-Y79AA1000131  
 35 C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//  
 AF132936  
 C-Y79AA1000202  
 C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//  
 345bp//100%//AF081192  
 40 C-Y79AA1000230  
 C-Y79AA1000258  
 C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207  
 C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910  
 C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25 %//Q93794  
 45 C-Y79AA1000355  
 C-Y79AA1000368//REDUCED VIABILTY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343  
 C-Y79AA1000420  
 C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-  
 plete cds."//8.30E-252//1207bp//85%//U41736  
 50 C-Y79AA1000480  
 C-Y79AA1000540  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT).//0//652aa//98%//P17427  
 55 C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801  
 C-Y79AA1000627//"Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds."//2E-287//203  
 lbp//82%//AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

C-Y79AA1000734//&quot;Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.&quot;/  
 0//1594bp//99%//AF093670  
 C-Y79AA1000748//&quot;Homo sapiens CGI-05 protein mRNA, complete cds.&quot;//1.9E-239//1367bp//91%//  
 AF152097  
 5 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//  
 4.9E-91//200aa//64%//Q61990  
 C-Y79AA1000774  
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3E-37//469aa//27%//P49902  
 10 C-Y79AA1000784//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//1.10E-236//1076bp//  
 99%//AF098799  
 C-Y79AA1000794//&quot;Homo sapiens actin-associated protein 2E4/kaptein (2E4) mRNA, 2E4-1 allele, complete  
 cds.&quot;//0//1610bp//99%//AF105369  
 C-Y79AA1000800//&quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&quot;//1.6E-  
 284//1288bp//99%//AF072733  
 15 C-Y79AA1000805  
 C-Y79AA1000824  
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209  
 C-Y79AA1000850  
 C-Y79AA1000962//&quot;MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).&quot;//  
 20 4.2E-17//430aa//27%//Q99323  
 C-Y79AA1000968//&quot;Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, com-  
 plete cds.&quot;//3.9E-248//1468bp//87%//U38253  
 C-Y79AA1000976  
 C-Y79AA1001023  
 25 C-Y79AA1001041  
 C-Y79AA1001048//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.-) (VLCAD).&quot;//3.1E-138//583aa//47%//P45953  
 C-Y79AA1001077  
 C-Y79AA1001078  
 30 C-Y79AA1001145  
 C-Y79AA1001177  
 C-Y79AA1001185  
 C-Y79AA1001211//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.&quot;/  
 //0//1435bp//99%//AF139658  
 35 C-Y79AA1001228  
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
 DROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//P51657  
 C-Y79AA1001236//&quot;Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581  
 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin)).&quot;//0//1653bp//99%//AJ005892  
 40 C-Y79AA1001281  
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//  
 Q03309  
 C-Y79AA1001323//&quot;Mus musculus mRNA for GSG1, complete cds.&quot;//3.3E-172//1171bp//83%//  
 D87325  
 45 C-Y79AA1001391//HOMEODOMAIN PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%//P31271  
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746  
 C-Y79AA1001402//&quot;Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.  
 &quot;//8.50E-65//784bp//62%//AF083115  
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 50 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132  
 C-Y79AA1001533//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//  
 4.5E-193//1333bp//80%//D14336  
 C-Y79AA1001541  
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-  
 55 NASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356  
 C-Y79AA1001555  
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.9E-40//482aa//27%//P27550

C-Y79AA1001585  
 C-Y79AA1001603//&quot;POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PRO-  
 TEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALAC-  
 TOSAMINYLTRANSFERASE) (GALNAC-T1).&quot;//1.7E-84//313aa//48%//Q07537  
 5 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91//209aa//41%//P52740  
 C-Y79AA1001665  
 C-Y79AA1001679//&quot;Homo sapiens lambda-crystallin mRNA, complete cds.&quot;//3.4e-310//1430bp//98%//  
 AF077049  
 C-Y79AA1001696//&quot;Homo sapiens mRNA for KIAA1109 protein, partial cds.&quot;//0//1669bp//100%//  
 10 AB029032  
 C-Y79AA1001705//&quot;Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.  
 &quot;//3.4E-47//626bp//68%//AF033120  
 C-Y79AA1001711//&quot;Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.&quot;//1.2E-258//  
 1185bp//99%//J04137  
 15 C-Y79AA1001781  
 C-Y79AA1001805  
 C-Y79AA1001827//&quot;Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, com-  
 plete cds.&quot;//0//1689bp//98%//AF177145  
 C-Y79AA1001846  
 20 C-Y79AA1001923  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 SPAC10F6.02C.//1E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743  
 25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018  
 C-Y79AA1002089  
 C-Y79AA1002115  
 C-Y79AA1002125  
 C-Y79AA1002204  
 30 C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%//Q02357  
 C-Y79AA1002209//&quot;Homo sapiens CGI-04 protein mRNA, complete cds.&quot;//0//1617bp//99%//  
 AF132939  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620  
 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//32%//000445  
 35 C-Y79AA1002298  
 C-Y79AA1002307//&quot;Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.&quot;//0//1209bp//99%//  
 AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.9E-186//1130bp//82%//  
 X67877  
 40 C-Y79AA1002351  
 C-Y79AA1002407  
 C-Y79AA1002433//&quot;Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit  
 mRNA, complete cds.&quot;//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5E-136//472aa//  
 45 49%//Q05481

## Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
 50 es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,  
 and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//  
 55 AF196304  
 C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.50E-153//525bp//91%//Z70200  
 C-HEMBA1000213  
 C-HEMBA1000243

C-HEMBA1000244  
C-HEMBA1000251  
C-HEMBA1000338  
C-HEMBA1000357  
5 C-HEMBA1000376  
C-HEMBA1000428  
C-HEMBA1000469  
C-HEMBA1000497  
10 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//  
25%//Q05481  
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865  
C-HEMBA1000575  
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
15 C-HEMBA1000673  
C-HEMBA1000702  
C-HEMBA1000722  
C-HEMBA1000726  
C-HEMBA1000876  
C-HEMBA1000942  
20 C-HEMBA1000943  
C-HEMBA1000960  
C-HEMBA1000985  
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)  
25 (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
C-HEMBA1001020  
C-HEMBA1001024  
C-HEMBA1001026  
C-HEMBA1001051  
C-HEMBA1001060  
30 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461  
C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//  
432bp//94%//AF119043  
C-HEMBA1001099  
C-HEMBA1001121  
35 C-HEMBA1001123  
C-HEMBA1001208  
C-HEMBA1001213  
C-HEMBA1001226  
C-HEMBA1001247  
40 C-HEMBA1001299  
C-HEMBA1001319  
C-HEMBA1001323  
C-HEMBA1001327  
C-HEMBA1001361  
45 C-HEMBA1001375  
C-HEMBA1001377  
C-HEMBA1001383  
C-HEMBA1001391  
C-HEMBA1001411  
50 C-HEMBA1001432  
C-HEMBA1001433  
C-HEMBA1001435  
C-HEMBA1001442  
C-HEMBA1001463  
55 C-HEMBA1001515  
C-HEMBA1001522  
C-HEMBA1001557  
C-HEMBA1001566

C-HEMBA1001589  
C-HEMBA1001608  
C-HEMBA1001636  
C-HEMBA1001647  
5 C-HEMBA1001651  
C-HEMBA1001658  
C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//  
P54787  
C-HEMBA1001712  
10 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//  
1.10E-38//87aa//96%//P55288  
C-HEMBA1001745  
C-HEMBA1001750  
C-HEMBA1001784  
15 C-HEMBA1001791  
C-HEMBA1001803  
C-HEMBA1001820  
C-HEMBA1001835  
C-HEMBA1001888  
20 C-HEMBA1001912  
C-HEMBA1001915  
C-HEMBA1001918  
C-HEMBA1001940  
C-HEMBA1001942  
25 C-HEMBA1001964  
C-HEMBA1002022  
C-HEMBA1002039  
C-HEMBA1002100  
C-HEMBA1002113  
30 C-HEMBA1002119  
C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
C-HEMBA1002160  
C-HEMBA1002162  
C-HEMBA1002166  
35 C-HEMBA1002185  
C-HEMBA1002204  
C-HEMBA1002328  
C-HEMBA1002337  
C-HEMBA1002348  
40 C-HEMBA1002381  
C-HEMBA1002486  
C-HEMBA1002498  
C-HEMBA1002538  
C-HEMBA1002552  
45 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//  
68%//AF055993  
C-HEMBA1002558  
C-HEMBA1002621  
C-HEMBA1002629  
50 C-HEMBA1002645  
C-HEMBA1002659  
C-HEMBA1002661  
C-HEMBA1002666  
C-HEMBA1002678  
55 C-HEMBA1002679  
C-HEMBA1002712  
C-HEMBA1002716  
C-HEMBA1002742

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746  
C-HEMBA1002748  
C-HEMBA1002780  
C-HEMBA1002801  
5 C-HEMBA1002826  
C-HEMBA1002833  
C-HEMBA1002921  
C-HEMBA1002934  
C-HEMBA1002944  
10 C-HEMBA1002968  
C-HEMBA1003034  
C-HEMBA1003037  
C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858  
15 C-HEMBA1003078  
C-HEMBA1003083  
C-HEMBA1003086  
C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096  
20 C-HEMBA1003133  
C-HEMBA1003142  
C-HEMBA1003166  
C-HEMBA1003197  
C-HEMBA1003202  
C-HEMBA1003220  
25 C-HEMBA1003229  
C-HEMBA1003276  
C-HEMBA1003278  
C-HEMBA1003328  
C-HEMBA1003373  
30 C-HEMBA1003597  
C-HEMBA1003598  
C-HEMBA1003656  
C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//  
423aa//47%//P34629  
35 C-HEMBA1003733  
C-HEMBA1003742  
C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
(MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665  
40 C-HEMBA1003803  
C-HEMBA1003854  
C-HEMBA1003926  
C-HEMBA1003939  
C-HEMBA1003987  
C-HEMBA1004012  
45 C-HEMBA1004015  
C-HEMBA1004193  
C-HEMBA1004225  
C-HEMBA1004241  
C-HEMBA1004267  
50 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103  
C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516  
C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494  
C-HEMBA1004396  
C-HEMBA1004405  
55 C-HEMBA1004433  
C-HEMBA1004538  
C-HEMBA1004542  
C-HEMBA1004573



C-HEMBA1004577  
C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844  
C-HEMBA1004617  
C-HEMBA1004631  
5 C-HEMBA1004705  
C-HEMBA1004733  
C-HEMBA1004748  
C-HEMBA1004778  
C-HEMBA1004803  
10 C-HEMBA1004807  
C-HEMBA1004820  
C-HEMBA1004865  
C-HEMBA1004880  
C-HEMBA1004900  
15 C-HEMBA1004909  
C-HEMBA1004960  
C-HEMBA1004978  
C-HEMBA1004980  
C-HEMBA1004983  
20 C-HEMBA1004995  
C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548  
C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947  
C-HEMBA1005035  
C-HEMBA1005039  
25 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290  
C-HEMBA1005050  
C-HEMBA1005062  
C-HEMBA1005066  
C-HEMBA1005075  
30 C-HEMBA1005079  
C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//  
AF080561  
C-HEMBA1005123  
C-HEMBA1005149  
35 C-HEMBA1005152  
C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941  
C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//  
Q00004  
C-HEMBA1005223  
40 C-HEMBA1005232  
C-HEMBA1005241  
C-HEMBA1005275  
C-HEMBA1005293  
C-HEMBA1005311  
45 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581  
C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743  
C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//  
AF071787  
C-HEMBA1005374  
50 C-HEMBA1005382  
C-HEMBA1005411  
C-HEMBA1005426  
C-HEMBA1005443  
C-HEMBA1005447  
55 C-HEMBA1005497  
C-HEMBA1005500  
C-HEMBA1005506  
C-HEMBA1005508

C-HEMBA1005526  
 C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//  
 1578bp//98%//AF191340  
 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,  
 5 complete cds.//1.00E-220//1014bp//99%//AF134157  
 C-HEMBA1005552  
 C-HEMBA1005568  
 C-HEMBA1005588  
 C-HEMBA1005593  
 10 C-HEMBA1005606  
 C-HEMBA1005616  
 C-HEMBA1005627  
 C-HEMBA1005670  
 C-HEMBA1005679  
 15 C-HEMBA1005699  
 C-HEMBA1005705  
 C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697  
 C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789  
 20 C-HEMBA1005852  
 C-HEMBA1005894  
 C-HEMBA1005921  
 C-HEMBA1006035  
 C-HEMBA1006036  
 25 C-HEMBA1006090  
 C-HEMBA1006138  
 C-HEMBA1006173  
 C-HEMBA1006252  
 C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836  
 30 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193  
 C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160  
 C-HEMBA1006380  
 C-HEMBA1006416  
 C-HEMBA1006421  
 35 C-HEMBA1006424  
 C-HEMBA1006426  
 C-HEMBA1006446  
 C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//  
 97%//P55786  
 40 C-HEMBA1006486  
 C-HEMBA1006494  
 C-HEMBA1006546  
 C-HEMBA1006562  
 C-HEMBA1006595  
 45 C-HEMBA1006597  
 C-HEMBA1006631  
 C-HEMBA1006639  
 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
 C-HEMBA1006659  
 50 C-HEMBA1006665  
 C-HEMBA1006676  
 C-HEMBA1006695  
 C-HEMBA1006709  
 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//  
 91%//AF152492  
 55 C-HEMBA1006780  
 C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644  
 C-HEMBA1006824

C-HEMBA1006865  
C-HEMBA1006921  
C-HEMBA1006949  
5 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//  
447bp//89%//X74570  
C-HEMBA1007051  
C-HEMBA1007052  
C-HEMBA1007066  
C-HEMBA1007073  
10 C-HEMBA1007078  
C-HEMBA1007085  
C-HEMBA1007113  
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//  
92%//AF125042  
15 C-HEMBA1007129  
C-HEMBA1007147  
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929  
C-HEMBA1007178  
C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%//D86987  
20 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//  
AF196304  
C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060  
C-HEMBA1007251  
C-HEMBA1007288  
25 C-HEMBA1007322  
C-HEMBA1007341  
C-HEMBB1000050  
C-HEMBB1000054  
C-HEMBB1000059  
30 C-HEMBB1000089  
C-HEMBB1000113  
C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLA-  
SE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177  
C-HEMBB1000173  
35 C-HEMBB1000175  
C-HEMBB1000272  
C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888  
C-HEMBB1000318  
C-HEMBB1000336  
40 C-HEMBB1000341  
C-HEMBB1000343  
C-HEMBB1000354  
C-HEMBB1000374  
C-HEMBB1000434  
45 C-HEMBB1000441  
C-HEMBB1000491  
C-HEMBB1000493  
C-HEMBB1000510  
C-HEMBB1000652  
50 C-HEMBB1000672  
C-HEMBB1000684  
C-HEMBB1000709  
C-HEMBB1000726  
C-HEMBB1000770  
55 C-HEMBB1000827  
C-HEMBB1000831  
C-HEMBB1000883  
C-HEMBB1000888

C-HEMBB1000893  
 C-HEMBB1000913  
 C-HEMBB1000996  
 C-HEMBB1001004  
 5 C-HEMBB1001047  
 C-HEMBB1001060  
 C-HEMBB1001114  
 C-HEMBB1001119  
 C-HEMBB1001133  
 10 C-HEMBB1001142  
 C-HEMBB1001177  
 C-HEMBB1001208  
 C-HEMBB1001209  
 C-HEMBB1001249  
 15 C-HEMBB1001253  
 C-HEMBB1001254  
 C-HEMBB1001271  
 C-HEMBB1001304  
 C-HEMBB1001317  
 20 C-HEMBB1001348  
 C-HEMBB1001394  
 C-HEMBB1001410  
 C-HEMBB1001424  
 C-HEMBB1001426  
 25 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001436  
 C-HEMBB10014437//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 C-HEMBB1001449  
 30 C-HEMBB1001458  
 C-HEMBB1001521  
 C-HEMBB1001531  
 C-HEMBB1001535  
 C-HEMBB1001536  
 35 C-HEMBB1001564  
 C-HEMBB1001565  
 C-HEMBB1001585  
 C-HEMBB1001588  
 C-HEMBB1001603  
 40 C-HEMBB1001618  
 C-HEMBB1001635  
 C-HEMBB1001653  
 C-HEMBB1001668  
 C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546  
 45 C-HEMBB1001685  
 C-HEMBB1001695  
 C-HEMBB1001707  
 C-HEMBB1001735  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 50 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001747  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001753  
 C-HEMBB1001756  
 55 C-HEMBB1001760  
 C-HEMBB1001785  
 C-HEMBB1001797  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

C-HEM BB1001816  
 C-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEM BB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 5 P18720  
 C-HEM BB1001850  
 C-HEM BB1001863  
 C-HEM BB1001868  
 C-HEM BB1001874  
 10 C-HEM BB1001880  
 C-HEM BB1001899  
 C-HEM BB1001906  
 C-HEM BB1001910  
 C-HEM BB1001911  
 15 C-HEM BB1001921  
 C-HEM BB1001922  
 C-HEM BB1001930  
 C-HEM BB1001944  
 C-HEM BB1001945  
 20 C-HEM BB1001947  
 C-HEM BB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.)  
 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEM BB1001952  
 C-HEM BB1001957  
 25 C-HEM BB1001962  
 C-HEM BB1001983  
 C-HEM BB1001990  
 C-HEM BB1001996  
 C-HEM BB1002002  
 30 C-HEM BB1002005  
 C-HEM BB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981  
 C-HEM BB1002043  
 C-HEM BB1002045  
 C-HEM BB1002049  
 35 C-HEM BB1002050  
 C-HEM BB1002068  
 C-HEM BB1002092  
 C-HEM BB1002139  
 C-HEM BB1002142  
 40 C-HEM BB1002190  
 C-HEM BB1002193  
 C-HEM BB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEM BB1002218  
 45 C-HEM BB1002232  
 C-HEM BB1002247  
 C-HEM BB1002249  
 C-HEM BB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEM BB1002327  
 50 C-HEM BB1002329  
 C-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//  
 AJ010841  
 C-HEM BB1002358  
 C-HEM BB1002371  
 55 C-HEM BB1002387  
 C-HEM BB1002409  
 C-HEM BB1002425  
 C-HEM BB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

C-HEMBB1002453  
C-HEMBB1002458  
C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
C-HEMBB1002489  
5 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
C-HEMBB1002520  
C-HEMBB1002522  
C-HEMBB1002545  
C-HEMBB1002579  
10 C-HEMBB1002582  
C-HEMBB1002596  
C-HEMBB1002603  
C-HEMBB1002610  
C-HEMBB1002613  
15 C-HEMBB1002617  
C-HEMBB1002623  
C-HEMBB1002635  
C-HEMBB1002677  
C-HEMBB1002683  
20 C-HEMBB1002699  
C-HEMBB1002702  
C-MAMMA1000009  
C-MAMMA1000043  
C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
25 GP37].//1.90E-07//249aa//27%//P03396  
C-MAMMA1000057  
C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
C-MAMMA1000092  
30 C-MAMMA1000103  
C-MAMMA1000117  
C-MAMMA1000129  
C-MAMMA1000133  
C-MAMMA1000155  
35 C-MAMMA1000175  
C-MAMMA1000198  
C-MAMMA1000241  
C-MAMMA1000251  
C-MAMMA1000254  
40 C-MAMMA1000287  
C-MAMMA1000307  
C-MAMMA1000331  
C-MAMMA1000339  
C-MAMMA1000340  
45 C-MAMMA1000348  
C-MAMMA1000356  
C-MAMMA1000360  
C-MAMMA1000402  
C-MAMMA1000414  
50 C-MAMMA1000431  
C-MAMMA1000444  
C-MAMMA1000458  
C-MAMMA1000500  
C-MAMMA1000522  
55 C-MAMMA1000576  
C-MAMMA1000583  
C-MAMMA1000594  
C-MAMMA1000605

C-MAMMA1000616  
 C-MAMMA1000643  
 C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134  
 C-MAMMA1000696  
 5 C-MAMMA1000707  
 C-MAMMA1000714  
 C-MAMMA1000720  
 C-MAMMA1000744  
 C-MAMMA1000761  
 10 C-MAMMA1000776  
 C-MAMMA1000798  
 C-MAMMA1000839  
 C-MAMMA1000851  
 C-MAMMA1000863  
 15 C-MAMMA1000867  
 C-MAMMA1000876  
 C-MAMMA1000880  
 C-MAMMA1000883  
 C-MAMMA1000921  
 20 C-MAMMA1000931  
 C-MAMMA1000941  
 C-MAMMA1000957  
 C-MAMMA1000962  
 C-MAMMA1000975  
 25 C-MAMMA1000987  
 C-MAMMA1001003  
 C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)  
 (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674  
 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 30 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746  
 C-MAMMA1001082  
 C-MAMMA1001162  
 C-MAMMA1001186  
 C-MAMMA1001191  
 35 C-MAMMA1001206  
 C-MAMMA1001220  
 C-MAMMA1001243  
 C-MAMMA1001249  
 C-MAMMA1001256  
 40 C-MAMMA1001268  
 C-MAMMA1001271  
 C-MAMMA1001274  
 C-MAMMA1001292  
 C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)  
 45 (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)  
 (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960  
 C-MAMMA1001324  
 C-MAMMA1001341  
 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750  
 50 C-MAMMA1001397  
 C-MAMMA1001408  
 C-MAMMA1001420  
 C-MAMMA1001442  
 C-MAMMA1001452  
 55 C-MAMMA1001465  
 C-MAMMA1001487  
 C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001547  
C-MAMMA1001551  
C-MAMMA1001575  
C-MAMMA1001590  
5 C-MAMMA1001600  
C-MAMMA1001606  
C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989  
C-MAMMA1001663  
C-MAMMA1001670  
10 C-MAMMA1001671  
C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
C-MAMMA1001711  
C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
C-MAMMA1001744  
15 C-MAMMA1001745  
C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete  
cds.//0//2332bp//99%//AF117708  
C-MAMMA1001783  
C-MAMMA1001788  
20 C-MAMMA1001806  
C-MAMMA1001812  
C-MAMMA1001815  
C-MAMMA1001817  
C-MAMMA1001818  
25 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
C-MAMMA1001824  
C-MAMMA1001851  
C-MAMMA1001854  
C-MAMMA1001864  
30 C-MAMMA1001878  
C-MAMMA1001890  
C-MAMMA1001907  
C-MAMMA1001908  
C-MAMMA1001931  
35 C-MAMMA1001969  
C-MAMMA1002011  
C-MAMMA1002032  
C-MAMMA1002041  
C-MAMMA1002047  
40 C-MAMMA1002056  
C-MAMMA1002058  
C-MAMMA1002078  
C-MAMMA1002082  
C-MAMMA1002084  
45 C-MAMMA1002093  
C-MAMMA1002094  
C-MAMMA1002118  
C-MAMMA1002125  
C-MAMMA1002132  
50 C-MAMMA1002140  
C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds//1.70E-252//1170bp//99%//  
AF099664  
C-MAMMA1002145  
C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE  
55 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR  
B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
C-MAMMA1002230  
C-MAMMA1002250



C-MAMMA1002282  
 C-MAMMA1002293  
 C-MAMMA1002298  
 C-MAMMA1002299  
 5 C-MAMMA1002308  
 C-MAMMA1002310  
 C-MAMMA1002311  
 C-MAMMA1002322  
 C-MAMMA1002339  
 10 C-MAMMA1002352  
 C-MAMMA1002359  
 C-MAMMA1002360  
 C-MAMMA1002392  
 C-MAMMA1002411  
 15 C-MAMMA1002413  
 C-MAMMA1002417  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE  
 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 C-MAMMA1002434  
 20 C-MAMMA1002446  
 C-MAMMA1002454  
 C-MAMMA1002461  
 C-MAMMA1002475  
 C-MAMMA1002556  
 25 C-MAMMA1002566  
 C-MAMMA1002612  
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 30 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//  
 1942bp//85%//AF018261  
 C-MAMMA1002727  
 C-MAMMA1002748  
 C-MAMMA1002758  
 35 C-MAMMA1002780  
 C-MAMMA1002820  
 C-MAMMA1002833  
 C-MAMMA1002843  
 C-MAMMA1002895  
 40 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
 C-MAMMA1003004  
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//  
 1533bp//99%//AF077952  
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110  
 45 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886  
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590  
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775 C-NT2RM1000499  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//  
 50 Q99383  
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//  
 52%//Q05481  
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990  
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518  
 55 C-NT2RM2001637  
 C-NT2RM2001641  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001699

C-NT2RM2001706  
 C-NT2RM2001718  
 C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931  
 C-NT2RM2001805  
 5 C-NT2RM4000086  
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962  
 C-NT2RM4000414  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000634  
 10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%//AB028992  
 C-NT2RM4000783  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000971  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//  
 15 50%//Q05481  
 C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532  
 C-NT2RM4001569  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
 20 8.10E-300//1395bp//98%//M37712  
 C-NT2RM4001905  
 C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%//AB020705  
 C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//  
 25 1.90E-31//80aa//52%//P36419  
 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//  
 AF072758  
 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//  
 2550bp//99%//AF176085  
 C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%//  
 30 AF071592  
 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940  
 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430  
 C-NT2RM4002390  
 C-NT2RM4002398  
 35 C-NT2RM4002420  
 C-NT2RM4002534  
 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962  
 C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//  
 4.60E-78//921bp//69%//X85019  
 40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//  
 88%//AL050019  
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//8.20E-83//345aa//47%//Q61068  
 45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//  
 99%//AL050118  
 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
 PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
 50 1687bp//99%//AF145020  
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//  
 98%//AF047020  
 C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094  
 C-NT2RP1000916  
 55 C-NT2RP1000944  
 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//  
 U82267  
 C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113  
 C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%//AL080222  
 C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139  
 5 C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192  
 C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513  
 10 C-NT2RP1001311  
 C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799  
 C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034  
 C-NT2RP2000027  
 15 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675  
 C-NT2RP2000198  
 C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238  
 20 C-NT2RP2000551  
 C-NT2RP2000644  
 C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955  
 C-NT2RP2000678  
 C-NT2RP2000715  
 25 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811  
 C-NT2RP2000970  
 C-NT2RP2001347  
 C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709  
 30 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391  
 C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067  
 C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%//AF058718  
 35 C-NT2RP2001677  
 C-NT2RP2001678  
 C-NT2RP2001720  
 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068  
 40 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523  
 C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009  
 C-NT2RP2001861  
 45 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//014754  
 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008  
 C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161  
 50 C-NT2RP2001936  
 C-NT2RP2001943  
 C-NT2RP2001946  
 C-NT2RP2002032  
 C-NT2RP2002033  
 55 C-NT2RP2002041  
 C-NT2RP2002047  
 C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020  
 C-NT2RP2002172  
 C-NT2RP2002219  
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418  
 5 C-NT2RP2002316  
 C-NT2RP2002373  
 C-NT2RP2002439  
 C-NT2RP2002475  
 C-NT2RP2002546  
 10 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//  
 P51523  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
 C-NT2RP2002643  
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
 15 C-NT2RP2002736  
 C-NT2RP2002740  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
 C-NT2RP2002752  
 C-NT2RP2002753  
 20 C-NT2RP2002857  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//1.90E-11//132aa//38%//Q13829  
 C-NT2RP2003073  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
 25 C-NT2RP2003206  
 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794  
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//  
 1551bp//77%//AF023657  
 C-NT2RP2003237  
 30 C-NT2RP2003272//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2003280  
 C-NT2RP2003293  
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//  
 P25386  
 35 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//9.60E-78//346aa//43%//061068  
 C-NT2RP2003456  
 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//  
 40 95%//M12783  
 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//  
 99%//AF125158  
 C-NT2RP2003559  
 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 45 2.10E-59//270aa//46%//P19474  
 C-NT2RP2003581  
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//  
 82%//AJ006215  
 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete  
 50 cds.//2.1e-313//978bp//99%//AF098786  
 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//  
 AJ132637  
 C-NT2RP2003727  
 C-NT2RP2003751  
 55 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//  
 Q09201  
 C-NT2RP2003825  
 C-NT2RP2003871

C-NT2RP2003885  
 C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954  
 C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%//AB007916  
 5 C-NT2RP2003988  
 C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//2.30E-53//141aa//78%//P20290  
 C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%//Q01513  
 10 C-NT2RP2004142  
 C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781  
 C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//AF003998  
 C-NT2RP2004207  
 15 C-NT2RP2004226  
 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//AB015982  
 C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//427aa//26%//P19246  
 20 C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857  
 C-NT2RP2004321  
 C-NT2RP2004339  
 C-NT2RP2004347  
 C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//99%//AB028069  
 25 C-NT2RP2004399  
 C-NT2RP2004400  
 C-NT2RP2004412  
 C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739  
 30 C-NT2RP2004490  
 C-NT2RP2004523  
 C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//AF090190  
 C-NT2RP2004580  
 35 C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695  
 C-NT2RP2004594  
 C-NT2RP2004681  
 C-NT2RP2004709  
 C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231  
 40 C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%//AB020691  
 C-NT2RP2004767  
 C-NT2RP2004775  
 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-228//1666bp//75%//U56732  
 45 C-NT2RP2004962  
 C-NT2RP2004982  
 C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//1.80E-99//376aa//43%//P19474  
 C-NT2RP2005018  
 50 C-NT2RP2005020  
 C-NT2RP2005022  
 C-NT2RP2005031  
 C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0//4069bp//99%//AB014564  
 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921  
 55 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509  
 C-NT2RP2005254  
 C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

99%//AF124735

C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709

C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%//P32660

5 C-NT2RP2005360

C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059

C-NT2RP2005454

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652

10 C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418

C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005501

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171

15 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943

C-NT2RP2005645

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158

20 C-NT2RP2005741

C-NT2RP2005806

C-NT2RP2005815

C-NT2RP2005841

C-NT2RP2005882

25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500

C-NT2RP2006103

C-NT2RP2006166

C-NT2RP2006258

30 C-NT2RP2006261

C-NT2RP2006321

C-NT2RP2006454

C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538

35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559

C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755

C-NT2RP3000418

C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-1511319aa//26%//P37908

40 C-NT2RP3000487

C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667

C-NT2RP3000526

C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562

C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265

45 C-NT2RP3000628

C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%//Q10149

C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.).//8.30E-108//331aa//50%//P27448

50 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027

C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%//Q05481

C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//P25386

55 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140

C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%//P32380

C-NT2RP3001356

C-NT2RP3001383  
 C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538  
 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//  
 388aa//32%//P46821  
 5 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534  
 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-  
 240//902bp//99%//AF054177  
 C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//  
 774bp//88%//AF008554  
 10 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141  
 C-NT2RP3001739  
 C-NT2RP3001777  
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575  
 15 C-NT2RP3001944  
 C-NT2RP3002033  
 C-NT2RP3002054  
 C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956  
 C-NT2RP3002099  
 20 C-NT2RP3002102  
 C-NT2RP3002147  
 C-NT2RP3002163  
 C-NT2RP3002173  
 C-NT2RP3002255  
 25 C-NT2RP3002303//PROBABLE UNDECAPRENYL-PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYN-  
 THETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767  
 C-NT2RP3002343  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase  
 (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396  
 30 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-  
 79//416aa//34%//P33991  
 C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578  
 C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//  
 99%//AL050092  
 35 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//  
 52%//Q10010  
 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60)  
 (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598  
 C-NT2RP3002603  
 40 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//  
 90aa//42%//P38660  
 C-NT2RP3002659  
 C-NT2RP3002660  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903  
 45 C-NT2RP3002687  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002701  
 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371  
 C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430  
 50 C-NT2RP3002876  
 C-NT2RP3002877  
 C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314  
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053  
 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333  
 55 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mR-  
 NA, complete cds.//0//2656bp//99%//AF084555  
 C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357  
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

C-NT2RP3003078  
 C-NT2RP3003139  
 C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//  
 AF07773 8  
 5 C-NT2RP3003150  
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//  
 31%//Q09674  
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-  
 210//1851bp//76%//AF110267  
 10 C-NT2RP3003210  
 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-  
 187//1750bp//75%//U20286  
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656  
 C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//  
 15 AF098462  
 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 4.20E-86//366aa//48%//P19474  
 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//  
 585aa//54%//064948  
 20 C-NT2RP3003311  
 C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//  
 782bp//65%//U90653  
 C-NT2RP3003427  
 C-NT2RP3003543  
 25 C-NT2RP3003552  
 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//  
 191aa//40%//P40529  
 C-NT2RP3003564  
 C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//  
 30 AF106681  
 C-NT2RP3003621  
 C-NT2RP3003625  
 C-NT2RP3003656  
 C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843  
 35 C-NT2RP3003686  
 C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446  
 C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014  
 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//  
 U28164  
 40 C-NT2RP3003795  
 C-NT2RP3003805  
 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590  
 C-NT2RP3003819  
 C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//  
 45 P02720  
 C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete  
 cds.//2.2e-316//1436bp//99%//AB020523  
 C-NT2RP3003833  
 C-NT2RP3003842  
 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//  
 AB019435  
 C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343  
 C-NT2RP3003876  
 C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 55 (DUGT).//2.20E-20//76aa//64%//Q09332  
 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//  
 AF086628  
 C-NT2RP3003989



C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)  
(KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263

C-NT2RP3004070

C-NT2RP3004145

5 C-NT2RP3004215

C-NT2RP3004253

C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871

C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//  
X67877

10 C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982

C-NT2RP3004503

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//  
P51523

15 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST),  
complete cds.//0//2393bp//99%//AB014679

C-NT2RP4000023

C-NT2RP4000218

C-NT2RP4000424

20 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676

C-NT2RP4001447

C-NT2RP4001841

C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194

C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618

C-NT2RP4002075

25 C-NT2RP4002083

C-OVARC1000001/Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//  
99%//AB029290

C-OVARC1000008

C-OVARC1000017

30 C-OVARC1000058

C-OVARC1000068

C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//  
727bp//67%//AF156957

C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761

35 C-OVARC1000109

C-OVARC1000114

C-OVARC1000145

C-OVARC1000240

40 C-OVARC1000302

C-OVARC1000408

C-OVARC1000414

C-OVARC1000440

C-OVARC1000442

C-OVARC1000496

45 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)  
(RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349

C-OVARC1000557

C-OVARC1000578

C-OVARC1000622

50 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888

C-OVARC1000681

C-OVARC1000700

C-OVARC1000724

55 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//  
74aa//37%//P49596

C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED  
PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501

C-OVARC1000885//OXIDOREDUCTASE UCFA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%//P32943  
 C-OVARC1000960  
 C-OVARC1000971  
 5 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527  
 C-OVARC1001000  
 C-OVARC1001029  
 C-OVARC1001040  
 10 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//  
 AF051782  
 C-OVARC1001118  
 C-OVARC1001129  
 15 C-OVARC1001169  
 C-OVARC1001240  
 C-OVARC1001261  
 C-OVARC1001339  
 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058  
 20 C-OVARC1001357  
 C-OVARC1001442  
 C-OVARC1001611  
 C-OVARC1001813  
 25 C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0//1760bp//99%//AF054174  
 C-OVARC1002143  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213  
 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-  
 09//207aa//30%//Q91854  
 30 C-PLACE1000014  
 C-PLACE1000078  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//  
 U35245  
 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645  
 35 C-PLACE1000814  
 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742  
 C-PLACE1001007  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//  
 1355bp//100%//AB024301  
 40 C-PLACE1001088  
 C-PLACE1001136  
 C-PLACE1001241  
 C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//  
 AF009615  
 45 C-PLACE1001395  
 C-PLACE1001740  
 C-PLACE1001746  
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//  
 319aa//26%//P37908  
 50 C-PLACE1002066  
 C-PLACE1002115  
 C-PLACE1002213  
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0//1657bp//98%//AB018271  
 C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274  
 55 C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262  
 C-PLACE1002499  
 C-PLACE1002578  
 C-PLACE1002714

C-PLACE1002772  
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201  
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522  
 5 C-PLACE1002993  
 C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387  
 C-PLACE1003205  
 C-PLACE1003249  
 10 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481  
 C-PLACE1003553  
 C-PLACE1003592  
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975  
 15 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793  
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//1316bp//98%//AF053305  
 C-PLACE1003870  
 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500  
 20 C-PLACE1003892  
 C-PLACE1003900  
 C-PLACE1004336  
 C-PLACE1004384  
 25 C-PLACE1004425  
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%//P51522  
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878  
 30 C-PLACE1004518  
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954  
 C-PLACE1004681  
 C-PLACE1004693  
 C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099  
 35 C-PLACE1004815  
 C-PLACE1004836  
 C-PLACE1004838  
 C-PLACE1004840  
 C-PLACE1004900  
 40 C-PLACE1004985  
 C-PLACE1005085  
 C-PLACE1005086  
 C-PLACE1005108  
 C-PLACE1005146  
 45 C-PLACE1005409  
 C-PLACE1005453  
 C-PLACE1005477  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005595  
 50 C-PLACE1005603  
 C-PLACE1005639  
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680  
 C-PLACE1005799  
 55 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 C-PLACE1005884  
 C-PLACE1005968  
 C-PLACE1006002

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C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852  
C-PLACE1006017  
C-PLACE1006037  
C-PLACE1006076  
5 C-PLACE1006143  
C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548  
C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//  
4.60E-117//147aa//80%//P21796  
10 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374  
C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
1.30E-18//460aa//24%//Q00547  
C-PLACE1006371  
15 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
TIVATING ENZYME).//1.20E-83//313aa//49%//P27550  
C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//  
2170bp//99%//AF191338  
C-PLACE1006521  
20 C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//  
883bp//99%//AL110144  
C-PLACE1006617  
C-PLACE1006640  
C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//  
6.20E-63//191aa//43%//P13688  
25 C-PLACE1006760  
C-PLACE1006779  
C-PLACE1006805  
C-PLACE1006815  
C-PLACE1006867  
30 C-PLACE1007045  
C-PLACE1007097  
C-PLACE1007111  
C-PLACE1007112  
C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226  
35 C-PLACE1007218  
C-PLACE1007454  
C-PLACE1007478  
C-PLACE1007677  
C-PLACE10077057//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//  
40 82%//AB033922  
C-PLACE1007737  
C-PLACE1007743  
C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//  
AB020685  
45 C-PLACE1007877  
C-PLACE1008045  
C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326  
C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
50 C-PLACE1008231  
C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-  
TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315  
C-PLACE1008331  
55 C-PLACE1008369  
C-PLACE1008392  
C-PLACE1008405  
C-PLACE1008424

C-PLACE1008584  
 C-PLACE1008625  
 C-PLACE1008630  
 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
 5 H2).//5.20E-90//483aa//38%//002668  
 C-PLACE1008715  
 C-PLACE1008748  
 C-PLACE1008757  
 C-PLACE1008798  
 10 C-PLACE1008851  
 C-PLACE1008947  
 C-PLACE1009039  
 C-PLACE1009048  
 C-PLACE1009050  
 15 C-PLACE10091137//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//  
 0//2529bp//99%//AF035586  
 C-PLACE1009150  
 C-PLACE1009200  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 20 C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//  
 AF191298  
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742  
 C-PLACE1009410  
 25 C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584  
 C-PLACE1009493  
 C-PLACE1009539  
 C-PLACE1009595  
 C-PLACE1009637  
 30 C-PLACE1009639  
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552  
 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//  
 209aa//38%//P43510  
 C-PLACE1009888  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963  
 C-PLACE1009947  
 C-PLACE1010069  
 C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020  
 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//  
 40 5.10E-27//371aa//28%//Q14246  
 C-PLACE1010270  
 C-PLACE1010562  
 C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//  
 1362bp//99%//AF200715  
 45 C-PLACE1010624  
 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and  
 S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907  
 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//1.80E-222//808aa//52%//Q09332  
 50 C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160  
 C-PLACE1010761  
 C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209  
 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//  
 23%//P35580  
 55 C-PLACE1010916  
 C-PLACE1010947  
 C-PLACE1010965  
 C-PLACE1011032

C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019  
 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
 C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//  
 99%//AL050159  
 5 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
 C-PLACE1011214  
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//  
 701bp//99%//AF153604  
 C-PLACE1011273  
 10 C-PLACE1011291  
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
 C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN  
 H2).//1.70E-78//383aa//39%//Q61703  
 C-PLACE1011503  
 15 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA,  
 complete cds.//0//1559bp//99%//AF105377  
 C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752  
 C-PLACE1011650  
 C-PLACE1011675  
 20 C-PLACE1011725  
 C-PLACE1011749  
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
 B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
 C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256  
 25 C-PLACE2000006  
 C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720  
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//  
 212aa//35%//P10586  
 C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-  
 30 291//1167bp//89%//L08505  
 C-PLACE2000061  
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219  
 C-PLACE2000097  
 C-PLACE2000103  
 35 C-PLACE2000115  
 C-PLACE2000124  
 C-PLACE2000140  
 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736  
 C-PLACE2000176  
 40 C-PLACE2000223  
 C-PLACE2000235  
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098  
 C-PLACE2000302  
 C-PLACE2000347  
 45 C-PLACE2000359  
 C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205  
 C-PLACE2000379  
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//1.60E-14//180aa//39%//P14209  
 50 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 (LEURS).//9.90E-229//821aa//54%//Q09996  
 C-PLACE2000450  
 C-PLACE2000455  
 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267  
 55 C-PLACE3000070  
 C-PLACE3000119  
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224  
 C-PLACE3000136

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084  
 C-PLACE3000148  
 C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//AB014572  
 C-PLACE3000160  
 C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742  
 C-PLACE3000194  
 C-PLACE3000199  
 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020  
 C-PLACE3000230  
 C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aay//92%//P53995  
 C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946  
 C-PLACE3000276  
 C-PLACE3000310  
 C-PLACE3000320  
 C-PLACE3000331  
 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640  
 C-PLACE3000352  
 C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739  
 C-PLACE3000362  
 C-PLACE3000365  
 C-PLACE3000388  
 C-PLACE3000413  
 C-PLACE3000425  
 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580  
 C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100  
 C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281  
 C-PLACE4000089  
 C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//AF091234  
 C-PLACE4000129  
 C-PLACE4000147  
 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746  
 C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//AF000422  
 C-PLACE4000222  
 C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990  
 C-PLACE4000270  
 C-PLACE4000300  
 C-PLACE4000387  
 C-PLACE4000392  
 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200  
 C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217b.p//98%//AF000422  
 C-PLACE4000465  
 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002  
 C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267  
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

C-SKNC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800  
 C-SKNC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655  
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709  
 5 C-THYRO1000070  
 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC  
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799  
 C-THYRO1000092  
 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039  
 10 C-THYRO1000124  
 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698  
 C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552  
 C-THYRO1000206  
 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//  
 15 P51523  
 C-THYRO1000253  
 C-THYRO1000270  
 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068  
 C-THYRO1000320  
 20 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563  
 C-THYRO1000368  
 C-THYRO1000381  
 C-THYRO1000387  
 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//  
 25 1325bp//99%//AF072864  
 C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857  
 C-THYRO1000401  
 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663  
 C-THYRO1000501//52 KD RO PROTEIN (SJOOREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//  
 30 4.20E-98//408aa//42%//P19474  
 C-THYRO1000558  
 C-THYRO1000570  
 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//  
 AF140360  
 35 C-THYRO1000625  
 C-THYRO1000637  
 C-THYRO1000676  
 C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679  
 C-THYRO1000712  
 40 C-THYRO1000805  
 C-THYRO1000815  
 C-THYRO1000855  
 C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
 7.50E-57//315aa//43%//P32322  
 45 C-THYRO1000988  
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948  
 C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//  
 1479bp//66%//U38252  
 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and  
 50 TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276  
 C-THYRO1001262  
 C-THYRO1001271  
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-  
 ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701  
 55 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861  
 C-THYRO1001347  
 C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//  
 99%//AL080120



C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%//AB014607  
 C-THYRO1001403  
 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427  
 C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//  
 5 AF078850  
 C-THYRO1001426  
 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580  
 C-THYRO1001480  
 10 C-THYRO1001487  
 C-THYRO1001584  
 C-THYRO1001661  
 C-THYRO1001746  
 C-THYRO1001772  
 15 C-THYRO1001854  
 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//  
 AF171060  
 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484  
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//  
 20 AF123534  
 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835  
 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692  
 C-Y79AA1000410  
 C-Y79AA1000539  
 25 C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//  
 AF091080  
 C-Y79AA1000802  
 C-Y79AA1000827  
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 30 C-Y79AA1000969  
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962  
 C-Y79AA1001061  
 C-Y79AA1001068  
 C-Y79AA1001216  
 35 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738  
 C-Y79AA1001511  
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 2.50E-14//410aa//24%//Q00547  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78//  
 40 227aa//40%//Q01820  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 45 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002210//YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//016264  
 50 C-Y79AA1002220  
 C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 55 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//1444bp//98%//AF129534  
 5 C-HEMBA1000290  
 C-HEMBA1000459  
 C-HEMBA1000505  
 C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088  
 10 C-HEMBA1002503  
 C-HEMBA1002508  
 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972  
 C-HEMBA1003480  
 15 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%//P00736  
 C-HEMBA10036451//TPPD PROTEIN.//2.40E-10//289aa//23%//015736  
 C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%//AB023230  
 C-HEMBA1003667  
 20 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253  
 C-HEMBA1003827  
 C-HEMBA1003838  
 C-HEMBA1004055  
 25 C-HEMBA1004056  
 C-HEMBA1004086  
 C-HEMBA1004335  
 C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471  
 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221  
 30 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333  
 C-HEMBA1004507  
 C-HEMBA1004638  
 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583  
 35 C-HEMBA1004709  
 C-HEMBA1004860  
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308  
 C-HEMBA1005472  
 C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//002193  
 40 C-HEMBA1005572  
 C-HEMBA1005780  
 C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516  
 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001  
 45 C-HEMBA1006124  
 C-HEMBA1006461  
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716  
 C-HEMBA1006617  
 50 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//015509  
 C-HEMBA1006779  
 C-HEMBA1006796  
 C-HEMBA1006812  
 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832  
 55 C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%//AB028988  
 C-HEMBA1000240  
 C-HEMBA1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

C-HEMBB1000335  
 C-HEMBB1000337  
 C-HEMBB1000554  
 C-HEMBB1000573  
 5 C-HEMBB1000749  
 C-HEMBB1000774  
 C-HEMBB1000835  
 C-HEMBB1001197  
 C-HEMBB1001315  
 10 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001500  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001619  
 15 C-HEMBB1001630  
 C-HEMBB1001665  
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031  
 C-HEMBB1001812  
 C-HEMBB1001834  
 20 C-HEMBB1001869  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//  
 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 25 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 30 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001925  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002152  
 35 C-HEMBB1002300  
 C-HEMBB1002381  
 C-HEMBB1002383  
 C-HEMBB1002534  
 C-MAMMA1000143  
 40 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//  
 P51523  
 C-MAMMA1000227  
 C-MAMMA1000257  
 C-MAMMA1000264  
 45 C-MAMMA1000270  
 C-MAMMA1000279  
 C-MAMMA1000372  
 C-MAMMA1000559  
 C-MAMMA1000752  
 50 C-MAMMA1000760  
 C-MAMMA1000778  
 C-MAMMA1000855  
 C-MAMMA1000859  
 C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN  
 55 H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033  
 C-MAMMA1000940  
 C-MAMMA1001073  
 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//

AF067420

C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001202

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978

5 C-MAMMA1001252

C-MAMMA1001296

C-MAMMA1001502

C-MAMMA1001630

C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

10 C-MAMMA1001683

C-MAMMA1001715

C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687

C-MAMMA1001760

15 C-MAMMA1001769

C-MAMMA1001785

C-MAMMA1001848

C-MAMMA1001874

C-MAMMA1001956

20 C-MAMMA1002009

C-MAMMA1002033

C-MAMMA1002155

C-MAMMA1002498

C-MAMMA1002545

25 C-MAMMA1002571

C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640

C-MAMMA1002590

C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742

30 C-MAMMA1002618

C-MAMMA1002636

C-MAMMA1002646

C-MAMMA1002665

C-MAMMA1002708

35 C-MAMMA1002728

C-MAMMA1002744

C-MAMMA1002764

C-MAMMA1002765

C-MAMMA1002830

40 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178

C-MAMMA100285 8//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590

C-MAMMA1002880

C-MAMMA1002892

45 C-MAMMA1002909

C-MAMMA1002941

C-MAMMA1002947

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343

50 C-MAMMA1002973

C-MAMMA1002987

C-MAMMA1003003

C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542

C-MAMMA1003031

55 C-MAMMA1003089

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843

C-NT2RM1000272

C-NT2RM1000341

C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097

C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731

C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775

C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695

C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458

C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516

C-NT2RM1001082

C-NT2RM1001112

C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091

C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798

C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//2300bp//100%//AL110217

C-NT2RM2001803//Homo sapiens IkappaB kinase cbmplex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195

C-NT2RM4002504

C-NT2RP1000409

C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991

C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//99%//AF173378

C-NT2RP1000796

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP2001214

C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481

C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334

C-NT2RP2002056

C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634

C-NT2RP2002333

C-NT2RP2002677

C-NT2RP2002755

C-NT2RP2002843

C-NT2RP2003101

C-NT2RP2003668

C-NT2RP2003799

C-NT2RP2004095

C-NT2RP2004300

C-NT2RP2004675

C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//22%//Q61687

C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//AF045583

C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444

C-NT2RP2005726

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-TRANSFERASE).//4.40E-55//358aa//42%//P51005

C-NT2RP2005980

C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%//AB020725

C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131

C-NT2RP2006554

C-NT2RP3000584  
 C-NT2RP3001115  
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//  
 1138bp//63%//AF193613  
 5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458  
 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791  
 C-NT2RP3002402  
 C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215  
 C-NT2RP3002512  
 10 C-NT2RP3002713  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//  
 41%//P17564  
 C-NT2RP3002799  
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125  
 15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//  
 P51026  
 C-NT2RP3002955  
 C-NT2RP3002985  
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//  
 20 82%//U78090  
 C-NT2RP3003121  
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//  
 91%//AB011414  
 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//  
 25 AF071592  
 C-NT2RP3003155  
 C-NT2RP3003157  
 C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455  
 C-NT2RP3003264  
 30 C-NT2RP3003346  
 C-NT2RP3003403  
 C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//  
 743bp//90%//AF071317  
 C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009  
 35 C-NT2RP3003572  
 C-NT2RP3003576  
 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885  
 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-  
 TEIN) (12E7).//2.20E-13//146aa//42%//P14209  
 40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//  
 2047bp//95%//AL080155  
 C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294  
 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//  
 924bp//89%//AF130457  
 45 C-NT2RP3003828  
 C-NT2RP3003932  
 C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//2739bp//  
 99%//AL050019  
 C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692  
 50 C-NT2RP3004028  
 C-NT2RP3004041  
 C-NT2RP3004051  
 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091  
 C-NT2RP3004093  
 55 C-NT2RP3004095  
 C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-  
 229//1560bp//78%//AF126747  
 C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640  
 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948  
 C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.30E-14//242aa//24%//Q00808  
 C-NT2RP3004332  
 5 C-NT2RP3004349  
 C-NT2RP3004470  
 C-NT2RP4000035  
 C-NT2RP4000049  
 C-NT2RP4000102  
 10 C-NT2RP4000167  
 C-NT2RP4000515  
 C-NT2RP4000517  
 C-NT2RP4000519  
 C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117  
 15 C-OVARC1000092  
 C-OVARC1000533  
 C-OVARC1000678  
 C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//  
 0//2032bp//99%//AL133014  
 20 C-OVARC1000802  
 C-OVARC1000890  
 C-OVARC1000891  
 C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//  
 82%//AB005549  
 25 C-OVARC1001072  
 C-OVARC1001117  
 C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192  
 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//  
 X62083  
 30 C-OVARC1001329  
 C-OVARC1001341  
 C-OVARC1001376  
 C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
 AF016507  
 35 C-OVARC1001873  
 C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//1.60E-81//212aa//70%//P34547  
 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-  
 40 241//1124bp//98%//AF135421  
 C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234  
 C-PLACE1001076  
 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742  
 C-PLACE1001366  
 45 C-PLACE1001545  
 C-PLACE1001608  
 C-PLACE1002004  
 C-PLACE1002256  
 C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233  
 50 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146  
 C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//  
 AF079765  
 C-PLACE1003383  
 C-PLACE1003864  
 55 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267  
 C-PLACE1004913  
 C-PLACE1004979  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

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C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148  
C-PLACE1005128  
C-PLACE1005162  
5 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//  
96%//AF113539  
C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//  
7.60E-97//1287bp//67%//AJ010046  
10 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//  
6.80E-09//267aa//30%//P29128  
C-PLACE1005611//Mus musculus mRNA for mDjIO, complete cds.//2.00E-33//379bp//66%//AB028860  
C-PLACE1005802  
C-PLACE1005850  
C-PLACE1005898  
15 C-PLACE1005932  
C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542  
C-PLACE1006360  
C-PLACE1006795  
C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
20 NUCLEASE).//1.90E-08//122aa//36%//P16658  
C-PLACE1007557  
C-PLACE1007807  
C-PLACE1008181  
C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114  
25 C-PLACE1008455  
C-PLACE1008941  
C-PLACE1009935  
C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804  
C-PLACE1011891  
30 C-PLACE10118967//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969  
C-PLACE2000003  
C-PLACE2000132  
C-PLACE2000170  
C-PLACE2000335  
35 C-PLACE3000124  
C-PLACE3000158  
C-PLACE3000207  
C-PLACE3000221  
C-PLACE3000271  
40 C-PLACE3000304  
C-PLACE3000322  
C-PLACE3000341  
C-PLACE3000373  
C-PLACE3000399  
45 C-PLACE3000401  
C-PLACE3000402  
C-PLACE3000406  
C-PLACE3000475  
C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
50 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640  
C-PLACE4000093  
C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//  
AF146689  
55 C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//  
1612bp//97%//AL117455  
C-PLACE4000247  
C-PLACE4000250  
C-PLACE4000252



C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200  
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201  
 C-PLACE4000320  
 C-PLACE4000344  
 5 C-PLACE4000367  
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//7.20E-22//54aa//62%//Q01576  
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//  
 0//2159bp//98%//AL117654  
 10 C-PLACE4000487  
 C-PLACE4000494  
 C-PLACE4000521  
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164  
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mito-  
 15 chondrial protein, complete cds.//0//2384bp//99%//AF047690  
 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//  
 AB021663  
 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333  
 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//  
 20 AF118566  
 C-THYRO1001142  
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//  
 62%//005481  
 C-THYRO1001320  
 25 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//  
 0//1010bp//98%//AL050159  
 C-THYRO1001602  
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652  
 C-THYRO1001828  
 30 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//  
 AF157833  
 C-Y79AA1001167  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//  
 4708bp//99%//AF055084  
 35 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 C-HEMBA1006092  
 C-HEMBA1006406  
 C-HEMBB1000790  
 40 C-HEMBB1000917  
 C-HEMBB1002280  
 C-MAMMA1000802  
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//  
 P20931  
 45 C-MAMMA1002597  
 C-MAMMA1002868  
 C-NT2RP2003161  
 C-NT2RP2003339  
 C-NT2RP3001282  
 50 C-PLACE1001761  
 C-PLACE1004491  
 C-PLACE1004686  
 C-PLACE1005574  
 C-PLACE1006382  
 55 C-PLACE1006792  
 C-PLACE3000455  
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430  
 C-THYRO1000916

C-HEMBA1000327  
 C-HEMBA1000637  
 C-HEMBA1001967  
 C-MAMMA1000266  
 5 C-NT2RP2002979  
 C-PLACE1007866  
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)  
 (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%//Q13177  
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%//P52740  
 10 C-THYRO1001637  
 C-MAMMA1002215  
 C-MAMMA1002721  
 C-NT2RP2002070

15 Homology search result 14.

**[0334]** Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%//061712  
 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 25 (LEURS).//6.40E-99//457aa//45%//Q09996  
 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%//X02344  
 C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.//0//1759bp//99%//  
 AF124490  
 C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME 1.//3.80E-25//166aa//36%//  
 30 Q09884  
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//  
 AF196304  
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%//  
 AF085356  
 35 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
 1.90E-12//368aa//24%//P08553  
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%//P35584  
 C-HEMBA1000168//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%//P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31 %//P48555  
 40 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738  
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
 TEIN).//1.00E-86//146aa//56%//Q61221  
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%//  
 AF030131  
 45 C-HEMBA1000304//Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-  
 131//712bp//91%//U16802  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-  
 49//107aa//91%//035594  
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//  
 50 AF174601  
 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%//AB026491  
 C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%//Q02357  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa//31%//P22279  
 55 C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa//38%//P18490  
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa//36%//Q01755  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS).//2.60E-12//73aa//41%//P02826

C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340  
 C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529  
 5 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25 %//Q05481  
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabb//32%//Q60865  
 C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573  
 10 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
 C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//O43295  
 C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776  
 15 C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868  
 C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689  
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366  
 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124  
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//25 1.40E-12//131aa//38%//Q01485  
 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088  
 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461  
 30 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730  
 35 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646  
 C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733  
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401  
 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081  
 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091  
 C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221  
 C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599  
 50 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850  
 55 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166  
 C-HEMBA1001569//SYNAPTOSOMAL VESICLE ASSOCIATED MEMBRANE PROTEIN 2 (VAMP-2).//2.30E-53//110aa//100%//P19065  
 C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

- C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141  
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803
- 5 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%//Q63679  
 C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//365aa//33%//P33450
- 10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%//AF072247  
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//P54787
- 15 C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//100%//AB029042  
 C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%//AF195883  
 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).//1.10E-38//87aa//96%//P55288
- 20 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009  
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.60E-59//998bp//64%//AF098066  
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1637bp//99%//AF125158
- 25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676  
 C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479  
 C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//AF159025
- 30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%//Q07230  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.70E-51//234aa//41%//Q09332  
 C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.30E-36//395aa//26%//Q63342
- 35 C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535  
 C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//1850bp//99%//AF000145  
 C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114  
 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete cds.//0//2149bp//99%//AB032252
- 40 C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-271//1583bp//88%//U92703  
 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
- 45 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//P79293
- 50 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//P43694  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.00E-17//267aa//29%//P18161  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226  
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
- 55 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537  
 C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//96%//Q62415  
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

- 1847bp//99%//AF092563  
 C-HEMBA1002417//mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//1.00E-121//489aa//52%//P39447  
 C-HEMBA1002419//TRICHOHYALIN.//1.90E-09//299aa//24%//P22793  
 5 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.20E-24//109aa//55%//Q00994  
 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.50E-50//199aa//61%//P98175  
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-12//285aa//31%//P17437  
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.80E-53//257aa//36%//P48732  
 10 C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972  
 C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0//1605bp//97%//AF016903  
 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993  
 15 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.80E-305//951bp//99%//AF075587  
 C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746  
 C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds.//7.80E-237//1522bp//85%//AB011126  
 20 C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds.//2.90E-176//1024bp//88%//D87671  
 C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.//3.40E-54//319bp//76%//AF153879  
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185  
 25 C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2.00E-304//1383bp//99%//AJ132819  
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n.//1.50E-44//188aa//52%//Q09297  
 C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-15//371aa//25%//Q05481  
 30 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2.00E-34//300aa//34%//P16157  
 C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//4.40E-06//324aa//24%//P32380  
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.20E-27//63aa//100%//P14646  
 35 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.80E-25//534aa//24%//Q02224  
 C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-171//1552bp//75%//U20286  
 C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA.//0//1558bp//99%//AF054182  
 40 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858  
 C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.60E-15//199aa//31%//P24014  
 C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-117//1139bp//72%//M32486  
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096  
 45 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.50E-51//221aa//33%//P41940  
 C-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//0//1583bp//99%//AJ005670  
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.90E-74//134aa//53%//P44551  
 50 C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87//285bp//90%//AF129534  
 C-HEMBA1003235//TROPOMYOSIN.//2.30E-06//109aa//33%//Q02088  
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.20E-41//245aa//42%//Q06548  
 55 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6.00E-11//239aa//32%//P32506  
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229//1043bp//99%//AB024436  
 C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10).//7.6.20E-28//126aa//51%//

Q38997

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%/Q02224

C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//7.80E-13//297aa//30%/P18616

5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-255//1179bp//99%/AF095192

C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%/P37709

C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139

10 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%/P00736

C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%/P50480

C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%/P53384

C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.20E-31//71aa//100%/P16874

15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//7.90E-49//279aa//32%/P19474

C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%/Q13330

C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%/P26039

20 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10//118aa//35%/P19682

C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%/AB026125

C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//97%/AB015344

C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%/O15736

25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%/Q13207

C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%/P23253

C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%/P34629

30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%/Q13105

C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%/P53973

C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//1.70E-44//501bp//67%/AF037339

35 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%/Q16665

C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-81//511bp//86%/U17343

C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//1204bp//84%/AF084259

40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp//95%/AF090402

C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%/P40484

C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//1.20E-105//1192bp//70%/AF030430

45 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//89aa//46%/P16372

C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%/AF091234

C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%/Q14141

C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%/AF067855

50 C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%/P34529

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%/P51153

C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%/P40991

C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/U50748

55 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.70E-217//1217bp//88%/AF095927

C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//2.00E-43//98aa//84%/Q08755

C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds.//1.10E-152//1403bp//69%//AF043725

C-HEMBA1004276//Homo sapiens AP-4 adaptor complex .beta4 subunit mRNA, complete cds.//4.80E-257//738bp//99%//AF092094

5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp//99%//AF022795

C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103

C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676

C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471

10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516

C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494

C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1437bp//99%//AF125158

C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-CLOPHILIN-10).//3.20E-32//148aa//52%//P52017

15 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221

C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333

C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME ,4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107

20 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841

C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291

25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844

C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583

C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749

C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITTIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743

30 C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405

C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082

C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%//L39060

35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547

C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851

C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%//Q00004

C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aabp//26%//U72515

40 C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%//P25386

C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401

C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036

45 C-HEMBA1004973//ZINC-BINDING PROTEIN A337.//4.10E-08//121aa//33%//Q02084

C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474

C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947

C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290

C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//AF080561

50 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941

C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004

C-HEMBA1005206//Drosophila simulans anon73Bl gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308

55 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%//P39929

C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581

C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743

C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

AF071787

C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//3.90E-126//1097bp//75%//AF200357

C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//2.00E-213//537bp//99%//AF041248

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//O02193

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%//Q60809

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340

C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157

C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929

C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%//D86949

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270

C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN).//0.00000009//213aa//27%//P09492

C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.30E-54//562aa//29%//P34036

C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds.//8.00E-211//962bp//99%//AF072933

C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%//AJ249128

C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81 %//Q15768

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.40E-17//167aa//34%//P25296

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789

C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%//P51522

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516

C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%//AB019435

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001

C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%//AF098066

C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25 %//Q93794

C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//155 lbp//99%//AF048693

C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.90E-19//215aa//39%//P05142

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23//151aa//37%//P16372

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//62aa//53%//P42698

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265

C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.00E-210//490aa//77%//P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//30%//P32505

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.20E-12//215aa//23%//P70473

C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%//AF005050

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043

C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//O02193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160

C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds.//2.00E-277//1729bp//85%//U93563

C-HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.//1.40E-270//1224bp//



100%//U96750  
 C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%//Q01552  
 C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786  
 5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%//O60879  
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716  
 C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//2.80E-206//1107bp//83%//U06944  
 10 C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%//AF190774  
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%//Q58323  
 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//O15509  
 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
 15 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.30E-22//241aa//31%//P53196  
 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.00000043//111aa//40%//Q01485  
 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492  
 20 C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644  
 C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN.//2.00E-59//378aa//39%//P16258  
 C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%//AB018566  
 25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832  
 C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271//1234bp//99%//AF118649  
 C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%//AF004828  
 30 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/l-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//447bp//89%//X74570  
 C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//2.40E-188//391aa//89%//Q90828  
 35 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568  
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%//AF125042  
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929  
 40 C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085  
 C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1588bp//99%//AF139658  
 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//AF196304  
 45 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060  
 C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.//5.00E-58//330bp//95%//AF176707  
 C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%//AF127479  
 50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941  
 C-HEMBA1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%//AF151809  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187//1582bp//80%//AF084928  
 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799  
 55 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521  
 C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

C-HEM BB1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385  
 C-HEM BB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEDB.5//2.70E-12//112aa//47%//Q09530  
 5 C-HEM BB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516  
 C-HEM BB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256  
 C-HEM BB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888  
 10 C-HEM BB1000593//Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864  
 C-HEM BB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970  
 C-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671  
 15 C-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723  
 C-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475  
 C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847  
 C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105  
 20 C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956  
 C-HEM BB1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008  
 25 C-HEM BB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122  
 C-HEM BB1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598  
 C-HEM BB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910  
 30 C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974  
 C-HEM BB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575  
 C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523  
 35 C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087  
 C-HEM BB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.60E-52//331bp//80%//AF010144  
 C-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803  
 40 C-HEM BB1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032  
 C-HEM BB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
 C-HEM BB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267  
 C-HEM BB1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357  
 45 C-HEM BB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938  
 C-HEM BB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897  
 C-HEM BB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157  
 50 C-HEM BB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719  
 C-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081  
 C-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703  
 C-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//2.10E-65//458bp//79%//D63850  
 55 C-HEM BB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175  
 C-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441

C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-AT-  
 PASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342  
 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167  
 15 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 P18720  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//  
 20 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 25 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)  
 30 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN  
 35 KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//  
 40 1045bp//99%//AF118649  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544  
 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749  
 C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-  
 136//660bp//98%//AF105421  
 C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//  
 50 Z47553  
 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226  
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 55 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//  
 2.60E-164//1044bp//87%//AF197060  
 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

P51523

C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.20E-109//864bp//76%//X99836

C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%//AB015132

5 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%//Q09232

C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883

C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%//P48365

10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.)/4.40E-33//250aa//33%//P42660

C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%//AF172451

C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524

15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%//O14646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9.00E-299//1033aa//55%//P87115

20 C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%//P53500

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711

25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%//AF117892

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674

30 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]//2.60E-107//190aa//95%//Q15746

C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946

C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%//AF151830

35 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//AF067420

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338

40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978

C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%//AF184275

45 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa//30%//P34537

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//P20931

50 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.50E-129//260aa//92%//P52623

C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

55 C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.50E-276//1561bp//90%//M61764

C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989

C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687  
 C-MAMMA1001735/TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653  
 5 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa//36%//P21573  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//1987bp//99%//AF112204  
 10 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%//Q58556  
 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 15 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230  
 C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664  
 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880  
 20 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667  
 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.80E-217//310aa//86%//PP70541  
 25 C-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.00E-190//1624bp//76%//AF068748  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//AJ011679  
 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//AF190795  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108  
 35 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623  
 C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//AF098462  
 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//337aa//31%//P43571  
 C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0//1910bp//99%//AF065214  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640  
 45 C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.50E-16//159aa//37%//Q09931  
 50 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.10E-45//618aa//26%//P27550  
 55 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//1942bp//85%//AF018261  
 C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

2.20E-25//330bp//77%//AF011794

C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%//U58883

C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178

C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590

C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//85%//P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//35%//P48060

C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343

C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851

C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//1533bp//99%//AF077952

C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584

C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//1178bp//86%//AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735

C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062

C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//5.00E-13//592aa//24%//P47179

C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//592bp//97%//AF123052

C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596

C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671

C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190

C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//32%//P34537

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aa//47%//O42643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AJ245820

C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//U81002

C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882

C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//3012bp//99%//AB016789

C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028

C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds.//0//2766bp//99%//AF055995

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.7/0//1599bp//99%//AF152462  
 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775  
 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185//1486bp//81%//AF084928  
 C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700  
 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097  
 C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731  
 15 C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395  
 C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372  
 C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775  
 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636  
 C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440  
 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695  
 C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208  
 C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227//1043bp//99%//AF141310  
 30 C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202  
 C-NT2RM1000772//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808  
 C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%//Z97207  
 C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208  
 35 C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395  
 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8  
 C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157  
 C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0//2206bp//99%//AF077033  
 40 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.40E-244//1113bp//99%//AF043733  
 C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%//AF126799  
 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516  
 C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537  
 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700  
 50 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583  
 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa//26%//P46577  
 C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2230bp//99%//AF030233  
 55 C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.60E-13//119aa//36%//Q09701  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

Q99383

C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%//P08487

5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481

C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%//P54197

10 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%//P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703

15 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.30E-36//160aa//40%//P50102

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%//P14918

20 C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%//O48660

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251

25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.70E-68//419aa//36%//P50849

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.60E-54//344aa//33 %//P32802

30 C-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//9.70E-201//826bp//84%//AF030430

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%//Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%//P36113

35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%//P22211

C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%//P41823

C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304

C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243

40 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%//P17437

C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108

C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-187//741aa//46%//P73505

45 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%//P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%//AF179221

50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620

C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170

55 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.70E-142//285aa//90%//P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa//36%//Q15404

C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141



C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%//P28160  
 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.70E-53//266aa//43%//  
 P41877  
 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa//  
 98%//P23514  
 C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%//  
 AB015046  
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%//Q60809  
 C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%//AF100757  
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//  
 26%//P46577  
 C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//  
 AF053091  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%//P05143  
 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//  
 177aa//32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 DOHYDROLASE).//1.30E-180//328aa//99%//P13264  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%//  
 P53995  
 C-NT2RM2001324//ZYXIN.//6.80E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%//Q00808  
 C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%//AJ007509  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121//  
 437aa//57%//P52569  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//  
 90aa//42%//P38660  
 C-NT2RM2001575//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 4.30E-61//312aa//44%//P19474  
 C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%//AF032667  
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440  
 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%//AF084458  
 C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844  
 C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-  
 TEIN OF 121 KD) (P145).//1.20E-142//566aa//56%//P52591  
 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%//AF084458  
 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%//  
 AF111162  
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%//P20107  
 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0//  
 2471bp//99%//AF044195  
 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in  
 intron 11, complete cds.//6.20E-16//464bp//62%//AFQ83391  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0//  
 1843bp//94%//U21155  
 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//  
 30%//Q09674  
 C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253//  
 1170bp//99%//AB028600  
 C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD)  
 (FRAGMENT).//5.70E-130//536aa//49%//P50544  
 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//  
 0//1774bp//98%//AB032251  
 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

ZYME).//7.20E-16//381aa//27%//Q09931

C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792

C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609

C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458

C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742

C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422

C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799

C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195

C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa//39%//P32657

C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759

C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010

C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692

C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818

C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182

C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320

C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250

C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838

C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L//3.10E-12//206aa//30%//Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796

C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789

C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990

C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//AF053091

C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%//P49695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805

C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928

C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167

C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146

C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003

C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742

C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//1.20E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21//785bp//60%//X67336  
 C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//1946bp//99%//AJ271784  
 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//686aa//23%//P25386  
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%//P16381  
 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%//Q16600  
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962  
 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%//L20303  
 C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%//AF030430  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%//M99438  
 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%//Q24371  
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%//P35292  
 C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%//AF195418  
 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769  
 C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271//2085bp//77%//AF062476  
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%//Q10297  
 25 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%//P04280  
 C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//29%//P39955  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.10E-11//394aa//24%//P16884  
 30 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%//Q07230  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%//P26337  
 35 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%//Q00808  
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%//P27550  
 C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%//P51178  
 40 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747/1.20E-28//180aa//30%//P74168  
 C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136//1104bp//77%//AF022789  
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154  
 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%//AF221712  
 45 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.//0//2184bp//99%//D88208  
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%//Q99676  
 C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%//AF084521  
 50 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%//Q05481  
 55 C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%//Q06138  
 C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%//AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%//Q09820

- C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%/P38682  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II./5.90E-86//292aa//48%/Q09417  
 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D./1.00E-11//103aa//38%/Q01704  
 5 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN./4.10E-197//445aa//78%/Q27969  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1./1.10E-48//218aa//43%/Q03532  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135./9.50E-135//375aa//60%/P52742  
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds./0//2310bp//99%/AF004828  
 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds./3.10E-148//1445bp//72%/U65079  
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds./4.30E-55//289bp//77%/AF129131  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)./3.50E-35//124aa//65%/P54676  
 15 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD)./2.30E-31//334aa//30%/P08503  
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds./1.80E-39//728bp//64%/D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)./1.00E-28//171aa//37%/P32626  
 20 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION./8.10E-30//265aa//33%/P53742  
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds./0//2300bp//99%/AF155103  
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds./0//2524bp//99%/AB019494  
 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds./2.20E-237//1079bp//99%/AF098799  
 25 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds./0//1962bp//87%/AF020526  
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds./0//1918bp//99%/AF047711  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)./1.40E-118//444aa//46%/P73505  
 30 C-NT2RM4001483//ZINC FINGER PROTEIN 136./5.10E-106//357aa//55%/P52737  
 C-NT2RM4001566//NECDIN./9.80E-44//227aa//41%/P25233  
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds./1.50E-284//1082bp//90%/AF071317  
 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION./7.60E-56//213aa//49%/P31380  
 C-NT2RM4001597//M.musculus red-1 gene./12.10E-171//1414bp//78%/X92750  
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)J/2.60E-32//203aa//39%/Q12600  
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)./1.50E-93//278aa//38%/Q13368  
 40 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION./2.70E-84//410aa//42%/P37339  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT)./8.90E-141//354aa//72%/Q14141  
 C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds./0//1922bp//100%/AF179221  
 45 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.)./4.10E-186//639aa//58%/Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1)./7.90E-66//311aa//35%/Q03164  
 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1)./5.10E-07//263aa//30%/P16112  
 50 C-NT2RM4001813//LECTIN BRA-2./0.00000048//114aa//30%/P17346  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds./8.10E-300//1395bp//98%/M37712  
 55 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)/7.2.90E-55//325aa//37%/P28160  
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)./5.90E-161//481aa//56%/P51523  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT)./6.50E-22//126aa//46%/P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%//Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%//Q15404

5 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486

C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851

C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330

10 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%//P51523

C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170

C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935

15 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260

C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419

C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%//U82267

20 C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71 %//AF117755

C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//AF072758

25 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652

C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%//AF176085

C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014

30 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940

C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535

C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590

C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640

35 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430

C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%//Q07803

C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%//AF157028

40 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809

C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778

45 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%//P27095

C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%//AF129131

C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515

50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137

C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%//AF055899

55 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962

C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).//  
 2.30E-101//488aa//45%//O32038  
 C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385  
 C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449  
 5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//  
 AF193608  
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834  
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471  
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859  
 10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//  
 951bp//98%//AF011792  
 C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357  
 C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//  
 1155bp//87%//AB015895  
 15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
 plete cds.//1.30E-275//1249bp//99%//AF053551  
 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447  
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343  
 C-NT2RP1000363//R.norvegicus LL5 mRNA7//7.90E-262//1175bp//83%//X74226  
 20 C-NT2RP1000376//Homo sapiens Ca<sup>2+</sup>-independent phospholipase A2 long isoform (iPLA2) mRNA, complete  
 cds.//0//2252bp//96%//AF102989  
 C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%//  
 P55161  
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-  
 25 94//1019bp//63%//AF111423  
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-  
 CRYSTALLIN).//2.40E-10//227aa//25%//Q08257  
 C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624  
 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//  
 30 254aa//47%//P34580  
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653  
 C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%//  
 AF039688  
 C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM  
 35 GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194  
 C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101  
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//8.20E-83//345aa//47%//Q61068  
 40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-  
 27//193aa//35%//P49020  
 C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%//  
 P97367  
 C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233  
 45 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
 PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
 1687bp//99%//AF145020  
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379  
 50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
 cds.//0//2186bp//99%//AF101434  
 C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//  
 99%//AF173378  
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 55 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566  
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN  
 ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960  
 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase AI (PDE9A) mRNA, complete cds.//0//1494bp//99%//

AF067223

C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%//L01790

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291

C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//284aa//25%//P40074

C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917

C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//100%//AJ005257

C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//O35566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//271aa//89%//P47758

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//79aa//55%//O34136  
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-177//726aa//47%//P51523  
 5 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//1.80E-22//184aa//34%//Q01730  
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749  
 10 C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//2245bp//99%//AF155109  
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON).//9.40E-16//45aa//100%//P49446  
 C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418  
 15 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51//383aa//32%//P33450  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//AJ242730  
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356  
 20 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//P41877  
 C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//AF175966  
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585  
 25 C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891  
 C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329  
 C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632  
 30 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675  
 C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//99%//AF153605  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568  
 35 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//7.10E-12//213aa//23%//P35251  
 40 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//1043bp//99%//U78723  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.60E-27//576aa//25%//Q10297  
 45 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676  
 C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//1193bp//99%//U82381  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760  
 50 C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//99%//U83981  
 C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265  
 55 C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844  
 C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238  
 C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955



C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.30E-27//349aa//32%//Q01577  
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%//O32038  
 5 C-NT2RP2000764//NIFS PROTEIN.//6.60E-36//252aa//42%//P12623  
 C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195  
 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//5-.60E-08//179aa//29%//Q99104  
 10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//1.10E-07//96aa//29%//P13466  
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//7.90E-08//172aa//28%//P26174  
 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811  
 15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%//O60841  
 C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135  
 C-NT2RP2000931//MATRIN 3.//2.40E-289//467aa//95%//P43244  
 C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds.//0//2767bp//99%//AF130464  
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704  
 20 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.80E-46//222aa//45%//Q20939  
 C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.20E-118//430aa//54%//P50232  
 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440  
 C-NT2RP2001168//VERPROLIN.//1.50E-09//143aa//33%//P37370  
 25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLGCF46.1 (FRAGMENT).//6.00E-10//88aa//38%//P18722  
 C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481  
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.20E-10//366aa//28%//P14105  
 30 C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.40E-91//179aa//99%//P28663  
 C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.30E-39//161aa//34%//P20107  
 C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//5.50E-116//311aa//71%//Q13829  
 35 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.00E-11//403aa//25%//Q02817  
 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.40E-192//581aa//54%//P93647  
 C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004  
 40 C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds.//1.9e-316//1428bp//100%//AB020981  
 C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//9.00E-112//742bp//82%//U76759  
 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334  
 C-NT2RP2001460//TRICHOHYAUN.//1.00E-14//521aa//24%//P37709  
 C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//3.20E-297//2206bp//75%//AF093097  
 45 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494  
 C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2326bp//99%//AF035586  
 C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992  
 50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.20E-29//294aa//31%//Q09837  
 C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE.//0.000000036//127aa//36%//P30957  
 C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1748bp//99%//AF196304  
 55 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391  
 C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067  
 C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

NA, complete cds.//0//1287bp//99%//AF058718

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897

C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//79%//P14324

C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009

C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754

C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008

C-NT2RP2001883//Homo sapiens CGI-01- protein mRNA, complete cds.//0//2306bp//99%//AF132936

C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161

C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946

C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177//1538bp//74%//AF062378

C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%//AF090989

C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%//Q08469

C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%//P35331

C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0//1664bp//99%//AJ130894

C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0//2510bp//99%//AF083217

C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490

C-NT2RP2002079//HISTONE HI, GONADAL.//4.40E-11//214aa//34%//P02256

C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//33 89bp//99%//AJ007509

C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634

C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107

C-NT2RP2002185//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%//AF176069

C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.//0//2809bp//99%//AB021868

C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0//3118bp//91%//L38621

C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418

C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568

C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521

C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp//99%//AB015594

C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240//1105bp//99%//AF038958

C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp//93%//AJ242972

C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037

C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289

C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%//Q02386

C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.//3.70E-34//668bp//61%//AF105427

C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa//26%//Q11073  
 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523  
 5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%//P12815  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076  
 10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%//P55345  
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa//30%//O14345  
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%//P55194  
 15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%//P29764  
 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922  
 20 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%//AF038392  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%//Q18964  
 C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%//P52737  
 25 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%//P51669  
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%//P10129  
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190  
 30 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%//Q13829  
 C-NT2RP2003121//Mus musculus enhancer of polycbmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%//AF079765  
 35 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%//Q04652  
 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117  
 C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%//Q08170  
 40 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%//D67025  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
 C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%//AF006264  
 C-NT2RP2003228//H.sapiens PI-Cdc21 mRNA.//0//2870bp//98%//X74794  
 45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657  
 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978  
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811  
 50 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%//P30771  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%//Q23400  
 55 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%//Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%//P17886

C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.60E-14//332aa//32%//P26337

C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754

5 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769

C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386

C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-

10 ZYME 1).//9.60E-78//346aa//43%//Q61068

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5.00E-131//269aa//91%//P38378

C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2194bp//99%//AF126799

15 C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//3012bp//99%//AF125158

C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.40E-14//106aa//46%//P04175

C-NT2RP2003513//Homo sapiens mRNA for paralemmin.//0//2137bp//97%//Y14770

20 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783

C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158

C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.70E-17//148aa//34%//P74261

25 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//2.10E-59//270aa//46%//P19474

C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds.//4.80E-82//530bp//85%//AF130367

30 C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2442bp//99%//AF030233

C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215

C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete

35 cds.//2.1e-313//978bp//99%//AF098786

C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637

C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.//0//2018bp//99%//AF073344

40 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.40E-29//85aa//72%//Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.70E-75//147aa//93%//P51669

C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620

45 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201

C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.70E-21//137aa//43%//Q11076

50 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955

C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.//0//2807bp//99%//AF205601

C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954

55 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.50E-23//200aa//30%//O09175

C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//1.40E-16//664aa//20%//

P39702

C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//  
2.30E-53//141aa//78%/P20290

C-NT2RP2004041//SYNAPSINS IA AND B.//0.00000074//159aa//32%/P17599

C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288//  
1994bp//81%/AF156529

C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%/Q01513

C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%/Y12781

C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//  
5.60E-31//424aa//28%/Q07231

C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%/AF003998

C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%/AB015982

C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%/AB015718

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
9.90E-12//427aa//26%/P19246

C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//6.40E-117//  
1122bp//72%/AF200357

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%/P32857

C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13.//1.30E-51//505aa//  
29%/Q07878

C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.30E-15//  
126aa//39%/P38120

C-NT2RP2004392//MNN4 PROTEIN7//1.40E-11//143aa//27%/P36044

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//  
99%/AB028069

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%/AF155739

C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%/AF180920

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%/AF090190

C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%/Q09903

C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
7.30E-07//352aa//23%/P07197

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%/AJ006291

C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
2.60E-07//426aa//23%/P19246

C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.60E-64//616aa//  
33%/Q92355

C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%/U40750

C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
7.30E-07//352aa//23%/P07197

C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-  
26//190aa//41%/P38692

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA  
LIGASE) (LEURS).//9.50E-73//153aa//59%/Q10490

C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.70E-135//414aa//62%/P53588

C-NT2RP2004816//H58 PROTEIN.//9.00E-173//327aa//98%/P40336

C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//  
22%/Q61687

C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%/AB007144

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%/P13692

C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-

228//1666bp//75%//U56732

C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386

C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//1.80E-99//376aa//43%//P19474

5 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779

C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447

C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4.00E-91//218aa//44%//Q92089

10 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//2.00E-173//273aa//57%//P34466

C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743

15 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921

C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%//AF045583

C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050

C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509

20 C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0//1262bp//99%//AF090385

C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025

C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053

25 C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%//AF060219

C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//780bp//100%//AF036144

C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//99%//AF124735

30 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709

C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%//P32660

C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247

35 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SENP1) mRNA, complete cds.//1.30E-52//753bp//67%//AF149770

C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823

C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059

40 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.20E-13//185aa//38%//Q08170

C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%//AF113540

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-13 0//608bp//99%//AF070652

45 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127

C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032

C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.//1.80E-175//1102bp//83%//AF053628

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418

50 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.20E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803

55 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563

C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.40E-304//1687bp//85%//AF035526

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171

C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (AL-DOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2.00E-20//181aa//36%//Q39366

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%//AF062529

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%//O32053

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//74aa//45%//P56101

C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.60E-248//1129bp//99%//AF043733

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%//AF089814

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158

C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//0//2681 bp//99%//AF132022

C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444

C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//2545bp//99%//AB011414

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09//169aa//28%//P38074

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%//P47943

C-NT2RP2005767//G.gallus PB1 gene.//5.00E-163//1158bp//81%//X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.70E-180//656bp//99%//AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%//Q02038

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%//P51005

C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//0//2191bp//92%//AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39//318aa//31%//P40004

C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%//P34223

C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%//AB039669

C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%//P48837

C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500

C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%//Q08170

C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%//AF169797

C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.10E-214//1026bp//97%//X96484

C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1669bp//88%//U49055

C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//388aa//32%//P46821

C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%//AF035262

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

- 3.40E-07//50aa//50%//Q61658  
 C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.//1.30E-37//484bp//65%//AF055636
- 5 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266  
 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131  
 C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966
- 10 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%//P24461  
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543  
 C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538
- 15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973  
 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559  
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755  
 C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%//Q05481
- 20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1 ).//2.20E-06//165aa//27%//Q62245  
 C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//P46401
- 25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692  
 C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640  
 C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652  
 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
- 30 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%//D29766  
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978  
 C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
- 35 C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622  
 C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334  
 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
- 40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293  
 C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%//AF061817
- 45 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.70E-139//679aa//41%//O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185  
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//319aa//26%//P37908
- 50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066  
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667  
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160  
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%//P15151
- 55 C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%//AF093097  
 C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843



C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%/P33288  
 C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%/Q07283  
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%/Q13562  
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%/AB012265  
 5 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//5.80E-234//1562bp//81%/AJ251245  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%/P51523  
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%/Q10149  
 10 C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%/P10895  
 C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.00E-10//565aa//24%/P12036  
 15 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%/Q94650  
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%/Q61982  
 C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0//2522bp//99%/AB032470  
 20 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%/P27448  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%/U53445  
 C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138//1673bp//67%/AF227209  
 25 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%/Q03426  
 C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%/P40848  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.70E-185//585bp//88%/AF015264  
 30 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%/P39027  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159  
 C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.80E-38//462bp//70%/AF225902  
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%/Q05481  
 35 C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.10E-47//537bp//74%/AF060219  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%/AF087433  
 40 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.00E-44//260aa//40%/P55201  
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%/AF097725  
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%/P25386  
 45 C-NT2RP3001120//ZINC FINGER, PROTEIN 136.//7.80E-170//512aa//58%/P52737  
 C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%/P35446  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%/P52154  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.70E-10//196aa//27%/P53154  
 50 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%/P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%/P80193  
 55 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%/P14873  
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%/P32380

C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.30E-99//669bp//83 %//Y18101

5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508

C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089

10 C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%//AF133913

C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0//1214bp//99%//AJ243467

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

15 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529

C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG.//2.70E-10//159aa//33%//O09053

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P12270

C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371

20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%//AF205831

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801

25 C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-290//793bp//93%//U63420

C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//345aa//42%//P20964

C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%//Q10022

30 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821

C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0//1730bp//85%//AF163665

C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//2617bp//99%//U35832

35 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609

C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.80E-09//132aa//31%//O22468

C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449

C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0//2836bp//99%//AF149046

40 C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0//2495bp//99%//AB023584

C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1869bp//99%//AF173868

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386

45 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356

C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534

C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%//AF193613

50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177

C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554

C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141

55 C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.40E-15//190aa//32%//Q09701

C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.80E-117//462aa//55%//P52272

C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.60E-11//348aa//27%//P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652  
 C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.//0//2742bp//99%//AF155135  
 5 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347  
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808  
 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.//0//1587bp//100%//AB000624  
 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.//4.30E-91//656bp//81%//AF177478  
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458  
 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//3.10E-92//314aa//51%//Q09251  
 15 C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23%//P37709  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//X86779  
 C-NT2RP3002007//SAP1 PROTEIN.//1.1 OE-68//474aa//32%//P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232  
 20 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT.//1.00E-299//397aa//94%//P18484  
 C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374  
 C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3764bp//99%//AF095195  
 25 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//4.10E-233//1896bp//69%//AF111423  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170  
 30 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.90E-151//223aa//91%//Q02614  
 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978  
 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767  
 35 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396  
 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991  
 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792  
 C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45.//8.90E-95//542aa//38%//P38932  
 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010  
 45 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598  
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660  
 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//1703bp//99%//AF111109  
 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%//AF165163  
 C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//97%//AF103731  
 55 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060  
 C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-93//1205bp//69%//D17577  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//

41%//P17564

C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371

C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125

C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//P51026

C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430

C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%//AF053091

C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%//Q13625

C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%//Q04652

C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%//AF152498

C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053

C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333

C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%//AF080158

C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555

C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%//U78090

C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357

C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%//AB027149

C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%//D88315

C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%//AB011414

C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//AF071592

C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF077738

C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455

C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%//P52742

C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//31%//Q09674

C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%//AF110267

C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286

C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656

C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//AF098462

C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366aa//48%//P19474

C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%//L36983

C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%//AB033922

C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%//O64948

C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%//AF117657

C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.30E-35//178aa//44%//Q62191

C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084

C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%//U09874

- C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
- 5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%//AB019435
- C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
- C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
- 10 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
- C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
- C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 15 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
- C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
- C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
- C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
- 20 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
- C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
- C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
- 25 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
- C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- 30 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
- C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181
- C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- 35 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
- C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
- C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
- 40 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
- C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
- C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
- 45 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
- C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
- C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
- C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
- 50 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
- C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%//AF065391
- 55 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%//AF088982
- C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871
- C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

X67877

C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.90E-38//462bp//70%//AF225902

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798

5 C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839

C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//42%//P34110

10 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%//AB012851

C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%//U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484

15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%//L11316

C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%//Q15642

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523

20 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%//Q01484

C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0//1853bp//99%//AF040701

C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922

25 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097

30 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%//P54352

C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375

35 C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%//AJ012449

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568

C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%//AF176667

40 C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%//U35776

C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579

C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%//P15287

45 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE.2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.50E-297//1024aa//55%//P87115

50 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.50E-26//237aa//28%//Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%//P26372

55 C-NT2RP4000367//Homo sapiens I kappa B kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%//O75570

- C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738  
 C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//AF221546
- 5 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701  
 C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp//99%//AF083106  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.50E-37//291aa//38%//P50101
- 10 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.90E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484  
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818  
 C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962  
 C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//99%//AF067730
- 20 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//30%//P39625  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa//27%//Q11073
- 25 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267  
 C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00000032//67aa//31%//P53915
- 30 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265  
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175
- 35 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314  
 C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//D45913
- 40 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//227aa//36%//Q06828  
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.50E-76//346aa//43%//Q61068
- 45 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505.//1.40E-07//185aa//25%//Q58900  
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//90aa//42%//P38660
- 50 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//100%//AF094583  
 C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579  
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
- 55 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.70E-16//401aa//26%//P39968  
 C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//3.50E-257//1377bp//91%//U67140  
 C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

AF198487

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%//Q09996

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65//6.70E-51//335aa//37%//Q64375

5 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2<sup>+</sup>-ATPASE)//1.30E-123//563aa//46%//P13586

C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967

C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//2.30E-07//474aa//22%//P12036

10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1)//2.60E-17//121aa//36%//P51400

C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.90E-115//224aa//100%//P38378

C-NT2RP4001122//mPD PROTEIN//1.40E-65//253aa//741%//O15736

15 C-NT2RP4001126//TRICHOHYALIN//2.90E-18//380aa//26%//Q07283

C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP)//2.10E-07//93aa//33%//P44514

C-NT2RP4001148//SOF1 PROTEIN//1.30E-104//236aa//52%//P33750

20 C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//4.40E-187//731bp//100%//AF037339

C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//3.40E-29//385aa//29%//P35331

C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//4.70E-29//227aa//35%//P52178

25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%//U95760

C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.70E-141//511aa//43%//Q99676

30 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.20E-27//90aa//42%//P38660

C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//1.80E-103//508aa//43%//Q04652

C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene)//0//2006bp//100%//AJ249677

35 C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601

C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082

C-NT2RP4001276//TRICHOHYALIN//7.90E-09//126aa//32%//Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//5.90E-17//296aa//29%//P24391

40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5//8.50E-213//1129bp//92%//AJ001119

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%//O24076

C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein//9.20E-160//736bp//99%//AJ007014

45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%//AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445

50 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.60E-19//222aa//30%//Q08180

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1)//9.20E-17//146aa//35%//P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I//2.00E-53//436aa//30%//Q10085

55 C-NT2RP4001389//KESIPROTEIN//1.70E-31//342aa//34%//P35844

C-NT2RP4001407//TRICHOHYALIN//1.90E-05//298aa//21%//P22793

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//7.70E-190//422aa//82%//Q14141

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.20E-138//419aa//54%//Q99676



C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds//2.70E-66//738bp//71%//  
 AF129131  
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (AL-  
 PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218  
 5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1.00E-27//374aa//29%//P39010  
 C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//  
 AF198487  
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.70E-  
 54//242aa//38%//P25656  
 10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//3202bp//99%//AF152961  
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.70E-09//216aa//24%//P96902  
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//5.40E-07//213aa//26%//Q02453  
 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.80E-10//109aa//36%//P35197  
 15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//874aa//  
 96%//P53620  
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830  
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//  
 1.70E-141//373aa//47%//P73505  
 20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.80E-14//652aa//22%//Q02224  
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.10E-46//234aa//32%//  
 P40469  
 C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.40E--19//111aa//45%//P25323  
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//  
 25 P12868  
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF  
 100 KD SUBUNIT).//4.00E-10//243aa//25%//Q10568  
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3.00E-10//128aa//32%//  
 Q10282  
 30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//6.40E-170//1168aa//33%//Q09332  
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.90E-236//665aa//58%//  
 P51523  
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 CIOGENITAL DYSPLASIA PROTEIN).//4.10E-16//263aa//27%//P98174  
 35 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds.//  
 0//3053bp//99%//AF170025  
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//241aa//30%//O35566  
 40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.10E-19//77aa//54%//P55083  
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.30E-99//555bp//73%//  
 AF155595  
 C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194  
 C-NT2RP4001861//HTUCHOHYALIN.//1.00E-35//307aa//34%//P37709  
 45 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.40E-08//345aa//25%//Q00808  
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.30E-38//258aa//32%//Q12024  
 C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.80E-60//303aa//38%//P49711  
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-  
 ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-  
 50 ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.50E-13//211aa//28%//Q43209  
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.20E-13//356aa//27%//P13816  
 C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3203bp//87%//AF195418  
 C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//0//3024bp//99%//  
 AF236056  
 55 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.90E-24//370aa//27%//Q04652  
 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//O67618  
 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//  
 1.00E-137//679aa//40%//O43143

- C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa//39%//Q05481
- C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIAL).//6.70E-06//250aa//31%//P52655
- 5 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938
- C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270
- C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552
- C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808
- 10 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565
- C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0//2289bp//99%//AF095448
- C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116
- 15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290
- C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262
- C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//O14727
- 20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.60E-295//1393bp//97%//AF058922
- C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45 %//P80022
- C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957
- 25 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
- C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874
- C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610
- C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455
- 30 C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107
- C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.50E-95//461bp//98%//AJ242975
- 35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332
- C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665
- C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904
- 40 C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249
- C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363
- C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614
- 45 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004
- C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205
- C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075
- 50 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452
- C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671
- C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850
- C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349
- 55 C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0e-310//1440bp//98%//AF121855
- C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-

plete cds.//0//1812bp//98%//D43772

C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888

C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.10E-209//293aa//95%//P39098

5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0//759bp//98%//AF038661

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159

C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%//P49596

10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886

C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//O35501

C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711

C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199

15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584

C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963

C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484

C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%//AF132608

20 C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398

C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabbp//49%//P32943

C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549

25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343

C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978

C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566

30 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490

C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946

C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%//AF082657

35 C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//2.00E-214//769bp//97%//AJ005897

C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//98%//AF167572

C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//AF051782

40 C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp//93%//AF055008

C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//436bp//92%//U94855

45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510

C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192

C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568

C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//X62083

50 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444

C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058

55 C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%//AF034801

C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp//99%//AJ224819

C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

mRNA, complete cds.//0//1715bp//99%//AF135802

C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426

C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111

C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%//AB017616

C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//AF016507

C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161

C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081

C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//AF031165

C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0//1870bp//99%//AF068302

C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp//61%//AF133670

C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//38%//Q62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106

C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796

C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%//P08942

C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945

C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//0//963bp//99%//U97670

C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.70E-190//1624bp//76%//AF068748

C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945

C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859

C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//0//1083bp//99%//AF203687

C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%//AB029290

C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//Q35913

C-OVARC1002138//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955

C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851

C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213

C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%//Q91854

C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602

C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70%//P34547

C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154

C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538

C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127

C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.80E-62//158aa//81%//P20290

C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//134aa//43%//P52046

C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291  
 C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910  
 C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640  
 5 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246  
 10 C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%//P53368  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245  
 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421  
 15 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455  
 20 C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449  
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201  
 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891  
 25 C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%//AF180371  
 C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896  
 C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043  
 30 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449  
 C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952  
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734  
 35 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070  
 40 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742  
 C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278//1476bp//92%//AF110195  
 C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301  
 45 C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
 C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323  
 50 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742  
 C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496  
 C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202//1333bp//80%//D14336  
 55 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652  
 C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds.//6.20E-223//1092bp//78%//AF120207  
 C-PLACE1001304//Homo sapiens C2H2 (Krueppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

99%//AF159567

C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615

C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-UIEM).//3.00E-33//138aa//42%//Q61103

C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//132aa//46%//Q12929

C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137

C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809

C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//P51523

C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408

C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635

C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381

C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243

C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276

C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290

C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953

C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159

C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524

C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935

C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908

C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091

C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211

C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.30E-07//188aa//29%//P49606

C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//O76094

C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679

C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591

C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505

C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533

C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233

C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105

C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274

C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262

C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273

C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//U50927

C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396

C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890

C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//P39087

C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146

C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.50E-17//76aa//56%//P45340

C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046

C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180

C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//9.40E-13//500aa//21%//Q99323

5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%//Q15391

C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201

C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%//U50927

10 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973

C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522

C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//0//1654bp//99%//AB028600

15 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091

C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387

C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTIN) (R48321).//1.70E-05//150aa//24%//Q13563

20 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743

C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds.//1.70E-148//687bp//99%//AF182003

25 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//Q15391

C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%//P51522

30 C-PLACE10033537//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715

C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403

C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//AF152463

35 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556

C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475

40 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE- ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO- NENT).//7.70E-68//404aa//33%//P32802

C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975

45 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200

C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//Q02516

C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-169//683bp//99%//AF191338

50 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824

C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793

C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8.00E-19//209aa//34%//Q08170

C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282//1316bp//98%//AF053305

55 C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742

C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%//AF133423

C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%/P25500

C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//6.70E-113//501aa//46%/P10895

C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.40E-243//584aa//74%/P17812

C-PLACE1003915//PROBABLE ARGINYLYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA UGASE) (ARGRS).//2.40E-108//581aa//40%/Q05506

C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//0//1670bp//99%/AF033120

C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.40E-124//326aa//73%/P80385

C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//0//2384bp//86%/AF032666

C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.10E-181//340aa//96%/P29387

C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds.//3.30E-41//452bp//65%/AF195534

C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ010071

C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.50E-10//208aa//27%/Q62556

C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%/AF069493

C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.//2.00E-93//960bp//76%/AF115778

C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA//0//1144bp//98%/AF129112

C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.70E-36//389aa//31%/O15393

C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/AF084830

C-PLACE1004302//SOF1 PROTEIN.//1.90E-110//325aa//48%/P33750

C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588

C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%/AF100153

C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.20E-39//385aa//33%/Q63448

C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283

C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%/P25823

C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)7/2.90E-56//276aa//41%/P51522

C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%/U90878

C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.40E-227//1037bp//99%/AF040701

C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%/AF132954

C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568

C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.70E-18//264aa//32%/Q13438

C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.40E-42//985bp//59%/X66277

C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.30E-195//982bp//96%/AF035606

C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N- RECOGNIN).//4.40E-35//578aa//27%/O60152

C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.10E-224//790bp//98%/AB022918

C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.90E-32//259aa//32%/P30337

C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%/P10267

C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.70E-65//695aa//29%/Q01631



C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170  
 C-PLACE1004868//MALE STERILITY PROTEIN 27//3.90E-39//261aa//27%//Q08891  
 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 5 SPAC10F6.02C.//9.30E-11//94aa//47%//O42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%//P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%//AF099936  
 C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794  
 10 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa//26%//Q11073  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950  
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652  
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539  
 15 C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577  
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352  
 20 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760  
 C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//O33335  
 25 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251  
 30 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288  
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128  
 35 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.10E-148//321aa//83%//P31350  
 40 C-PLACE10057277//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680  
 C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//1.30E-237//585aa//72%//Q60710  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.50E-79//209aa//53%//P08635  
 45 C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//AF027156  
 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482  
 50 C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069  
 C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120  
 C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//1.10E-264//661bp//99%//AF203687  
 55 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE).//5.40E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)7/1.40E-07//  
 254aa//25%/P38129  
 C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%/AF151852  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%/AJ236876  
 5 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%/X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%/AF039023  
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
 (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//  
 10 236aa//30%/P98110  
 C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%/P38351  
 C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT).//1.70E-169//373aa//88%/P17427  
 15 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.70E-116//496aa//48%/Q09747  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%/P28675  
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-  
 LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//  
 20 4.60E-117//147aa//80%/P21796  
 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%/U76374  
 C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%/AF155112  
 C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//  
 1.30E-18//460aa//24%/Q00547  
 25 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%/AF062085  
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%/P49910  
 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//1.20E-83//313aa//49%/P27550  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%/Q90595  
 30 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%/Q00004  
 C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%/AF137030  
 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//  
 35 2170bp//99%/AF191338  
 C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%/AF093097  
 C-PLACE1006534//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-  
 UDP ACETYL GALACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAM-  
 40 INYLTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%/Q10472  
 C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%/P39922  
 C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
 0//1464bp//99%/U97670  
 C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
 45 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-  
 24//734bp//62%/AB015630  
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC  
 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-13//177aa//33%/Q59263  
 C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//  
 50 6.20E-63//191aa//43%/P13688  
 C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%/P08547  
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
 TOUS NUCLEAR PROTEIN).//2.00E-15//188aa//29%/P35123  
 55 C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-  
 NUCLEASE).//1.90E-08//122aa//36%/P16658  
 C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35%/Q99181  
 C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.70E-48//278aa//41%/

Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30E-86//522aa//36%//P97998

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421

5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542

C-PLACE1007105//Homo sapiens muskellin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489

C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22%//P37709

10 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.50E-216//1068bp//96%//D50495

C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908

15 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.10E-17//1037bp//56%//AF117649

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

20 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007409//WHTTE PROTEIN.//1.10E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487

25 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45%//P08728

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164

30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%//P34537

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506

35 C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa//28%//Q26457

C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535

40 C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602

C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415

45 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//370aa//25%//Q99323

C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%//P38226

50 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272

55 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

- C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179  
 C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//3.00E-25//208aa//37%//Q03326  
 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%//Q09531
- 5 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709  
 C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077  
 C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%//P53620
- 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689  
 C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%//AF078779  
 C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315
- 15 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.7//1.90E-170//780bp//100%//AF036144  
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432  
 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
- 20 C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%//O42184  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527  
 C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275
- 25 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%//P22620  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
- 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2).//5.20E-90//483aa//38%//O02668  
 C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406
- 35 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.30E-269//1225bp//99%//AJ004974  
 C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668  
 C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623
- 40 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
 C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582  
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//30%//P30432  
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814
- 45 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586  
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086  
 C-PLACE1009158//Mus musculus mRNA for death inducer-obliterators-1 (Dio-1).//5.40E-200//1790bp//75%//AJ238332
- 50 C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//1179bp//98%//AF150105  
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675  
 C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//P34110
- 55 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922  
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%//AF107295

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%/Q12067  
 C-PLACE1009398//ZINC FINGER PROTEIN 135./6.20E-97//361aa//51%/P52742  
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I./4.70E-08//165aa//33%/Q09820  
 5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds./1.00E-173//1367bp//77%/AF176523  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA)./7.80E-71//82aa//89%/P42356  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)./3.10E-289//550aa//93%/P54319  
 10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III./3.90E-40//179aa//37%/P34580  
 C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds./6.60E-147//592bp//99%/AF043117  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)/7.8.10E-99//228aa//75%/Q99418  
 15 C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds./5.90E-185//857bp//99%/AF078857  
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1./5.10E-54//291aa//40%/Q00808  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN./1.30E-60//209aa//41%/P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)./1.50E-285//538aa//99%/P55161  
 20 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds./0//1854bp//100%/AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I./7.00E-33//166aa//43%/Q09876  
 C-PLACE1009721//MSF1 PROTEIN./1.70E-22//176aa//33%/P35200  
 25 C-PLACE1009731//AIG1 PROTEIN./1.60E-22//274aa//28%/P54120  
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds./4.30E-294//1329bp//100%/AB012190  
 C-PLACE1009798//RLR1 PROTEIN./1.60E-18//270aa//23%/P53552  
 C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)./2.30E-59//405aa//33%/P38968  
 30 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-)./6.50E-28//209aa//38%/P43510  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION./1.90E-108//277aa//43%/P53145  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds./0//1730bp//99%/AF038963  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84)./4.60E-59//450aa//34%/P28175  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds./5.20E-70//736bp//73 %//U48288  
 40 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein./6.00E-279//1402bp//94%/X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./0//2019bp//99%/AF065482  
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)./1.40E-268//506aa//98%/Q62671  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)./7.30E-114//537aa//44%/Q04652  
 45 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3)./1.70E-20//156aa//42%/P22082  
 C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I)./4.60E-07//431aa//23%/P35662  
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)./9.80E-11//95aa//49%/Q01130  
 50 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)./5.1 OE-27//371aa//28%/Q14246  
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN./1.60E-77//214aa//62%/P25722  
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)./1.20E-18//467aa//30%/P46804  
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)./1.10E-09//350aa//22%/P52178  
 55 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)./2.00E-09//126aa//29%/P34024  
 C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds./0//2082bp//91%/AF003927

- C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981 bp//99%//AB022718
- C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%//AF191838
- 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aa//24%//P25386
- C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771
- 10 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546
- C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
- C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
- C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
- 15 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
- C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
- C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
- 20 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267
- C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205
- C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
- 25 C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392
- C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
- C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481
- 30 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
- C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
- C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487
- 35 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
- C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
- C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894
- 40 C-PLACE1011056//HISTONE HI, GONADAL.//6.80E-13//154aa//37%//P02256
- C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
- C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
- C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
- 45 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
- C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.20E-12//212aa//29%//Q03326
- C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
- C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
- 50 C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265
- C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
- C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
- 55 C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830
- C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695
- C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
- C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

4.90E-11//147aa//32%//P52178

C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%//L11672

C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.//4.10E-259//1538bp//87%//AF177476

C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377

C-PLACE1011664//CROOKED NECK PROTEIN.//1.60E-187//505aa//64%//P17886

C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%//AF095192

C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969

C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580

C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%//AF059617

C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%//AF121862

C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.60E-42//104aa//49%//Q09475

C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%//P42566

C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%//AF082556

C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586

C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%//P38650

C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347.//6.30E-166//656bp//94%//AB015629

C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219

C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736

C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%//Q01082

C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%//Q04652

C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098

C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0//1554bp//99%//AF069307

C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205

C-PLACE2000373//F-SPONDIN PRECURSOR.//8.60E-16//371aa//28%//P35446

C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//90aa//98%//P10586

C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209

C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996

C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085

C-PLACE2000427//PROBABLE HELICASE MOT1.//1.20E-26//200aa//27%//P32333

C-PLACE2000438//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%//Q10472

C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25//165aa//40%//P33450

C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//6.70E-127//671bp//94%//AF072733

C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAGMENT).//3.50E-30//400aa//30%//P11414

C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.//0//2253bp//99%//AF033861

C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267

C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157.//1.90E-08//281aa//22%//P22224

C-PLACE3000145//TENSIN.//1.00E-108//277aa//75%//Q04205

- C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
- C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
- 5 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020
- C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811
- C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995
- C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
- 10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640
- C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549
- 15 C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290
- C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085
- C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
- 20 C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100
- C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
- C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
- 25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689
- C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabbp//88%//AF091234
- 30 C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481
- C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
- C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
- 35 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
- C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protem.//0//5143bp//90%//Z70200
- C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
- C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667
- C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 40 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754
- C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
- C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
- 45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
- C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)7/5.70E-60//254aa//44%//P13002
- 50 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783
- C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640
- C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
- 55 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//226aa//52%//P10079
- C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//



P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267

C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

5 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800

C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655

10 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663

C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709

C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799

15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710

C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%//U49055

C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%//U97018

20 C-THYRO1000173//Homo sapiens AP-mu chain family member muB (HSMU1B) mRNA, complete cds.//0//1713bp//99%//AF020797

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523

25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068

C-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%//AF124145

C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06//280aa//31%//P54259

30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864

C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857

C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085

35 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474

C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566

40 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//AF075587

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360

45 C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889

C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195

50 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171

C-THYRO1000756//ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686

C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//2.40E-157//1656bp//70%//U37373

55 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-137//689bp//96%//U62739

C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2387bp//99%//AF079529

C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//  
 7.50E-57//315aa//43%/P32322  
 C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//  
 566aa//37%/P43550  
 5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%/P35132  
 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%/P52491  
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%/P31948  
 10 C-THYRO1001100//ZINC FINGER X-UNKEK PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%/P98168  
 C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%/AF053700  
 C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%/AF151835  
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//  
 62%/Q05481  
 15 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS Z) gene, exons 4, 5, and 6 and complete cds; and  
 TH1 gene partial sequence.//3.80E-100//478bp//99%/AF136276  
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-  
 ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%/P45701  
 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%/AF121861  
 20 C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%/AF064729  
 C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN  
 ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%/O00154  
 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%/P30427  
 25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%/O70503  
 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,  
 TYPE B) (NMMHC-B).//2.70E-171//559aa//59%/P35580  
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//  
 99%/AJ002190  
 30 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//  
 82%/AF175968  
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%/AJ225089  
 35 C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa//32%/P45672  
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%/Q04652  
 C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%/P38584  
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%/P42128  
 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%/AF171060  
 40 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%/AF126484  
 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%/P25916  
 C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds.//0//  
 980bp//96%/AF180472  
 45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%/AF132936  
 C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp//  
 100%/AF081192  
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%/AF123534  
 50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%/AF035207  
 C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%/Q02910  
 C-Y79AA1000328//SEL-10 PROTEIN.//0.00000067//219aa//25%/Q93794  
 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%/AB030835  
 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%/AF157833  
 55 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%/X84692  
 C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa//27%/P25343  
 C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete

cds.//8.30E-252//1207bp//85%//U41736

C-Y79AA1000540//CELL POLARITY PROTEIN TEA1.//2.10E-12//211aa//33%//P87061

C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)7/0//652aa//98%//P17427

C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.40E-27//216aa//34%//P28320

C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//2.00E-287//2031bp//82%//AF060503

C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//0//1594bp//99%//AF093670

C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//6.60E-286//1832bp//84%//AF177477

C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.90E-91//200aa//64%//Q61990

C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902

C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//1.10E-236//1076bp//99%//AF098799

C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds.//0//1610bp//99%//AF105369

C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//1.60E-284//1288bp//99%//AF072733

C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5.00E-173//220aa//79%//P05209

C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17//430aa//27%//Q99323

C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757

C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//3.90E-248//1468bp//87%//U38253

C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962

C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953

C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1435bp//99%//AF139658

C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657

C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds.//0//1612bp//99%//AF063015

C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738

C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//Q03309

C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.//3.30E-172//1171bp//83%//D87325

C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%//AF055084

C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271

C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746

C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.//8.50E-65//784bp//62%//AF083115

C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132

C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//4.50E-193//1333bp//80%//D14336

C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356

C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.90E-40//482aa//27%//P27550

C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547

C-Y79AA1001603//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-

AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537  
 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740  
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//  
 227aa//40%//Q01820  
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-  
 47//626bp//68%//AF033120  
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//  
 J04137  
 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//  
 0//1689bp//98%//AF177145  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489  
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//  
 AF174602  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 SPAC10F6.02C.//1.00E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743  
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329  
 C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357  
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-  
 72//437aa//39%//P00952  
 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN).//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//  
 146aa//35%//O16264  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620  
 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384  
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//  
 X67877  
 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//  
 Y18208  
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//  
 86%//U49385  
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725  
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds.//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//  
 49%//Q05481  
 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//  
 51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//  
 1444bp//98%//AF129534

## Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

- 5 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
- 10 3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:
- 15

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

- 5      4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
- 10      6. A substantially pure protein encoded by polynucleotide of claim 4.
7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
- 15            (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following  
SEQ ID NOs:

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SEQ ID NO: 10468, SEQ ID NO: 10470, SEQ ID NO: 10471, SEQ ID NO: 10472, SEQ ID  
NO: 10473, SEQ ID NO: 10475, SEQ ID NO: 10477, SEQ ID NO: 10479, SEQ ID NO: 10481,  
SEQ ID NO: 10483, SEQ ID NO: 10485, SEQ ID NO: 10487, SEQ ID NO: 10488, SEQ ID  
5 NO: 10489, SEQ ID NO: 10491, SEQ ID NO: 10493, SEQ ID NO: 10495, SEQ ID NO: 10496,  
SEQ ID NO: 10497, SEQ ID NO: 10498, SEQ ID NO: 10500, SEQ ID NO: 10502, SEQ ID  
NO: 10503, SEQ ID NO: 10504, SEQ ID NO: 10505, SEQ ID NO: 10507, SEQ ID NO: 10508,  
SEQ ID NO: 10510, SEQ ID NO: 10511, SEQ ID NO: 10512, SEQ ID NO: 10514, SEQ ID  
10 NO: 10516, SEQ ID NO: 10517, SEQ ID NO: 10519, SEQ ID NO: 10521, SEQ ID NO: 10523,  
SEQ ID NO: 10524, SEQ ID NO: 10526, SEQ ID NO: 10528, SEQ ID NO: 10529, SEQ ID  
NO: 10530, SEQ ID NO: 10532, SEQ ID NO: 10534, SEQ ID NO: 10535, SEQ ID NO: 10537,  
SEQ ID NO: 10539, SEQ ID NO: 10540, SEQ ID NO: 10542, SEQ ID NO: 10543, SEQ ID  
NO: 10545, SEQ ID NO: 10546, SEQ ID NO: 10548, SEQ ID NO: 10550, SEQ ID NO: 10551,  
15 SEQ ID NO: 10553, SEQ ID NO: 10555, SEQ ID NO: 10556, SEQ ID NO: 10557, SEQ ID  
NO: 10558, SEQ ID NO: 10560, SEQ ID NO: 10562, SEQ ID NO: 10564, SEQ ID NO: 10566,  
SEQ ID NO: 10567, SEQ ID NO: 10569, SEQ ID NO: 10571, SEQ ID NO: 10573, SEQ ID  
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20 SEQ ID NO: 10584, SEQ ID NO: 10586, SEQ ID NO: 10588, SEQ ID NO: 10590, SEQ ID  
NO: 10592, SEQ ID NO: 10594, SEQ ID NO: 10596, SEQ ID NO: 10597, SEQ ID NO: 10599,  
SEQ ID NO: 10601, SEQ ID NO: 10603, SEQ ID NO: 10604, SEQ ID NO: 10606, SEQ ID  
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NO: 10637, SEQ ID NO: 10639, SEQ ID NO: 10641, SEQ ID NO: 10642, SEQ ID NO: 10644,  
30 SEQ ID NO: 10646, SEQ ID NO: 10647, SEQ ID NO: 10648, SEQ ID NO: 10649, SEQ ID  
NO: 10650, SEQ ID NO: 10652, SEQ ID NO: 10654, SEQ ID NO: 10655, SEQ ID NO: 10656,  
SEQ ID NO: 10658, SEQ ID NO: 10659, SEQ ID NO: 10661, SEQ ID NO: 10663, SEQ ID  
NO: 10665, SEQ ID NO: 10667, SEQ ID NO: 10669, SEQ ID NO: 10670, SEQ ID NO: 10671,  
SEQ ID NO: 10673, SEQ ID NO: 10674, SEQ ID NO: 10676, SEQ ID NO: 10678, SEQ ID  
35 NO: 10680, SEQ ID NO: 10682, SEQ ID NO: 10683, SEQ ID NO: 10685, SEQ ID NO: 10687,  
SEQ ID NO: 10689, SEQ ID NO: 10691, SEQ ID NO: 10693, SEQ ID NO: 10695, SEQ ID  
NO: 10696, SEQ ID NO: 10698, SEQ ID NO: 10700, SEQ ID NO: 10702, SEQ ID NO: 10704,  
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SEQ ID NO: 10754, SEQ ID NO: 10756, SEQ ID NO: 10757, SEQ ID NO: 10758, SEQ ID  
NO: 10760, SEQ ID NO: 10761, SEQ ID NO: 10763, SEQ ID NO: 10765, SEQ ID NO: 10767,  
SEQ ID NO: 10769, SEQ ID NO: 10771, SEQ ID NO: 10773, SEQ ID NO: 10774, SEQ ID  
50 NO: 10776, SEQ ID NO: 10778, SEQ ID NO: 10780, SEQ ID NO: 10781, SEQ ID NO: 10783,





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SEQ ID NO: 18938, SEQ ID NO: 18940, SEQ ID NO: 18941, SEQ ID NO: 18943, SEQ ID  
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SEQ ID NO: 18953, SEQ ID NO: 18955, SEQ ID NO: 18956, SEQ ID NO: 18957, SEQ ID  
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10 SEQ ID NO: 18981, SEQ ID NO: 18982, SEQ ID NO: 18983, SEQ ID NO: 18984, SEQ ID  
NO: 18985, SEQ ID NO: 18986, SEQ ID NO: 18987, SEQ ID NO: 18988, SEQ ID NO: 18989,  
SEQ ID NO: 18990, SEQ ID NO: 18992, SEQ ID NO: 18993, SEQ ID NO: 18995, SEQ ID  
NO: 18997, SEQ ID NO: 18998, SEQ ID NO: 18999, SEQ ID NO: 19000, SEQ ID NO: 19001,  
15 SEQ ID NO: 19002, SEQ ID NO: 19004, SEQ ID NO: 19006  
SEQ ID NO: 19007, SEQ ID NO: 19009, SEQ ID NO: 19011, SEQ ID NO: 19012, SEQ ID  
NO: 19013, SEQ ID NO: 19014, SEQ ID NO: 19016, SEQ ID NO: 19018, SEQ ID NO: 19020,  
SEQ ID NO: 19022, SEQ ID NO: 19024, and SEQ ID NO: 19025

20 (b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence  
set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:10469, SEQ ID NO:10474, SEQ ID NO:10476, SEQ ID NO:10478, SEQ ID  
NO:10480, SEQ ID NO:10482, SEQ ID NO:10484, SEQ ID NO:10486, SEQ ID NO:10490,  
SEQ ID NO:10492, SEQ ID NO:10494, SEQ ID NO:10499, SEQ ID NO:10501, SEQ ID  
NO:10506, SEQ ID NO:10509, SEQ ID NO:10513, SEQ ID NO:10515, SEQ ID NO:10518,  
SEQ ID NO:10520, SEQ ID NO:10522, SEQ ID NO:10525, SEQ ID NO:10527, SEQ ID  
NO:10531, SEQ ID NO:10533, SEQ ID NO:10536, SEQ ID NO:10538, SEQ ID NO:10541,  
SEQ ID NO:10544, SEQ ID NO:10547, SEQ ID NO:10549, SEQ ID NO:10552, SEQ ID  
NO:10554, SEQ ID NO:10559, SEQ ID NO:10561, SEQ ID NO:10563, SEQ ID NO:10565,  
SEQ ID NO:10568, SEQ ID NO:10570, SEQ ID NO:10572, SEQ ID NO:10575, SEQ ID  
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SEQ ID NO:10587, SEQ ID NO:10589, SEQ ID NO:10591, SEQ ID NO:10593, SEQ ID  
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SEQ ID NO:10608, SEQ ID NO:10610, SEQ ID NO:10612, SEQ ID NO:10617, SEQ ID  
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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence  
 selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted,  
 45 inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino  
 acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the  
 nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equiv-  
 50 alent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein  
 encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence  
 of (a).

55 9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

20 19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and

b) recovering the synthesized product.

25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

30 22. A method for detecting the polynucleotide of claim 8, the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and

b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

35 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

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Figure 1

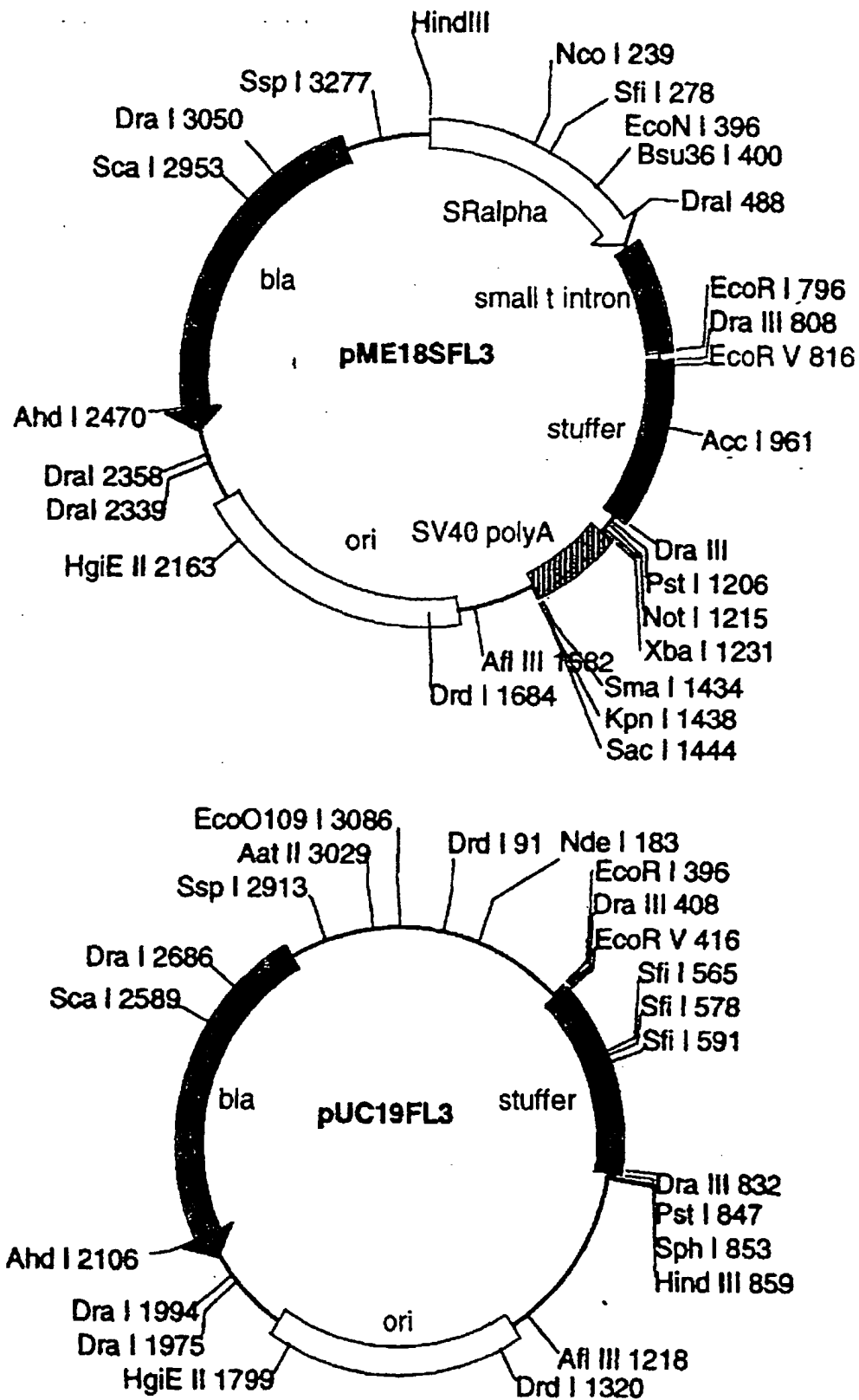


Figure 2

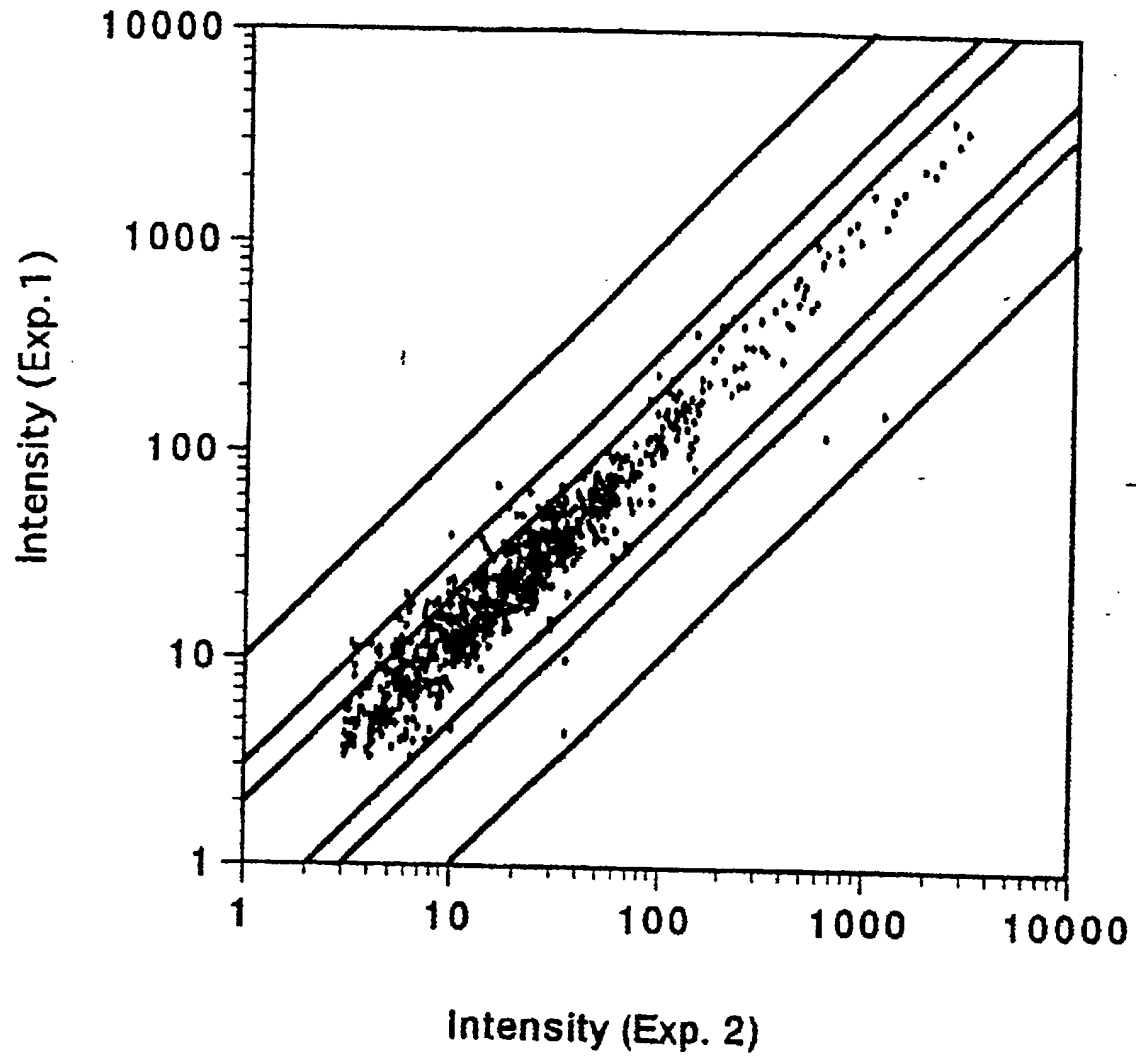
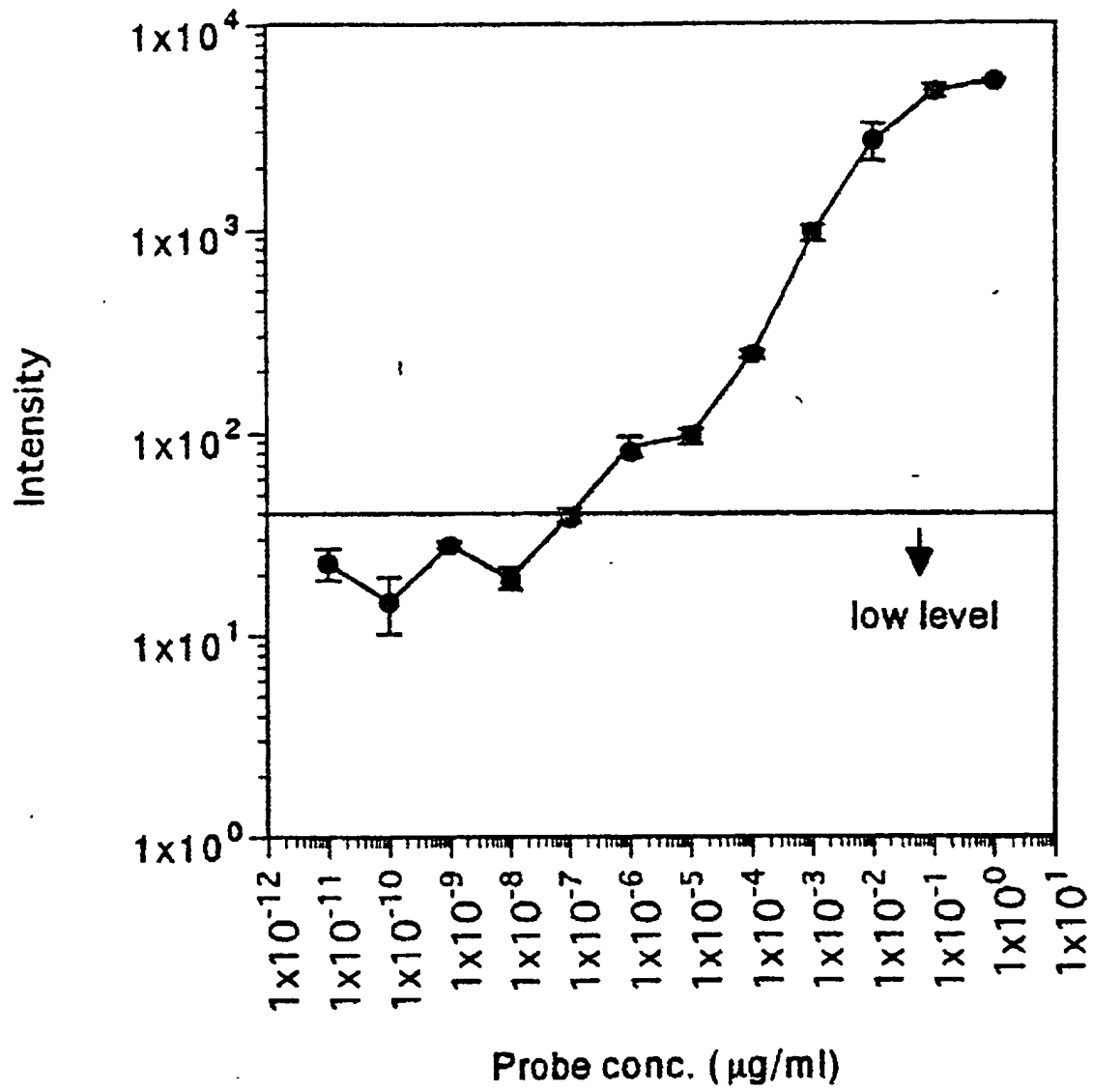




Figure 3



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